SEARCH REQUEST FORM

5-54

Requestor's
Name: _____

Serial
Number: _____

Date: _____   Phone: _____   Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevent citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevent claim(s).

STAFF USE ONLY

Date completed: 5-7-98

Searcher: MARK

Terminal time: 6

Elapsed time: prep 10

CPU time: _____

Total time: 16

Number of Searches: 1

Number of Databases: 11

Search Site

_____ STIC

__✓__ CM-1

_____ Pre-S

Type of Search

__✓__ N.A. Sequence

__✓__ A.A. Sequence

_____ Structure

_____ Bibliographic

Vendors

__✓__ IG MPSRCH

_____ STN

_____ Dialog

_____ APS

_____ Geninfo

_____ SDC

_____ DARC/Questel

_____ Other

MPSRCH (TM)

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*************************************************************
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Distribution rights by Oxford Molecular Ltd
*************************************************************
```

MPsrch.pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 6 08:18:28 1998; MasPar time 3.90 Seconds
     375.094 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-2
Description: (1-256) from US0804166.pep
Perfect Score: 1994
Sequence: 1 SRTSLLIAFGLLCLPWLOBG.........GFKVENHTGCHCSTCYYHKS 256

Scoring table: PAM 150
      Gap 11

Searched: 62627 seqs, 5720858 residues

Post-processing: Minimum Match 0%

Database: a-issued
    Listing first 45 summaries

Statistics: Mean 29.680; Variance 124.309; scale 0.239
    1:back1 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:PCT90
    10:PCT91 11:PCT92 12:PCT93 13:PCT94 14:PCT95 15:PCT96

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1124	56.4	455	7	US-08-321-	Sequence 2, Applicatio	1.28e-100
2	1124	56.4	455	7	US-08-321-	Sequence 25, Applicatio	1.28e-100
3	1115	55.9	199	7	US-08-050-	Sequence 48, Applicatio	1.05e-99
4	996	49.9	167	7	US-08-050-	Sequence 2, Applicatio	1.15e-87
5	996	49.9	167	7	US-08-050-	Sequence 57, Applicati	1.15e-87
6	981	49.2	124	7	US-08-050-	Sequence 4, Applicati	3.70e-86
7	800	40.1	157	7	US-08-050-	Sequence 50, Applicati	6.45e-68
8	666	33.4	158	7	US-08-050-	Sequence 54, Applicati	1.67e-54
9	477	23.9	153	7	US-08-050-	Sequence 52, Applicati	8.82e-36
10	339	17.0	41	7	US-08-050-	Sequence 36, Applicati	2.30e-22
11	324	16.2	40	7	US-08-050-	Sequence 26, Applicati	2.30e-21
12	318	15.9	43	7	US-08-050-	Sequence 31, Applicati	2.36e-20
13	225	11.3	325	5	US-08-292-	Sequence 2, Applicatio	1.31e-11
14	225	11.3	325	5	US-08-292-	Sequence 2, Applicatio	1.31e-11
15	221	11.1	326	5	US-08-292-	Sequence 4, Applicatio	3.06e-11
16	221	11.1	326	10	PCT-US91-0	Sequence 4, Applicatio	3.06e-11
17	212	10.6	474	1	5395760-4	Patent No. 5395760.	2.05e-10
18	210	10.5	355	5	US-08-292-	Sequence 6, Applicatio	3.12e-10
19	183	9.2	283	15	PCT-US96-1	Sequence 2, Applicatio	8.68e-08
20	183	9.2	595	5	US-08-225-	Sequence 2, Applicatio	8.68e-08
21	183	9.2	595	7	US-08-570-	Sequence 2, Applicatio	8.68e-08
22	181	9.1	228	12	PCT-US93-0	Sequence 8, Applicatio	1.31e-07
23	181	9.1	228	13	PCT-US94-0	Sequence 4, Applicatio	1.31e-07
24	181	9.1	228	14	PCT-US95-0	Sequence 4, Applicatio	1.31e-07
25	181	9.1	228	7	US-08-188-	Sequence 8, Applicatio	1.31e-07
26	181	9.1	228	7	US-08-453-	Sequence 8, Applicatio	1.31e-07
27	180	9.0	461	7	US-08-385-	Sequence 2, Applicatio	1.61e-07
28	180	9.0	461	1	5395760-2	Patent No. 5395760.	1.61e-07
29	180	9.0	486	7	US-08-243-	Sequence 1, Applicatio	1.61e-07
30	180	9.0	518	7	US-08-305-	Sequence 4, Applicatio	1.61e-07
31	180	9.0	333	12	PCT-US93-0	Sequence 12, Applicati	1.61e-07
32	169	8.5	333	7	US-08-453-	Sequence 12, Applicati	1.53e-06
33	169	8.5	399	7	US-08-453-	Sequence 10, Applicati	1.53e-06
34	169	8.5	399	12	PCT-US93-0	Sequence 10, Applicati	1.53e-06
35	167	8.4	70	4	US-07-920-	Sequence 24, Applicat	2.30e-06
36	167	8.4	71	6	US-08-314-	Sequence 24, Applicat	2.30e-06
37	167	8.4	93	7	US-08-445-	Sequence 4, Applicatio	2.30e-06
38	165	8.3	93	4	US-08-343-	Sequence 4, Applicatio	3.06e-06
39	165	8.3	186	7	US-08-089-	Sequence 6, Applicatio	3.06e-06
40	160	8.0	177	6	US-08-187-	Sequence 4, Applicatio	9.51e-06
41	160	8.0	198	6	US-08-187-	Sequence 6, Applicatio	9.51e-06
42	160	8.0	217	6	US-08-187-	Sequence 7, Applicatio	9.51e-06
43	156	7.8	206	5	US-08-097-	Sequence 4, Applicatio	2.13e-05
44	156	7.8	438	5	US-08-097-	Sequence 11, Applicati	2.13e-05
45	139	7.0	335	14	PCT-US95-1	Sequence 2, Applicatio	6.25e-04

ALIGNMENTS

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RESULT  1
ID   US-08-321-668-2   STANDARD;   PRT;   455 AA.
AC   xxxxxx
DT   01-JAN-1900
DE   Sequence 2, Application US/08321668.
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```
CC   Sequence 2, Application US/08321668.
CC   Patent No. 5665859
CC   GENERAL INFORMATION:
CC   APPLICANT:  WALLACH, David
CC   APPLICANT:  BRAKEBUSCH, Cord
CC   APPLICANT:  VARFOLOMEEV, Eugene
CC   APPLICANT:  BATKIN, Michael
CC   TITLE OF INVENTION:  MOLECULES INFLUENCING THE SHEDDING OF
CC   TITLE OF INVENTION:  THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
CC   NUMBER OF SEQUENCES:  42
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE:  BROWDY AND NEIMARK
CC   STREET:  419 Seventh Street, N.W., Suite 300
CC   CITY:  Washington
CC   STATE:  D.C.
CC   COUNTRY:  USA
CC   ZIP:  20004
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE:  Floppy disk
CC   COMPUTER:  IBM PC compatible
CC   OPERATING SYSTEM:  PC-DOS/MS-DOS
CC   SOFTWARE:  Patentin Release #1.0, Version #1.30
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER:  US/08/321,668
CC   FILING DATE:  12-OCT-1994
CC   CLASSIFICATION:  435
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER:  IL 107268
CC   FILING DATE:  12-OCT-1993
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME:  BROWDY, Roger L.
CC   REGISTRATION NUMBER:  25,618
CC   REFERENCE/DOCKET NUMBER:  WALLACH-13
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE:  202-628-5197
CC   TELEFAX:  202-737-3528
CC   TELEX:  248633
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CC   INFORMATION FOR SEQ ID NO: 2:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 455 amino acids
CC   TYPE: amino acid
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: protein
SQ   SEQUENCE   455 AA; 50494 MW; 1048031 CN;

Query Match
Best Local Similarity   99.3%; Score 1124; DB 7; Length 455;
                                 Pred. No. 1.28e-100;
Matches 142; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db   41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
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Qy   23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db 101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db 161 KQNTVCTCHAGFFLRENECVSCS 183
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Qy 143 KQNTVCTCHAGFFLRENECVSCA 165

RESULT 2
ID   US-08-050-319B-25   STANDARD;   PRT;   455 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 25, Application US/08050319B.

CC   GENERAL INFORMATION:
CC   Patent No. 5633145
CC   APPLICANT: M.Feldmann, P.W. Gray,
CC   APPLICANT: M.J.C. Turner, F.M Brennan
CC   TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC   TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC   NUMBER OF SEQUENCES: 57
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Reed & Robbins
CC   STREET: 635 Bryant Street
CC   CITY: Palo Alto
CC   STATE: California
CC   COUNTRY: USA
CC   ZIP: 94301
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: Patentin Release #1.0, version #1.25
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/050,319B
CC   FILING DATE: 10-May-1993
CC   CLASSIFICATION: 435
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Robbins, Roberta L.
CC   REGISTRATION NUMBER: 33,208
CC   REFERENCE/DOCKET NUMBER: 5150-0030
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (415) 617-8999
CC   TELEFAX: (415) 327-3231
CC   INFORMATION FOR SEQ ID NO: 25:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 455 amino acids
CC   TYPE: amino acid
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: protein
SQ   SEQUENCE   455 AA; 50579 MW; 1048388 CN;

Query Match
Best Local Similarity   99.3%; Score 1124; DB 7; Length 455;
                                 Pred. No. 1.28e-100;
Matches 142; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db   41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
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Qy   23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db 101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db 161 KQNTVCTCHAGFFLRENECVSCS 183
         ||||||||||||||||||||||:
Qy 143 KQNTVCTCHAGFFLRENECVSCA 165

RESULT 3
ID   US-08-050-319B-48   STANDARD;   PRT;   199 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 48, Application US/08050319B.

CC   GENERAL INFORMATION:
CC   Patent No. 5633145
CC   APPLICANT: M.Feldmann, P.W. Gray,
CC   APPLICANT: M.J.C. Turner, F.M Brennan
CC   TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC   TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC   NUMBER OF SEQUENCES: 57
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Reed & Robbins
CC   STREET: 635 Bryant Street
CC   CITY: Palo Alto
CC   STATE: California
CC   COUNTRY: USA
CC   ZIP: 94301
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: Patentin Release #1.0, version #1.25
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/050,319B
CC   FILING DATE: 10-May-1993
CC   CLASSIFICATION: 435
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Robbins, Roberta L.
CC   REGISTRATION NUMBER: 33,208
CC   REFERENCE/DOCKET NUMBER: 5150-0030
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (415) 617-8999
CC   TELEFAX: (415) 327-3231
CC   INFORMATION FOR SEQ ID NO: 48:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 199 amino acids
CC   TYPE: amino acid
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: protein
SQ   SEQUENCE   199 AA; 22186 MW; 195553 CN;

Query Match
Best Local Similarity   98.6%; Score 1115; DB 7; Length 199;
                                 Pred. No. 1.05e-99;
Matches 141; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db   41 DSVCPTGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
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Qy   23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db 101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
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Qy   83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db 161 KONTVCTCHAGFFLRENECVSCS 183
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Qy 143 KONTVCTCHAGFFLRENECVSCA 165

RESULT 4

ID US-08-050-319B-2   STANDARD;   PRT;   167 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 2, Application US/08050319B.
XX
CC Patent No. 5633145
CC GENERAL INFORMATION:
CC   APPLICANT: M.Feldmann, P.W. Gray,
CC   APPLICANT: M.J.C. Turner, F.M Brennan
CC   TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC   TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC   NUMBER OF SEQUENCES: 57
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Reed & Robbins
CC   STREET: 635 Bryant Street
CC   CITY: Palo Alto
CC   STATE: California
CC   COUNTRY: USA
CC   ZIP: 94301
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: PatentIn Release #1.0, version #1.25
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/050,319B
CC   FILING DATE: 10-May-1993
CC   CLASSIFICATION: 435
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Robbins, Roberta L.
CC   REGISTRATION NUMBER: 33,208
CC   REFERENCE/DOCKET NUMBER: 5150-0030
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (415) 617-8999
CC   TELEFAX: (415) 327-3231
CC INFORMATION FOR SEQ ID NO: 2:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 167 amino acids
CC   TYPE: amino acid
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: protein
SQ SEQUENCE 167 AA; 18626 MW; 139513 CN;

Query Match   49.9%; Score 996; DB 7; Length 167;
Best Local Similarity 100.0%; Pred. No. 1.15e-87;
Matches   127; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db   41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
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Qy   23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db 101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db 161 KONTVCT 167
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Qy 143 KONTVCT 149

RESULT 5

ID US-08-050-319B-57   STANDARD;   PRT;   167 AA.
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AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 57, Application US/08050319B.
XX
CC Patent No. 5633145
CC GENERAL INFORMATION:
CC   APPLICANT: M.Feldmann, P.W. Gray,
CC   APPLICANT: M.J.C. Turner, F.M Brennan
CC   TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC   TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC   NUMBER OF SEQUENCES: 57
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Reed & Robbins
CC   STREET: 635 Bryant Street
CC   CITY: Palo Alto
CC   STATE: California
CC   COUNTRY: USA
CC   ZIP: 94301
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: PatentIn Release #1.0, version #1.25
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/050,319B
CC   FILING DATE: 10-May-1993
CC   CLASSIFICATION: 435
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Robbins, Roberta L.
CC   REGISTRATION NUMBER: 33,208
CC   REFERENCE/DOCKET NUMBER: 5150-0030
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (415) 617-8999
CC   TELEFAX: (415) 327-3231
CC INFORMATION FOR SEQ ID NO: 57:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 167 amino acids
CC   TYPE: amino acid
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: protein
SQ SEQUENCE 167 AA; 18626 MW; 139513 CN;

Query Match   49.9%; Score 996; DB 7; Length 167;
Best Local Similarity 100.0%; Pred. No. 1.15e-87;
Matches   127; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db   41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
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Qy   23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db 101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
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Qy   83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db 161 KONTVCT 167
        |||||||
Qy 143 KONTVCT 149

RESULT 6

ID US-08-050-319B-4   STANDARD;   PRT;   124 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX

DE Sequence 4, Application US/08050319B.
XX
CC Patent No. 5633145
CC GENERAL INFORMATION:
CC APPLICANT: M.Feldmann, P.W. Gray,
CC APPLICANT: M.J.C. Turner, F.M Brennan
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC NUMBER OF SEQUENCES: 57
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Reed & Robbins
CC STREET: 635 Bryant Street
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/050,319B
CC FILING DATE: 10-May-1993
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Robbins, Roberta L.
CC REGISTRATION NUMBER: 33,208
CC REFERENCE/DOCKET NUMBER: 5150-0030
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 617-8999
CC TELEFAX: (415) 327-3231
CC INFORMATION FOR SEQ ID NO: 4:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 124 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
SQ MOLECULE TYPE: protein
SQ SEQUENCE 124 AA; 14047 MW; 75840 CN;

Query Match 49.2%; Score 981; DB 7; Length 124;
Best Local Similarity 100.0%; Pred. No. 3.78e-86;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   25 VCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC 84

Db   61 SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQ 120
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Qy   85 SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQ 144

Db  121 NTVC 124
        ||||
Qy  145 NTVC 148
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RESULT 7
ID US-08-050-319B-50   STANDARD;   PRT;   157 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 50, Application US/08050319B.
XX
CC Patent No. 5633145
CC GENERAL INFORMATION:
CC APPLICANT: M.Feldmann, P.W. Gray,
CC APPLICANT: M.J.C. Turner, F.M Brennan
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor

CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC NUMBER OF SEQUENCES: 57
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Reed & Robbins
CC STREET: 635 Bryant Street
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/050,319B
CC FILING DATE: 10-May-1993
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Robbins, Roberta L.
CC REGISTRATION NUMBER: 33,208
CC REFERENCE/DOCKET NUMBER: 5150-0030
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 617-8999
CC TELEFAX: (415) 327-3231
CC INFORMATION FOR SEQ ID NO: 50:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 157 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
SQ MOLECULE TYPE: protein
SQ SEQUENCE 157 AA; 17570 MW; 122247 CN;

Query Match 40.1%; Score 800; DB 7; Length 157;
Best Local Similarity 96.2%; Pred. No. 6.45e-68;
Matches 102; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Db   36 DREKRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWS 95
        | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   60 DTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWS 119

Db   96 ENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCS 141
        |||||||||||||||||||||||||||||||||||||||||||||
Qy  120 ENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCA 165
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RESULT 8
ID US-08-050-319B-54   STANDARD;   PRT;   158 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 54, Application US/08050319B.
XX
CC Patent No. 5633145
CC GENERAL INFORMATION:
CC APPLICANT: M.Feldmann, P.W. Gray,
CC APPLICANT: M.J.C. Turner, F.M Brennan
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC NUMBER OF SEQUENCES: 57
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Reed & Robbins
CC STREET: 635 Bryant Street
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible

Left panel

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RESULT 9
ID   US-08-050-319B-52    STANDARD;    PRT;    153 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 52, Application US/08050319B.
XX
CC   Patent No. 563145
CC   Sequence 52, Application US/0805 0319B.
XX
CC   GENERAL INFORMATION:
CC      APPLICANT: M.Feldmann, P.W. Gray,
CC      APPLICANT: M.J.C. Turner, F.M Brennan
CC      TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC      TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC      NUMBER OF SEQUENCES: 57
CC      CORRESPONDENCE ADDRESS:
CC         ADDRESSEE: Reed & Robbins
CC         STREET: 635 Bryant Street
CC         CITY: Palo Alto
CC         STATE: California
CC         COUNTRY: USA
CC         ZIP: 94301
CC      COMPUTER READABLE FORM:
CC         MEDIUM TYPE: Floppy disk
CC         COMPUTER: IBM PC compatible
CC         OPERATING SYSTEM: PC-DOS/MS-DOS
CC         SOFTWARE: Patentin Release #1.0, version #1.25
CC      CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER: US/08/050,319B
CC         FILING DATE: 10-May-1993
CC         CLASSIFICATION: 435
CC      ATTORNEY/AGENT INFORMATION:
CC         NAME: Robbins, Roberta L.
CC         REGISTRATION NUMBER: 33,208
CC         REFERENCE/DOCKET NUMBER: 5150-0030
CC      TELECOMMUNICATION INFORMATION:
CC         TELEFAX: (415) 327-3231
CC         TELEPHONE: (415) 617-8999
CC   INFORMATION FOR SEQ ID NO: 54:
CC      SEQUENCE CHARACTERISTICS:
CC         LENGTH: 158 amino acids
CC         TYPE: amino acid
CC         TOPOLOGY: linear
CC         MOLECULE TYPE: protein
SQ   SEQUENCE 158 AA; 17375 MW; 124033 CN;

Query Match             33.4%;  Score 666;  DB 7;  Length 158;
Best Local Similarity
Matches  86;  Conservative  97.7%;  Pred. No 1.67e-54;  Mismatches 1;  Indels 0;  Gaps 0;

Qy  23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGEQDTDCRECESGSFTASENHLRHCL  82
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGEQDTDCRECESGSFTASENHLRHCL 100

Qy  83 SCSKCRKEMGQVEISSCTVDRDTVCGCR 110
       ||||||||||||||||||||||||| |:
Db 101 SCSKCRKEMGQVEISSCTVDRDTVCTCH 128
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Right panel

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RESULT 10
ID   US-08-050-319B-36    STANDARD;    PRT;    41 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 36, Application US/08050319B.
XX
CC   Patent No. 563145
CC   Sequence 36, Application US/08050319B
XX
CC   GENERAL INFORMATION:
CC      APPLICANT: M.Feldmann, P.W. Gray,
CC      APPLICANT: M.J.C. Turner, F.M Brennan
CC      TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC      TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC      NUMBER OF SEQUENCES: 57
CC      CORRESPONDENCE ADDRESS:
CC         ADDRESSEE: Reed & Robbins
CC         STREET: 635 Bryant Street
CC         CITY: Palo Alto
CC         STATE: California
CC         COUNTRY: USA
CC         ZIP: 94301
CC      COMPUTER READABLE FORM:
CC         MEDIUM TYPE: Floppy disk
CC         COMPUTER: IBM PC compatible
CC         OPERATING SYSTEM: PC-DOS/MS-DOS
CC         SOFTWARE: Patentin Release #1.0, version #1.25
CC      CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER: US/08/050,319B
CC         FILING DATE: 10-May-1993
CC         CLASSIFICATION: 435
CC      ATTORNEY/AGENT INFORMATION:
CC         NAME: Robbins, Roberta L.
CC         REGISTRATION NUMBER: 33,208
CC         REFERENCE/DOCKET NUMBER: 5150-0030
CC      TELECOMMUNICATION INFORMATION:
CC         TELEFAX: (415) 327-3231
CC         TELEPHONE: (415) 617-8999
CC   INFORMATION FOR SEQ ID NO: 52:
CC      SEQUENCE CHARACTERISTICS:
CC         LENGTH: 153 amino acids
CC         TYPE: amino acid
CC         TOPOLOGY: linear
CC         MOLECULE TYPE: protein
SQ   SEQUENCE 153 AA; 17148 MW; 116104 CN;

Query Match             23.9%;  Score 477;  DB 7;  Length 153;
Best Local Similarity
Matches  66;  Conservative  66.0%;  Pred. No 8.82e-36;  Mismatches 19;  Indels 6;  Gaps 4;

Qy  44 CPQGKYIHPQNN-SIC--CTKCHK--GTYLYNDCPGPGQDT-DCRKNQYRHYWSENLFQC  97
       |||||||||||| ::|:  | ::|:  |  :|| | |  :| |||||||||||||||||||
Db  66 CESGSFTASENILRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC 125

Qy  98 FNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCS 137
       ||||||||||||||||||||||||||||||||||||||||:
Db 126 FNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCA 165

CC   INFORMATION FOR SEQ ID NO: 36:
CC      SEQUENCE CHARACTERISTICS:
CC         LENGTH: 41 amino acids
CC         TYPE: amino acid
CC         STRANDEDNESS: single
CC         TOPOLOGY: linear
CC         MOLECULE TYPE: peptide
SQ   SEQUENCE 41 AA; 4856 MW; 8601 CN;

Query Match             17.0%;  Score 339;  DB 7;  Length 41;
Best Local Similarity 100.0%;  Pred. No 2.30e-22;
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Matches  41;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Db    1  GCRKNQYRHYWSENLFQCFNGSLCLNGTVHLSCQEKQNTVC  41
         |||||||||||||||||||||||||||||||||||||||||
Qy  108  GCRKNQYRHYWSENLFQCFNGSLCLNGTVHLSCQEKQNTVC  148

RESULT  11
ID    US-08-050-319B-26          STANDARD;    PRT;    40 AA.
XX
AC    xxxxxx
XX
DT    01-JAN-1900
XX
DE    Sequence 26, Application US/08050319B.
XX
CC    Sequence 26, Application US/08050319B
CC    Patent No. 5633145
CC    GENERAL INFORMATION:
CC      APPLICANT: M.Feldmann, P.W. Gray,
CC      APPLICANT: M.J.C. Turner, F.M Brennan
CC      TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC      TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC      NUMBER OF SEQUENCES: 57
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE: Reed & Robbins
CC        STREET: 635 Bryant Street
CC        CITY: Palo Alto
CC        STATE: California
CC        COUNTRY: USA
CC        ZIP: 94301
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE: Floppy disk
CC        COMPUTER: IBM PC compatible
CC        OPERATING SYSTEM: PC-DOS/MS-DOS
CC        SOFTWARE: Patentin Release #1.0, version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER: US/08/050,319B
CC        FILING DATE: 10-May-1993
CC        CLASSIFICATION: 435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME: Robbins, Roberta L.
CC        REGISTRATION NUMBER: 33,208
CC        REFERENCE/DOCKET NUMBER: 5150-0030
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE: (415) 327-3231
CC        TELEFAX: (415) 327-3231
CC      INFORMATION FOR SEQ ID NO: 26:
CC        SEQUENCE CHARACTERISTICS:
CC          LENGTH: 40 amino acids
CC          TYPE: amino acid
CC          STRANDEDNESS: single
CC          TOPOLOGY: linear
CC      MOLECULE TYPE: protein
SQ    SEQUENCE  40 AA; 4459 MW; 7536 CN;

Query Match  16.2%;  Score 324;  DB 7;  Length 40;
Best Local Similarity 100.0%;  Pred. No. 6.30e-21;
Matches  40;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Db    1  VCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCR  40
         ||||||||||||||||||||||||||||||||||||||||
Qy   25  VCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCR  64

RESULT  12
ID    US-08-050-319B-31          STANDARD;    PRT;    43 AA.
XX
AC    xxxxxx
XX
DT    01-JAN-1900
XX
DE    Sequence 31, Application US/08050319B.
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CC    Sequence 31, Application US/08050319B
CC    Patent No. 5633145
CC    GENERAL INFORMATION:
CC      APPLICANT: M.Feldmann, P.W. Gray,
CC      APPLICANT: M.J.C. Turner, F.M Brennan
CC      TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC      TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC      NUMBER OF SEQUENCES: 57
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE: Reed & Robbins
CC        STREET: 635 Bryant Street
CC        CITY: Palo Alto
CC        STATE: California
CC        COUNTRY: USA
CC        ZIP: 94301
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE: Floppy disk
CC        COMPUTER: IBM PC compatible
CC        OPERATING SYSTEM: PC-DOS/MS-DOS
CC        SOFTWARE: Patentin Release #1.0, version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER: US/08/050,319B
CC        FILING DATE: 10-May-1993
CC        CLASSIFICATION: 435
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME: Robbins, Roberta L.
CC        REGISTRATION NUMBER: 33,208
CC        REFERENCE/DOCKET NUMBER: 5150-0030
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE: (415) 327-3231
CC        TELEFAX: (415) 327-3231
CC      INFORMATION FOR SEQ ID NO: 31:
CC        SEQUENCE CHARACTERISTICS:
CC          LENGTH: 43 amino acids
CC          TYPE: amino acid
CC          STRANDEDNESS: single
CC          TOPOLOGY: linear
CC      MOLECULE TYPE: protein
SQ    SEQUENCE  43 AA; 4767 MW; 9758 CN;

Query Match  15.9%;  Score 318;  DB 7;  Length 43;
Best Local Similarity 100.0%;  Pred. No. 2.36e-20;
Matches  43;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Db    1  ECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVC  43
         |||||||||||||||||||||||||||||||||||||||||||
Qy   65  ECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVC  107

RESULT  13
ID    US-08-292-549-2          STANDARD;    PRT;    325 AA.
XX
AC    xxxxxx
XX
DT    01-JAN-1900
XX
DE    Sequence 2, Application US/08292549.
XX
CC    Sequence 2, Application US/08292549
CC    Patent No. 5464938
CC    GENERAL INFORMATION:
CC      APPLICANT: Smith, Craig A.
CC      APPLICANT: Goodwin, Raymond G.
CC      TITLE OF INVENTION: Isolated Viral Protein TNF Antagonists
CC      NUMBER OF SEQUENCES: 10
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE: Immunex Corporation
CC        STREET: 51 University Street
CC        CITY: Seattle
CC        STATE: Washington
CC        COUNTRY: USA
CC        ZIP: 98101
```

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CC   COMPUTER READABLE FORM:
CC     MEDIUM TYPE: Floppy disk
CC     COMPUTER: IBM PC compatible
CC     OPERATING SYSTEM: PC-DOS/MS-DOS
CC     SOFTWARE: Patentin Release #1.0, Version #1.25
CC   CURRENT APPLICATION DATA:
CC     APPLICATION NUMBER: US/08/292,549
CC     FILING DATE:
CC     CLASSIFICATION: 530
CC   PRIOR APPLICATION DATA:
CC     APPLICATION NUMBER: 07/963,330
CC     FILING DATE: 10/19/92
CC   ATTORNEY/AGENT INFORMATION:
CC     NAME: Perkins, Patricia A.
CC     REGISTRATION NUMBER: 34,693
CC     REFERENCE/DOCKET NUMBER: 2602-A
CC   TELECOMMUNICATION INFORMATION:
CC     TELEPHONE: (206) 587-0430
CC     TELEFAX: (206) 233-0644
CC INFORMATION FOR SEQ ID NO: 2:
CC   SEQUENCE CHARACTERISTICS:
CC     LENGTH: 325 amino acids
CC     TYPE: amino acid
CC     TOPOLOGY: linear
CC     MOLECULE TYPE: protein
SQ SEQUENCE 325 AA; 35132 MW; 591446 CN;

Query Match  Best Local Similarity  11.3%;  Score 225;  DB 5;  Length 325;
             Matches  39;  Conservative  21;  Mismatches  45;  Indels  7;  Gaps  6;

Db     4  LIAL-LVCVVYVYGDDVPYSSNQGKGGHDYEKDGLCCASCHPGFYASRLC-GPGSNTVC  61
          |:|: |:|:              |||  : :::::||: || :||:|| |:|
Qy     6  LLAFGLLCLPWLQEGSADSVCPQGKYI-HP-QNNSICCTKCHKGTYLYNDCPGPGQDTDC  63

Db    62  SPCEDGTFTASTNHAPACVSCRGPCTGHLSESQ--PCDRTHDRVCNCSTGNY  111
          ||::|:|||||   ::|:  |   :::| | ||: :||  ::| | | || | |
Qy    64  RECESGSFTASENHLRHCLSC-SKCRKEMGQVEISSCTVDRDTVCGCRKNQY  114

RESULT  14
ID   PCT-US91-02207-2     STANDARD;     PRT;     325 AA.
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AC   xxxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 2, Application PC/TUS9102207.
XX
CC   GENERAL INFORMATION:
CC     APPLICANT: Smith, Craig A.
CC     APPLICANT: Goodwin, Raymond G.
CC     TITLE OF INVENTION: Isolated Viral Protein Cytokine Antagonists
CC     NUMBER OF SEQUENCES: 4
CC     CORRESPONDENCE ADDRESS:
CC       ADDRESSEE: Immunex Corporation
CC       STREET: 51 University Street
CC       CITY: Seattle
CC       STATE: Washington
CC       COUNTRY: USA
CC       ZIP: 98101
CC     COMPUTER READABLE FORM:
CC       MEDIUM TYPE: Floppy disk
CC       COMPUTER: IBM PC compatible
CC       OPERATING SYSTEM: PC-DOS/MS-DOS
CC       SOFTWARE: Patentin Release #1.24
CC     CURRENT APPLICATION DATA:
CC       APPLICATION NUMBER: PCT/US91/02207
CC       FILING DATE: 19910329
CC       CLASSIFICATION: 435
CC     ATTORNEY/AGENT INFORMATION:
CC       NAME: Wight, Christopher L.
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CC     REGISTRATION NUMBER: 31,680
CC     REFERENCE/DOCKET NUMBER: 2602
CC   TELECOMMUNICATION INFORMATION:
CC     TELEPHONE: (206) 587-0430
CC     TELEFAX: (206) 587-0606
CC INFORMATION FOR SEQ ID NO: 2:
CC   SEQUENCE CHARACTERISTICS:
CC     LENGTH: 325 amino acids
CC     TYPE: AMINO ACID
CC     TOPOLOGY: linear
CC     MOLECULE TYPE: protein
SQ SEQUENCE 325 AA; 35132 MW; 591446 CN;

Query Match  Best Local Similarity  11.3%;  Score 225;  DB 10;  Length 325;
             Matches  39;  Conservative  21;  Mismatches  45;  Indels  7;  Gaps  6;

Db     4  LIAL-LVCVVYVYGDDVPYSSNQGKGGHDYEKDGLCCASCHPGFYASRLC-GPGSNTVC  61
          |:|: |:|:              |||  : :::::||: || :||:|| |:|
Qy     6  LLAFGLLCLPWLQEGSADSVCPQGKYI-HP-QNNSICCTKCHKGTYLYNDCPGPGQDTDC  63

Db    62  SPCEDGTFTASTNHAPACVSCRGPCTGHLSESQ--PCDRTHDRVCNCSTGNY  111
          ||::|:|||||   ::|:  |   :::| | ||: :||  ::| | | || | |
Qy    64  RECESGSFTASENHLRHCLSC-SKCRKEMGQVEISSCTVDRDTVCGCRKNQY  114

RESULT  15
ID   US-08-292-549-4     STANDARD;     PRT;     326 AA.
XX
AC   xxxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 4, Application US/08292549.
XX
     Patent No. 5464938
XX
CC   GENERAL INFORMATION:
CC     APPLICANT: Smith, Craig A.
CC     APPLICANT: Goodwin, Raymond G.
CC     TITLE OF INVENTION: Isolated Viral Protein TNF Antagonists
CC     NUMBER OF SEQUENCES: 10
CC     CORRESPONDENCE ADDRESS:
CC       ADDRESSEE: Immunex Corporation
CC       STREET: 51 University Street
CC       CITY: Seattle
CC       STATE: Washington
CC       COUNTRY: USA
CC       ZIP: 98101
CC     COMPUTER READABLE FORM:
CC       MEDIUM TYPE: Floppy disk
CC       COMPUTER: IBM PC compatible
CC       OPERATING SYSTEM: PC-DOS/MS-DOS
CC       SOFTWARE: Patentin Release #1.0, Version #1.25
CC     CURRENT APPLICATION DATA:
CC       APPLICATION NUMBER: US/08/292,549
CC       FILING DATE:
CC       CLASSIFICATION: 530
CC     PRIOR APPLICATION DATA:
CC       APPLICATION NUMBER: 07/963,330
CC       FILING DATE: 10/19/92
CC     ATTORNEY/AGENT INFORMATION:
CC       NAME: Perkins, Patricia A.
CC       REGISTRATION NUMBER: 34,693
CC       REFERENCE/DOCKET NUMBER: 2602-A
CC     TELECOMMUNICATION INFORMATION:
CC       TELEPHONE: (206) 587-0430
CC       TELEFAX: (206) 233-0644
CC INFORMATION FOR SEQ ID NO: 4:
CC   SEQUENCE CHARACTERISTICS:
CC     LENGTH: 326 amino acids
CC     TYPE: amino acid
CC     TOPOLOGY: linear
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CC      MOLECULE TYPE:  protein
SQ      SEQUENCE  326 AA;  35208 MW;  586550 CN;

Query Match      11.1%;  Score 221;  DB 5;  Length 326;
Best Local Similarity  39.5%;  Pred. No. 3.06e-11;
Matches   32;  Conservative  15;  Mismatches  30;  Indels  4;  Gaps  3;

Qy   94  VEISSCTVDRDTVCGCRKNQY 114
             ||  ||  |   |
Db   93  SQ--SCDKTRDRVCDCSAGNY 111

Qy   35  QNNSICCIKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC-SKCRKEMGQ 93
             : :|||| || ||| |  | ::||  || :| | ||| |||| ::|   :::
Db   34  EKDGLCCTSCPPGSYASRLC-GPGSDTVCSPCKNETFTASTNHHAPACVSCRGRCTGHLSE 92
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***********************************
        M P S R C H (TM)
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Release 3.0.5AA John F. Collins, Biocomputing Research Unit.
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MPsrch.nn　n.a. - n.a. database search, using Smith-Waterman algorithm

Run on:　Wed May 6 10:00:45 1998; MasPar time 59.61 Seconds
　　　　　927.602 Million cell updates/sec

Tabular output not generated.

Title:　>US-08-804-166-1
Description:　(1-1049) from US08004166.seq
Perfect Score:　1049
N.A. Sequence:
Comp:　1 TCCACATGGCTACACAGGTAAG.........TTPATTATCACAAATCTTAAG 1049
　　　　AGGTGTACCGAGTCCATTC..........AATAATAGTGTTTAGAATTC

Scoring table:　TABLE default
　　　　　　　　Gap 6

Nmatch STD :　Dbase 0; Query 0

Searched:　102136 seqs, 26354296 bases x 2

Post-processing:　Minimum Match 0%
　　　　　　　　　Listing first 45 summaries

Database:　n-issued
　　　　　　1:back1 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:PCT90
　　　　　　10:PCT91 11:PCT92 12:PCT93 13:PCT94 14:PCT95 15:PCT96

Statistics:　Mean 8.672; Variance 4.371; scale 1.984

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result   Query %
No.   Score   Match   Length DB ID   Description   Pred. No.
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| Result No. | Score | Query % Match | Length | DB | ID | Description | Pred. No. |
|---|---|---|---|---|---|---|---|
| 1 | 424 | 40.4 | 2062 | 7 | US-08-050- | Sequence 24, Applicati | 0.00e+00 |
| 2 | 424 | 40.4 | 2175 | 7 | US-08-321- | Sequence 1, Applicatio | 0.00e+00 |
| 3 | 424 | 40.4 | 6889 | 6 | US-08-286- | Sequence 2, Applicatio | 0.00e+00 |
| 4 | 424 | 40.4 | 6889 | 14 | PCT-US95-0 | Sequence 1, Applicatio | 0.00e+00 |
| 5 | 420 | 40.0 | 600 | 7 | US-08-050- | Sequence 47, Applicati | 0.00e+00 |
| 6 | 381 | 36.3 | 504 | 7 | US-08-050- | Sequence 56, Applicati | 1.31e-290 |
| 7 | 379 | 36.1 | 501 | 7 | US-08-050- | Sequence 1, Applicatio | 2.58e-290 |
| 8 | 370 | 35.3 | 372 | 7 | US-08-050- | Sequence 3, Applicatio | 6.34e-289 |
| 9 | 302 | 28.8 | 474 | 7 | US-08-050- | Sequence 49, Applicati | 2.44e-281 |
| 10 | 300 | 28.6 | 2771 | 7 | US-08-273- | Sequence 5, Applicatio | 1.69e-222 |
| 11 | 298 | 28.4 | 4283 | 7 | US-08-343- | Sequence 5, Applicatio | 8.01e-222 |
| 12 | 298 | 28.4 | 4283 | 7 | US-08-445- | Sequence 1, Applicatio | 8.01e-221 |
| 13 | 255 | 24.3 | 477 | 7 | US-08-050- | Sequence 53, Applicati | 7.22e-185 |
| 14 | 169 | 16.1 | 462 | 7 | US-08-050- | Sequence 51, Applicati | 1.18e-113 |
| 15 | 69 | 6.6 | 534 | 6 | US-08-187- | Sequence 3, Applicatio | 9.14e-34 |
| 16 | 69 | 6.6 | 654 | 6 | US-08-187- | Sequence 1, Applicatio | 9.14e-34 |
| 17 | 59 | 5.6 | 321 | 4 | US-07-920- | Sequence 1, Applicatio | 3.06e-26 |
| 18 | 59 | 5.6 | 321 | 4 | US-08-314- | Sequence 23, Applicati | 3.06e-26 |
| 19 | 59 | 5.6 | 597 | 6 | US-08-187- | Sequence 2, Applicatio | 3.06e-26 |
| 20 | 57 | 5.4 | 7218 | 7 | US-08-232- | Sequence 14, Applicatio | 9.29e-25 |
| 21 | 52 | 5.0 | 2248 | 7 | US-08-475- | Sequence 1, Applicatio | 4.33e-21 |
| 22 | 52 | 5.0 | 2248 | 7 | US-08-780- | Sequence 1, Applicatio | 4.33e-21 |
| 23 | 52 | 5.0 | 2248 | 7 | US-08-636- | Sequence 1, Applicatio | 4.33e-21 |
| 24 | 52 | 5.0 | 2248 | 6 | US-08-369- | Sequence 1, Applicatio | 4.33e-21 |
| 25 | 38 | 3.6 | 633 | 7 | US-08-388- | Sequence 1, Applicati | 3.33e-11 |
| 26 | 36 | 3.4 | 4810 | 13 | PCT-US94-0 | Sequence 3, Applicati | 7.43e-10 |
| 27 | 36 | 3.4 | 4810 | 7 | US-08-453- | Sequence 3, Applicati | 7.43e-10 |
| 28 | 36 | 3.4 | 4810 | 7 | US-08-188- | Sequence 3, Applicati | 7.43e-10 |
| 29 | 36 | 3.4 | 4810 | 14 | PCT-US95-0 | Sequence 3, Applicati | 7.43e-10 |
| 30 | 36 | 3.4 | 5125 | 12 | PCT-US93-0 | Sequence 7, Applicati | 7.43e-10 |
| 31 | 36 | 3.4 | 5125 | 7 | US-08-453- | Sequence 11, Applicati | 7.43e-10 |
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| 33 | 36 | 3.4 | 5323 | 7 | US-08-453- | Sequence 9, Applicatio | 7.43e-10 |
| 34 | 36 | 3.4 | 5323 | 12 | PCT-US93-0 | Sequence 9, Applicatio | 7.43e-10 |
| 35 | 35 | 3.3 | 215 | 6 | US-08-238- | Sequence 14, Applicati | 1.76e-08 |
| 36 | 35 | 3.1 | 7218 | 7 | US-08-232- | Sequence 14, Applicati | 1.58e-08 |
| 37 | 30 | 2.9 | 33 | 7 | PCT-US94-0 | Sequence 5, Applicatio | 7.07e-06 |
| 38 | 29 | 2.8 | 215 | 6 | US-08-050- | Sequence 5, Applicatio | 2.58e-05 |
| 39 | 26 | 2.5 | 74 | 14 | PCT-US95-1 | Sequence 94, Applicati | 1.76e-03 |
| 40 | 26 | 2.5 | 81 | 14 | PCT-US95-1 | Sequence 92, Applicati | 1.76e-03 |
| 41 | 26 | 2.4 | 81 | 14 | PCT-US95-1 | Sequence 98, Applicati | 1.91e-03 |
| 42 | 25 | 2.4 | 82 | 14 | PCT-US95-1 | Sequence 97, Applicati | 6.91e-03 |
| 43 | 24 | 2.3 | 69 | 7 | US-08-471- | Sequence 142, Applicat | 2.64e-02 |
| 44 | 24 | 2.3 | 74 | 14 | PCT-US95-1 | Sequence 100, Applicat | 2.64e-02 |
| 45 | 24 | 2.3 | 82 | 14 | PCT-US95-1 | Sequence 97, Applicati | 2.64e-02 |

ALIGNMENTS

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RESULT 1
ID  US-08-050-3198-24 STANDARD; DNA; UNC; 2062 BP.
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DT  01-JAN-1900
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DE  Sequence 24, Application US/08050319B.
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CC  Sequence 24, Application US/08050319B.
CC  Patent No. 5633145
CC  GENERAL INFORMATION:
CC  APPLICANT: M.Feldmann, P.W. Gray,
CC  APPLICANT: M.J.C. Turner, F.M Brennan
CC  TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC  TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC  NUMBER OF SEQUENCES: 57
CC  CORRESPONDENCE ADDRESS:
CC  ADDRESSEE: Reed & Robbins
CC  STREET: 635 Bryant Street
CC  CITY: Palo Alto
CC  STATE: California
CC  COUNTRY: USA
CC  ZIP: 94301
CC  COMPUTER READABLE FORM:
CC  MEDIUM TYPE: Floppy disk
CC  COMPUTER: IBM PC compatible
CC  OPERATING SYSTEM: PC-DOS/MS-DOS
CC  SOFTWARE: Patentin Release #1.0, version #1.25
CC  CURRENT APPLICATION DATA:
CC  APPLICATION NUMBER: US/08/050,319B
CC  FILING DATE: 10-May-1993
CC  CLASSIFICATION: 435
CC  ATTORNEY/AGENT INFORMATION:
CC  NAME: Robbins, Roberta L.
CC  REGISTRATION NUMBER: 33,208
CC  REFERENCE/DOCKET NUMBER: 5150-0030
CC  TELECOMMUNICATION INFORMATION:
CC  TELEPHONE: (415) 617-8999
CC  TELEFAX: (415) 327-3231
CC  INFORMATION FOR SEQ ID NO: 24:
CC  SEQUENCE CHARACTERISTICS:
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CC   LENGTH: 2062 base pairs
CC   TYPE: nucleic acid
CC   STRANDEDNESS: double
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: cDNA to mRNA
CC   FEATURE:
CC   NAME/KEY: CDS
CC   LOCATION: 155..1519
SO   Sequence 2062 BP; 429 A; 617 C; 573 G; 443 T; 0 other;

Query Match             40.4%;  Score 424;  DB 7;  Length 2062;
Best Local Similarity   99.8%;  Pred. No. 0.00e+00;
Matches   425;  Conservative   0;  Mismatches 1;  Indels  0;  Gaps  0;

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Qy    344 GATAGTGTGTGTCCCCAAGGAAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403

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Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAAATGACTGTCCAGGCCCGGGGGGAGGATACGGAC 463

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Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAAACCACCTCAGACACTGCCTC 523

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Db    695 TCCTGT 700
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Qy    764 TCCTGT 769
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INFORMATION FOR SEQ ID NO: 1:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 2175 base pairs
CC   TYPE: nucleic acid
CC   STRANDEDNESS: single
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: cDNA
CC   FEATURE:
CC   NAME/KEY: CDS
CC   LOCATION: 256..1620
SO   Sequence 2175 BP; 474 A; 641 C; 604 G; 456 T; 0 other;

Query Match             40.4%;  Score 424;  DB 7;  Length 2175;
Best Local Similarity   99.8%;  Pred. No. 0.00e+00;
Matches   425;  Conservative   0;  Mismatches 1;  Indels  0;  Gaps  0;

Db    376 GATAGTGTGTGTCCCCAAGGAAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 435
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    344 GATAGTGTGTGTCCCCAAGGAAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403

Db    436 AAGTGCCACAAAGGAACCTACTTGTACAAATGACTGTCCAGGCCCGGGGGGAGGATACGGAC 495
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Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAAATGACTGTCCAGGCCCGGGGGGAGGATACGGAC 463

Db    496 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAAACCACCTCAGACACTGCCTC 555
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Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAAACCACCTCAGACACTGCCTC 523

Db    556 AGCTGCCTCCAAAATGCCGAAAAGGAAAATGGGTGCAGGTGGAGAATCTCTTCTTGCACAG 615
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Qy    524 AGCTGCCTCCAAAATGCCGAAAAGGAAAATGGGTGCAGGTGGAGAATCTCTTCTTGCACAG 583

Db    616 CGGGACACCGTGTGTGGCTGCAGGAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 675
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Qy    584 CGGGACACCGTGTGTGGCTGCAGGAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db    676 TTCCAGTGCTTCAATTGCAGCCTCTGCCCTCAATGGGACCGTGCACCTCTTCTTGCCAGGAG 735
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Qy    644 TTCCAGTGCTTCAATTGCAGCCTCTGCCCTCAATGGGACCGTGCACCTCTTCTTGCCAGGAG 703

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Qy    764 TCCTGT 769
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Left column:

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XX
DT    01-JAN-1900
XX
DE    Sequence 2, Application US/08286740.
XX
CC    Patent No. 5561053
CC    GENERAL INFORMATION:
CC       APPLICANT: Crowley, Craig W.
CC       TITLE OF INVENTION:  METHOD FOR SELECTING HIGH-EXPRESSING
CC       TITLE OF INVENTION:  HOST CELLS
CC       NUMBER OF SEQUENCES: 4
CC       CORRESPONDENCE ADDRESS:
CC          ADDRESSEE: Genentech, Inc.
CC          STREET: 460 Point San Bruno Blvd
CC          CITY:  South San Francisco
CC          STATE:  California
CC          COUNTRY:  USA
CC          ZIP:  94080
CC       COMPUTER READABLE FORM:
CC          MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
CC          COMPUTER: IBM PC compatible
CC          OPERATING SYSTEM:  PC-DOS/MS-DOS
CC          SOFTWARE:  patin (Genentech)
CC       CURRENT APPLICATION DATA:
CC          APPLICATION NUMBER:  US/08/286,740
CC          FILING DATE:  05-AUG-1994
CC          CLASSIFICATION:  435
CC       PRIOR APPLICATION DATA:
CC          APPLICATION NUMBER:
CC          FILING DATE:
CC       ATTORNEY/AGENT INFORMATION:
CC          NAME:  Lee, Wendy M.
CC          REGISTRATION NUMBER:
CC       REFERENCE/DOCKET NUMBER:  798
CC       TELECOMMUNICATION INFORMATION:
CC          TELEPHONE:  415/225-1994
CC          TELEFAX:  415/952-9881
CC          TELEX:  910/371-7168
CC    INFORMATION FOR SEQ ID NO:  2:
CC       SEQUENCE CHARACTERISTICS:
CC          LENGTH:  6889 bases
CC          TYPE:  nucleic acid
CC          STRANDEDNESS:  double
CC          TOPOLOGY:  linear
SQ    Sequence 6889 BP; 1729 A; 1826 C; 1681 G; 1653 T; 0 other;

      Query Match      40.4%;  Score 424;  DB 6;  Length 6889;
      Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
      Matches  425;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

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Qy    344 GATAGTGTGTGTCCCCAAGGAGAAAATATATCCACCCTCAAAATAATAATTCCATTTGCTGTACC 403

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Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 463

Db   1845 TGCAGGGAGTGTGAGAGCGGGCGCCTCCTTCACCGCCTTCAGAAAAACCACCTCAGACACTGCCTC 1904
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Qy    464 TGCAGGGAGTGTGAGAGCGGCTCCCTTCACCGCTTCAGAAAAACCACCTCAGACACTGCCTC 523

Db   1905 AGCTGCTCCAAAATGCCGAAAAGGAAATGGGTCAGGTGGGAGATCTCTTCTTCGCACAGTGGAC 1964
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Qy    704 AAACAGAACACCGTGTGCACCTGCCATGCAGAGGTTTCTTTCTAAGAGAAACGAGTGTGTC 763

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Qy    764 TCCTGT 769
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AC    xxxxxx
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DT    01-JAN-1900
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DE    Sequence 2, Application PC/TUS9509576.
XX
CC    GENERAL INFORMATION:
CC       APPLICANT: GENENTECH, INC.
CC       TITLE OF INVENTION:  METHOD FOR SELECTING HIGH-EXPRESSING
CC       TITLE OF INVENTION:  HOST CELLS
CC       NUMBER OF SEQUENCES: 4
CC       CORRESPONDENCE ADDRESS:
CC          ADDRESSEE: Genentech, Inc.
CC          STREET: 460 Point San Bruno Blvd
CC          CITY:  South San Francisco
CC          STATE:  California
CC          COUNTRY:  USA
CC          ZIP:  94080
CC       COMPUTER READABLE FORM:
CC          MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
CC          COMPUTER: IBM PC compatible
CC          OPERATING SYSTEM:  PC-DOS/MS-DOS
CC          SOFTWARE:  patin (Genentech)
CC       CURRENT APPLICATION DATA:
CC          APPLICATION NUMBER:  PCT/US95/09576
CC          FILING DATE:
CC          CLASSIFICATION:
CC       PRIOR APPLICATION DATA:
CC          APPLICATION NUMBER:  08/286740
CC          FILING DATE:  05-AUG-1994
CC       ATTORNEY/AGENT INFORMATION:
CC          NAME:  Lee, Wendy M.
CC          REGISTRATION NUMBER:  00,000
CC       REFERENCE/DOCKET NUMBER:  798PCT
CC       TELECOMMUNICATION INFORMATION:
CC          TELEPHONE:  415/225-1994
CC          TELEFAX:  415/952-9881
CC          TELEX:  910/371-7168
CC    INFORMATION FOR SEQ ID NO:  2:
CC       SEQUENCE CHARACTERISTICS:
CC          LENGTH:  6889 bases
CC          TYPE:  nucleic acid
CC          STRANDEDNESS:  double
CC          TOPOLOGY:  linear
SQ    Sequence 6889 BP; 1729 A; 1826 C; 1681 G; 1653 T; 0 other;

      Query Match      40.4%;  Score 424;  DB 14;  Length 6889;
      Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
      Matches  425;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Db   1725 GATAGTGTGTGTCCCCAAGGAGAAAATATATCCACCCTCAAAATAATAATTCGATTTGCTGTACC 1784
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    344 GATAGTGTGTGTCCCCAAGGAGAAAATATATCCACCCTCAAAATAATAATTCCATTTGCTGTACC 403

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Qy   464 TGCAGGGAGTGTGAGAGCGGCGTCCTTCACCGCTTCAGAAAAACCACCTCAGACACTGCCTC 523
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Db 1905 AGCTGCTCCAAATGCCAAAAGGAAAAAGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 1964

Db 1965 CGGGACACCGTGTGTGGGCTGCAGGAAGGAAGAAACCAGTACCGGGCGCCAATTATTGGAGTGAAAAACCTT 2024
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Qy   644 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCCCAAATGGGACCGTGCACCTCTCCCTGCCAGGAG 703

Db 2085 AAACAGAACACCGTGTGCCACCTGCCACCTGTTCTTTCTTCTAAGAGAGAAAACGAGTGTGTC 2144
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Qy   704 AAACAGAACACCGTGTGCCACCTGCCACCTGTTCTTTCTTCTAAGAGAGAAAACGAGTGTGTC 763

Db 2145 TCCTGT 2150
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Qy   764 TCCTGT 769

Query Match 40.0%;   Score 420; DB 7; Length 600;
Best Local Similarity 99.3%; Pred. No. 0.00e+00;
Matches 423; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy   764 TCCTGT 769

RESULT 7
ID US-08-050-319B-1 STANDARD; DNA; UNC; 501 BP.

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AC xxxxxx
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DT 01-JAN-1900
XX
DE Sequence 1, Application US/08050319B.
XX

Sequence 1, Application US/08050319B.
Patent No. 5633145
GENERAL INFORMATION:
CC APPLICANT: M.Feldmann, P.W.Gray,
CC APPLICANT: M.J.C.Turner, F.M Brennan

CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/050,319B
CC FILING DATE: 10-May-1993
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Robbins, Roberta L.
CC REGISTRATION NUMBER: 33,208
CC REFERENCE/DOCKET NUMBER: 5150-0030
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 617-8999
CC TELEFAX: (415) 327-3231
CC INFORMATION FOR SEQ ID NO: 56:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 504 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: double
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA to mRNA
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 1..501
SQ Sequence 504 BP; 122 A; 137 C; 138 G; 107 T; 0 other;

Query Match   36.3%; Score 381; DB 7; Length 504;
Best Local Similarity 99.7%; Pred. No. 1.31e-290;
Matches 382; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy  344 GATAGTGTGTGTCCCCAAGGAAAAATATATTCCACCCTCAAAATAATTCCAITTGCTGTACC 403

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Qy  464 TGCAGGGAGTGTGAGAGCGGGCTCCTTCACCGCTTCAGAAAAACCACCTCAGACACTGCCTC 523

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Qy  584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db  421 TTCCAGTGCTTCAAATTGCAGCCTCCTCCAAATGGGACCGTGCACCTCTCCTGCCAGGAG 480
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Qy  644 TTCCAGTGCTTCAAATTGCAGCCTCCTCCAAATGGGACCGTGCACCTCTCCTGCCAGGAG 703

Db  481 AAACAGAACACCGTGTGCACCTG 503
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Qy  704 AAACAGAACACCGTGTGCACCTG 726
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TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Reed & Robbins
CC STREET: 635 Bryant Street
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/050,319B
CC FILING DATE: 10-May-1993
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Robbins, Roberta L.
CC REGISTRATION NUMBER: 33,208
CC REFERENCE/DOCKET NUMBER: 5150-0030
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 617-8999
CC TELEFAX: (415) 327-3231
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 501 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: double
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 1..501
SQ Sequence 501 BP; 121 A; 137 C; 137 G; 106 T; 0 other;

Query Match   36.1%; Score 379; DB 7; Length 501;
Best Local Similarity 99.7%; Pred. No. 6.34e-289;
Matches 380; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db  121 GATAGTGTGTGTCCCCAAGGAGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  344 GATAGTGTGTGTCCCCAAGGAAAAATATATCCACCCTCAAAATAATTCCAITTGCTGTACC 403

Db  181 AAGTGCCACAAAAGGAAACCTACTTGTACAATGACTGTCCAGGCCCCGGGGCAGGATACGGAC 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  404 AAGTGCCACAAAAGGAAACCTACTTGTACAATGACTGTCCAGGCCCCGGGGCAGGATACGGAC 463

Db  241 TGCAGGGAGTGTGAGAGCGGGCTCCTTCACCGCTTCAGAAAAACCACCTCAGACACTGCCTC 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  464 TGCAGGGAGTGTGAGAGCGGGCTCCTTCACCGCTTCAGAAAAACCACCTCAGACACTGCCTC 523

Db  301 AGCTGCTCCAAATGCCGAAAAGGAAAATGGGTCAGGTGGGAGATCTCTTCTTCTTGCACAGTGGAC 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  524 AGCTGCTCCAAATGCCGAAAAGGAAAATGGGTCAGGTGGGAGATCTCTTCTTCTTGCACAGTGGAC 583

Db  361 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 420
        |||||||||||||||||||||||||||||||||||||||||||||||||
Qy  584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db  421 TTCCAGTGCTTCAAATTGCAGCCTCCTCGCCTCCAAATGGACCGTGCACCTCTCCTGCCAGGAG 480
        ||||||||||||||||||||||||||||||||||||||||||||||||
Qy  644 TTCCAGTGCTTCAAATTGCAGCCTCCTCGCCTCCAAATGGACCGTGCACCTCTCCTGCCAGGAG 703

Db  481 AAACAGAACACCGTGTGCACC 501
        |||||||||||||||||||||
Qy  704 AAACAGAACACCGTGTGCACC 724
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RESULT 8
ID US-08-050-319B-3 STANDARD; DNA; UNC; 372 BP.

Left column

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XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 3, Application US/08050319B.
     Patent No. 5633145
XX
CC   GENERAL INFORMATION:
CC    APPLICANT: M.Feldmann, P.W. Gray,
CC    APPLICANT: M.J.C. Turner, F.M Brennan
CC    TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC    TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC    NUMBER OF SEQUENCES: 57
CC    CORRESPONDENCE ADDRESS:
CC     ADDRESSEE: Reed & Robbins
CC     STREET: 635 Bryant Street
CC     CITY: Palo Alto
CC     STATE: California
CC     COUNTRY: USA
CC     ZIP: 94301
CC    COMPUTER READABLE FORM:
CC     MEDIUM TYPE: Floppy disk
CC     COMPUTER: IBM PC compatible
CC     OPERATING SYSTEM: PC-DOS/MS-DOS
CC     SOFTWARE: Patentin Release #1.0, version #1.25
CC    CURRENT APPLICATION DATA:
CC     APPLICATION NUMBER: US/08/050,319B
CC     FILING DATE: 10-May-1993
CC     CLASSIFICATION: 435
CC    ATTORNEY/AGENT INFORMATION:
CC     NAME: Robbins, Roberta L.
CC     REGISTRATION NUMBER: 33,208
CC     REFERENCE/DOCKET NUMBER: 5150-0030
CC    TELECOMMUNICATION INFORMATION:
CC     TELEPHONE: (415) 617-8999
CC     TELEFAX: (415) 327-3231
CC    INFORMATION FOR SEQ ID NO: 3:
CC     SEQUENCE CHARACTERISTICS:
CC      LENGTH: 372 base pairs
CC      TYPE: nucleic acid
CC      STRANDEDNESS: double
CC      TOPOLOGY: linear
CC     MOLECULE TYPE: DNA (genomic)
CC     FEATURE:
CC      NAME/KEY: CDS
CC      LOCATION: 1..372
SQ   Sequence 372 BP; 98 A; 102 C; 95 G; 77 T; 0 other;

Query Match    35.3%;  Score 370;  DB 7;  Length 372;
Best Local Similarity  99.7%;
Matches  371;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Qy      1 GTGTGTCCCCAAGGAAAAATATATTCACCTCAAAATAATTCGATTTGCTGTACCAAGTGC   60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    350 GTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCCATTTGCTGTACCAAGTGC  409

Qy     61 CACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGACTGCAGG  120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    410 CACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGACTGCAGG  469

Qy    121 GAGTGTGAGAGCGGCTCCTTCACCGGTTCAGAAAAACCACCTCAGACACTGCCTCAGCTGC  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    470 GAGTGTGAGAGCGGCTCCTTCACCGGTTCAGAAAAACCACCTCAGACACTGCCTCAGCTGC  529

Qy    181 TCCAAATGCCCAAAGCAAAATGGGTCACAGGTGGACTCTTCTTCTTGCACAGTGGACCGGGAC  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    530 TCCAAATGCCGAAAGCAAAATGGGTCACAGGTGGGAGAGATCTTCTTCTTGCACAGTGGACCGGGAC  589

Qy    241 ACCGGTGTGTGGCCTGCAGGAAGGAAACAGTACCGGGCATTATTGGAGTGAAAAACCTTTTCCAG  300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ACCGGTGTGTGGCCTGCAGGAAGGAAACAGTACCGGGCATTATTGGAGTGAAAAACCTTTTCCAG  300
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Right column

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RESULT   9
ID   US-08-050-319B-49 STANDARD; DNA; UNC; 474 BP.

XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 49, Application US/08050319B.
     Patent No. 5633145
XX
CC   GENERAL INFORMATION:
CC    APPLICANT: M.Feldmann, P.W. Gray,
CC    APPLICANT: M.J.C. Turner, F.M Brennan
CC    TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC    TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC    NUMBER OF SEQUENCES: 57
CC    CORRESPONDENCE ADDRESS:
CC     ADDRESSEE: Reed & Robbins
CC     STREET: 635 Bryant Street
CC     CITY: Palo Alto
CC     STATE: California
CC     COUNTRY: USA
CC     ZIP: 94301
CC    COMPUTER READABLE FORM:
CC     MEDIUM TYPE: Floppy disk
CC     COMPUTER: IBM PC compatible
CC     OPERATING SYSTEM: PC-DOS/MS-DOS
CC     SOFTWARE: Patentin Release #1.0, version #1.25
CC    CURRENT APPLICATION DATA:
CC     APPLICATION NUMBER: US/08/050,319B
CC     FILING DATE: 10-May-1993
CC     CLASSIFICATION: 435
CC    ATTORNEY/AGENT INFORMATION:
CC     NAME: Robbins, Roberta L.
CC     REGISTRATION NUMBER: 33,208
CC     REFERENCE/DOCKET NUMBER: 5150-0030
CC    TELECOMMUNICATION INFORMATION:
CC     TELEPHONE: (415) 617-8999
CC     TELEFAX: (415) 327-3231
CC    INFORMATION FOR SEQ ID NO: 49:
CC     SEQUENCE CHARACTERISTICS:
CC      LENGTH: 474 base pairs
CC      TYPE: nucleic acid
CC      STRANDEDNESS: double
CC      TOPOLOGY: linear
CC     MOLECULE TYPE: cDNA to mRNA
CC     FEATURE:
CC      NAME/KEY: CDS
CC      LOCATION: 1..471
SQ   Sequence 474 BP; 110 A; 126 C; 132 G; 106 T; 0 other;

Query Match    28.8%;  Score 302;  DB 7;  Length 474;
Best Local Similarity  97.8%;
Matches  309;  Conservative   0;  Mismatches   7;  Indels   0;  Gaps   0;

Qy    590 ACCGTGTGTGGCCTGCAGGAAGGAAACCAGTACCGGCATTATTGGAGTGAAAAACCTTTTCCAG  649
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TGCTTCAATTGCAGCCCTCTGCCTCAATGGGACCGGACCGTGCACCTCTCCTGCCTGCAGCTGC  360

Qy    650 TGCTTCAATTGCAGCCCTCTGCCTCAATGGGACCGGTGCACCTCTCCTGCCACAGCTGC  709
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 AACACCGTGTGC  372

Qy    710 AACACCGTGTGC  721
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Qy   514 ACACTGCCTCAGCTGCTCCAAATGCCGAAAAGGAAAAATGGGTCAGGTGGAGATCTCTTCTTG 573
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   225 CACAGTGGACCGGGACACCGTGTGTGCTGCAGGAGAGAAACAGTACCGGCACATTATTGGGAG 284

Qy   574 CACAGTGGACCGGGACACCGTGTGTGCTGCAGGAAGAACCAGTACCCGGCATTATTGGGAG 633
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   285 TGAAAACCTTTCCAGTGGCTTCAGTTCCAGCCTGCGTGCCACCTCTC 344

Qy   634 TGAAAACCTTTCCAGTGGCTTCAATTGCAGCCTGCGTGCCACCTCTC 693
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Db   345 CTGCCAGGAGAAACAGAACACCGTGTGCACCTCAGGTTTCTTTTCTAAGAGAAAA 404

Qy   694 CTGCCAGGAGAAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTTCTAAGAGAAAA 753
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   405 CGAGTGTGTCTCCTGT 420

Qy   754 CGAGTGTGTCTCCTGT 769
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Db   405 CGAGTGTGTCTCCTGT 420
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RESULT 10
ID   US-08-273-411-5 STANDARD; DNA; UNC; 2771 BP.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 5, Application US/08273411.
XX
CC   Patent No. 5625124
CC   GENERAL INFORMATION:
CC   APPLICANT: Falk, Per
CC   APPLICANT: Gordon, Jeffrey I.
CC   TITLE OF INVENTION: Animal Model for Gastro-Intestinal
CC      Disease
CC   NUMBER OF SEQUENCES: 10
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Patrea L. Pabst
CC   STREET: 1100 Peachtree Street, Suite 2800
CC   CITY: Atlanta
CC   STATE: Georgia
CC   COUNTRY: USA
CC   ZIP: 30309-4530
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: Patentin Release #1.0, Version #1.25
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/273,411
CC   FILING DATE:
CC   CLASSIFICATION: 435
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Pabst, Patrea L.
CC   REGISTRATION NUMBER: 31,284
CC   REFERENCE/DOCKET NUMBER: WU106
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (404) 815-6508
CC   TELEFAX: (404) 815-6555
CC   INFORMATION FOR SEQ ID NO: 5:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 2771 base pairs
CC   TYPE: nucleic acid
CC   STRANDEDNESS: double
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: DNA (genomic)
CC   HYPOTHETICAL: NO
CC   ANTI-SENSE: NO
CC   PUBLICATION INFORMATION:
CC   AUTHORS: Sweetser, et al.
CC   JOURNAL: Genes & Dev.
```

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CC   VOLUME: 2
CC   PAGES: 1318-1332
CC   DATE: 1988
CC   RELEVANT RESIDUES IN SEQ ID NO: 5: FROM 561 TO 629
CC   PUBLICATION INFORMATION:
CC   AUTHORS: Seeburg, et al.
CC   JOURNAL: DNA
CC   VOLUME: 1
CC   PAGES: 239-249
CC   DATE: 1982
CC   RELEVANT RESIDUES IN SEQ ID NO: 5: FROM 620 TO 2771
CC   PUBLICATION INFORMATION:
CC   AUTHORS: Sweetser, et al.
CC   JOURNAL: J. Biol. Chem.
CC   VOLUME: 261
CC   PAGES: 5553-5561
CC   DATE: 1986
CC   RELEVANT RESIDUES IN SEQ ID NO: 5: FROM 1 TO 617
SQ   Sequence 2771 BP; 666 A; 718 C; 704 G; 683 T; 0 other;

Query Match       28.6%; Score 300; DB 7; Length 2771;
Best Local Similarity  97.3%;
Matches  329; Conservative   0; Mismatches   5; Indels   4; Gaps  2;
                 Pred. No. 1.69e-222;
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Db   680 ATGGCTACAGGTAAGCGCCCCTAAAATCCCTTTGGGCACAATGTGTCCTGAGGGGGAGG 739
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     6 ATGGCTACAGGTAAGCGCCCCTAAAATCCCTTTGGGCACAATGTGTCCTGAGGGGGAGG 65

Db   740 CAGGGACCTGTAGATGGGACGGGGGCACTAAACCTCAGGTTTGGGGCTTCTGAATG--AG 797
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||
Qy    66 TATCGCCAATGTAAGCCCAGTATT----GGCCAAATCTCAGAGAAAGCTCTCAGGTTTGGGGCTTCTGAATG--AG 125

Db   798 TATGGCCAATGTAAGCCCAGTAT--GGCCAAATCTCAGAGAAAGCTCTCAGGTTTGGGGCTTCTGAATG 855
         |||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Qy   126 TATCGCCAATGTAAGCCCAGTATT----GGCCAAATCTCAGAGAAAGCTCTCAGGTTTGGGGCTTCTGAATG 185

Db   856 GGAGGAGAGAAAAACAAACAGCTCCTGGACGCAGGGAGAGTGCTGGCCCTCTTGGCCTCTCCGGC 915
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   186 GGAGGAGAGAAAAACAAACAGCTCCTGGACGCAGGGAGAGTGCTGGCCCTCTTGGCCTCTCCGGC 245

Db   916 TCCCTCTGTTGCCCTCTGGTTTCTCCCCAGGCTCCCGGACGCCCCGGCCTTTG 975
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   246 TCCCTCTGTTGCCCTCTGGTTTCTCCCCAGGCTCCCGGACGCCCCGGCCTTTG 305

Db   976 GCCTGCTCTGCCCTCCCCTGGCTTCAAGAGAGGCAGTGCC 1013
         ||||||||||||||||||||||||||||||||||||||||
Qy   306 GCCTGCTCTGCCCTCCCCTGGCTTCAAGAGAGGCAGTGCC 343
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RESULT 11
ID   US-08-343-401A-3 STANDARD; DNA; UNC; 4283 BP.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 3, Application US/08343401A.
XX
CC   Patent No. 5661132
CC   GENERAL INFORMATION:
CC   APPLICANT: Swain, William F
CC   APPLICANT: Macklin, Michael D
CC   APPLICANT: Eriksson, Elof
CC   APPLICANT: Andree, Christophe
CC   TITLE OF INVENTION: Improved Wound Healing
CC   NUMBER OF SEQUENCES: 4
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Quarles & Brady
CC   STREET: PO Box 2113
CC   CITY: Madison
CC   STATE: WI
```

Left column

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RESULT    12
ID   US-08-445-265A-1 STANDARD; DNA; UNC; 4283 BP.
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CC   COUNTRY: USA
CC      ZIP: 53701-2113
CC   COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Floppy disk
CC      COMPUTER: IBM PC compatible
CC      OPERATING SYSTEM: PC-DOS/MS-DOS
CC      SOFTWARE: Patentin Release #1.0, Version #1.30
CC   CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: US/08/343,401A
CC      FILING DATE: 22-NOV-1994
CC      CLASSIFICATION: 514
CC   ATTORNEY/AGENT INFORMATION:
CC      NAME: Seay, Nicholas J
CC      REGISTRATION NUMBER: 27,386
CC      REFERENCE/DOCKET NUMBER: 11-229-9103-9
CC   TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: 608-251-5000
CC      TELEFAX: 608-251-9166
CC   INFORMATION FOR SEQ ID NO: 3:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 4283 base pairs
CC      TYPE: nucleic acid
CC      STRANDEDNESS: double
CC      TOPOLOGY: circular
CC   MOLECULE TYPE: DNA (genomic)
CC   IMMEDIATE SOURCE:
CC      CLONE: pWRG1630
CC   FEATURE:
CC      NAME/KEY: sig_peptide
CC      LOCATION: 713..1049
CC   FEATURE:
CC      NAME/KEY: CDS
CC      LOCATION: join(713..721, 981..1253)
CC   FEATURE:
CC      NAME/KEY: exon
CC      LOCATION: 981..1253
CC   FEATURE:
CC      NAME/KEY: exon
CC      LOCATION: 713..721
SQ   Sequence 4283 BP; 1023 A; 1095 C; 1114 G; 1051 T; 0 other;

     Query Match    28.4%;  Score 298;  DB 7;  Length 4283;
     Best Local Similarity   96.2%;  Pred. No. 8.01e-221;
     Matches  326;  Conservative  0;  Mismatches 10;  Indels  3;  Gaps  3;

Db    713 ATGGCTACAGGTAAGCGCGCCCCTAAAAATCCCTTTGG-CACAAATGTGTCCTGAGGGGAGAGG 771
          ||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Qy      6 ATGGCTACAGGTAAGCGCCCCTAAAAATCCCTTTGGGCACAAATGTGTCCTGAGGGGAGAGG 65

Db    772 CAGGGACCTGTAGATGGGGACGGGGGGCACTAAACCCTCAGGGTTTGGGGTTCTGAATGTGAG 831
          |||| |||||||||||||||||| |||||||||||||||| ||||||||| ||||| ||| ||
Qy     66 CACCGACCTGTAGATGGGGACGGGGGCACTAAACCCTCAGGTTTGGGGCTTCTCAATCTCAC 125

Db    832 TATCGCCATCTAAGCCCACTATTTGGCCAATCTCAGAAAAGCTCCTCGGCCTCCCCTGGAGG-A 890
          |||||||| ||||||||| |||||||||||||||||||||||||||  ||||||||||||| ||
Qy    126 TATCGCCATGTAAGCCCAGTATTTGGCCAATCTCAGAAAAGCTCCTC-CTCCCCTGGAGGA 184

Db    891 TGGAGAGAGAGAAAAAACAAACAGCTCCTGGAGCAGCAGGGAGGAGAGTGTTGGCCTTGTGCCT 950
          |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    185 TGGAGAGAGAAAAAACAAACAGCTCCTGGAGCAGCAGGGAGGAGAGTGTTGGCCTTGTGCCT 244

Db    951 CTCCCTCTGTTGCCCTCTGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCCTGCTTTT 1010
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    245 CTCCCTCTGTTGCCCTCTGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCCTGCTTTT 304

Db   1011 GGCCTGCTGCTCTGCCTGCCTGCCTTCAAGAGGGCAGTGCC 1049
          |||||||||||||||||||||||||||||||||||||||||
Qy    305 GGCCTGCTGCTCTGCCTGCCTGCCTTCAAGAGGGCAGTGCC 343
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Right column

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SQ   Sequence 4283 BP; 1023 A; 1095 C; 1114 G; 1051 T; 0 other;

     Query Match    28.4%;  Score 298;  DB 7;  Length 4283;
     Best Local Similarity   96.2%;  Pred. No. 8.01e-221;
     Matches  326;  Conservative  0;  Mismatches 10;  Indels  3;  Gaps  3;

Db    713 ATGGCTACAGGTAAGCGCGCCCCTAAAAATCCCTTTGG-CACAAATGTGTCCTGAGGGGAGAGG 771
          ||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Qy      6 ATGGCTACAGGTAAGCGCCCCTAAAAATCCCTTTGGGCACAAATGTGTCCTGAGGGGAGAGG 65

Db    772 CAGGGACCTGTAGATGGGGACGGGGGGCACTAAACCCTCAGGGTTTGGGGTTCTGAATGTGAG 831
          |||| |||||||||||||||||| |||||||||||||||| ||||||||| ||||| ||| ||
Qy     66 CACCGACCTGTAGATGGGGACGGGGGCACTAAACCCTCAGGTTTGGGGCTTCTCAATCTCAC 125

Db    832 TATCGCCATCTAAGCCCACTATTTGGCCAATCTCAGAAAAGCTCCTCGGCCTCCCCTGGAGG-A 890
          |||||||| ||||||||| |||||||||||||||||||||||||||  ||||||||||||| ||
Qy    126 TATCGCCATGTAAGCCCAGTATTTGGCCAATCTCAGAAAAGCTCCTC-CTCCCCTGGAGGA 184

Db    891 TGGAGAGAGAGAAAAAACAAACAGCTCCTGGAGCAGCAGGGAGGAGAGTGTTGGCCTTGTGCCT 950
          |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    185 TGGAGAGAGAAAAAACAAACAGCTCCTGGAGCAGCAGGGAGGAGAGTGTTGGCCTTGTGCCT 244

Db    951 CTCCCTCTGTTGCCCTCTGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCCTGCTTTT 1010
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    245 CTCCCTCTGTTGCCCTCTGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCCTGCTTTT 304
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Db 1011 GGCCTGCGTCCTGCGCTGCGCCTGGCTTCAAGAGGCAGTGCC 1049
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Qy  305 GGCCTGCGTCCTGCCTGGCTTCAAGAGGCAGTGCC 343
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RESULT 13
ID US-08-050-319B-53 STANDARD; DNA; UNC; 477 BP.

XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 53, Application US/08050319B.
XX
CC GENERAL INFORMATION:
CC Patent No. 5633145
CC APPLICANT: M.Feldmann, P.W.Gray,
CC APPLICANT: M.J.C. Turner, F.M Brennan
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC NUMBER OF SEQUENCES: 57
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Reed & Robbins
CC STREET: 635 Bryant Street
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/050,319B
CC FILING DATE: 10-May-1993
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Robbins, Roberta L.
CC REGISTRATION NUMBER: 33,208
CC REFERENCE/DOCKET NUMBER: 5150-0030
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 617-8999
CC TELEFAX: (415) 327-3231
CC INFORMATION FOR SEQ ID NO: 53:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 477 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: double
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA to mRNA
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 1..474
SQ Sequence 477 BP; 117 A; 122 C; 131 G; 107 T; 0 other;

```
Query Match        24.3%;
Best Local Similarity   98.9%;
  Matches  258;  Conservative  0;  Mismatches  3;  Indels  0;  Gaps  0;
Score 255;  DB 7;  Length 477;
Pred. No. 7.22e-185;

Qy  121 GATAGTGTGTCCCAAGGAAAAATATACCACCCTCAAAATAATTCGATTTGCTGTACC 180
        |||||||||||||||||||||||| ||||||||||||||||||| ||||||||||||
Db  344 GATAGTGTGTCCCAAGGAAAATATATCCACCCTCAAAATAATTCCATTTGCTGTACC 403

Qy  181 AAGTGCCACAAAAGGAAACCTACTTGTACAATGACTGTCCAGGCCCGGGCAGGATACGGAC 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  404 AAGTGCCACAAAAGGAAACCTACTTGTACAATGACTGTCCAGGCCCGGGCAGGATACGGAC 463

Qy  241 TGCAGGGAGTGTGAGAGCGGCGCTCCTTCACCGCTTCAGAAAAACCACCTCAGACACTGCCTC 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  464 TGCAGGGAGTGTGAGAGCGGCGCTCCTTCACCGCTTCAGAAAAACCACCTCAGACACTGCCTC 523
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Db  361 CGGGACACCGTGTGTACCTGC 381
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Qy  584 CGGGACACCGTGTGGGCTGC 604
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Db  301 AGCTGCTCCAAATCGCCGAAAGGAAAAATGGGGTCAGGTGGGGAGAGATCTCTTGTTCCACACAGTGGAC 360
         |||||||||||  ||||||||||||||  |||||||||||||||   |||||||| |||||||||||||||
Qy  524 AGCTGCTCCAAAATGCCGAAAGGAAAATGGGGTCAGGTGGAGATCTCTTCTTCCACACAGTGGAC 583
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RESULT 14
ID US-08-050-319B-51 STANDARD; DNA; UNC; 462 BP.

XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 51, Application US/08050319B.
XX
CC GENERAL INFORMATION:
CC Patent No. 5633145
CC APPLICANT: M.Feldmann, P.W.Gray,
CC APPLICANT: M.J.C. Turner, F.M Brennan
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC NUMBER OF SEQUENCES: 57
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Reed & Robbins
CC STREET: 635 Bryant Street
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/050,319B
CC FILING DATE: 10-May-1993
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Robbins, Roberta L.
CC REGISTRATION NUMBER: 33,208
CC REFERENCE/DOCKET NUMBER: 5150-0030
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 617-8999
CC TELEFAX: (415) 327-3231
CC INFORMATION FOR SEQ ID NO: 51:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 462 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: double
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA to mRNA
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 1..459
SQ Sequence 462 BP; 116 A; 119 C; 121 G; 106 T; 0 other;

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Query Match        16.1%;
Best Local Similarity  100.0%;
  Matches  169;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
Score 169;  DB 7;  Length 462;
Pred. No. 1.18e-113;

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Qy  601 CTGCAGGAAGAACCAGTACCGGCCATTATTGGAGTGAAAAACCTTTTCCAGTGCTTCAATTG 660

Db  300 CAGCCTCTGCCTCAATTGGGACCGTGCACCTCTCCTGCCAGGAGAAACAGAACACCGTGTG 359
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Qy      CAGCCTCTGCCTCAATTGGGACCGTGCACCTCTCCTGCCAGGAGAAACAGAACACCGTGTG
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Qy    661  CAGCCTCTGCCTCAATGGACGGTGGACCGTGCCACCTCTCCTCCGCCAGGAGAAACAGAGAACACCGTGTG  720
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RESULT 15
ID   US-08-187-756C-3 STANDARD; DNA; UNC; 534 BP.
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AC   xxxxxx
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DT   01-JAN-1900
XX
DE   Sequence 3, Application US/08187756C.
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CC   Patent No. 5597709
CC   GENERAL INFORMATION:
CC   APPLICANT: ROSEN, ET AL.
CC   TITLE OF INVENTION: Human Growth Hormone
CC   NUMBER OF SEQUENCES: 7
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
CC   ADDRESSEE: CECCHI, STEWART & OLSTEIN
CC   STREET: 6 BECKER FARM ROAD
CC   CITY: ROSELAND
CC   STATE: NEW JERSEY
CC   COUNTRY: USA
CC   ZIP: 07068
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: 3.5 INCH DISKETTE
CC   COMPUTER: IBM PS/2
CC   OPERATING SYSTEM: MS-DOS
CC   SOFTWARE: WORD PERFECT 5.1
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/187,756C
CC   FILING DATE: January 27, 1994
CC   CLASSIFICATION: 435
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER:
CC   FILING DATE:
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: FERRARO, GREGORY D.
CC   REGISTRATION NUMBER: 36,134
CC   REFERENCE/DOCKET NUMBER: 325800-55
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: 201-994-1700
CC   TELEFAX: 201-994-1744
CC   INFORMATION FOR SEQ ID NO: 3:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 534 BASE PAIRS
CC   TYPE: NUCLEIC ACID
CC   STRANDEDNESS: SINGLE
CC   TOPOLOGY: LINEAR
CC   MOLECULE TYPE: CDNA
SQ   Sequence 534 BP; 108 A; 166 C; 143 G; 117 T; 0 other;

Query Match   98.6%; Score 69; DB 6; Length 534;
Best Local Similarity   98.6%;
Matches   70; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Db   8 CAGGCTCCCGGACGTCCCGCTTCCTGGCCTTTTGGCCTGCTCTGCCGTTCCTGGCTTCAAG 67
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Qy   273 CAGGCTCCCGGACGTCCCGCTTCCTGGCCTTTTGGCCTGCTCTGCCGTTCCTGGCTTCAAG 332

Db   68 AGGGCAGTGCC 78
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Qy   333 AGGGCAGTGCC 343
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Search completed: Wed May 6 10:02:47 1998

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MPSRCH (TM)
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Release 3.0.5AA John F. Collins, Biocomputing Research Unit.
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Distribution rights by Oxford Molecular Ltd

MPsrch.pp   protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 6 08:27:00 1998;   MasPar time 4.88 Seconds
                                     394.142 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-8
Description: (1-336) from US08804166.pep
Perfect Score: 2541
Sequence: 1 SRTSLLLAFGLLCLPWLQEG.........PSLPSPSRLPGPSDTPILPQ 336

Scoring table: PAM 150
                Gap 11

Searched: 62627 seqs, 5720858 residues

Post-processing: Minimum Match 0%
                   Listing first 45 summaries

Database: a-issued

Statistics: Mean 30.838;   Variance 140.153;   scale 0.220
            1:back1 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:PCT90
            10:PCT91 11:PCT92 12:PCT93 13:PCT94 14:PCT95 15:PCT96

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB	% ID	ID	Description	Pred. No.
1	1322	52.0	455	7	US-08-321-	Sequence 2, Applicatio	1.11e-110
2	1322	52.0	455	7	US-08-050-	Sequence 25, Applicati	1.11e-110
3	1243	48.9	199	7	US-08-050-	Sequence 48, Applicati	2.75e-103
4	1025	40.3	145	6	US-08-425-	Sequence 2, Applicatio	6.14e-83
5	1025	40.3	145	6	US-08-425-	Sequence 2, Applicatio	6.14e-83
6	1020	40.1	145	6	US-08-298-	Sequence 1, Applicatio	1.79e-82
7	995	39.2	145	6	US-08-425-	Sequence 10, Applicati	3.81e-80
8	996	39.2	167	7	US-08-050-	Sequence 57, Applicati	3.07e-80
9	996	39.2	167	7	US-08-050-	Sequence 2, Applicati	3.07e-80
10	981	38.6	124	7	US-08-050-	Sequence 4, Applicati	7.64e-79
11	928	36.5	157	7	US-08-050-	Sequence 50, Applicati	6.44e-74
12	740	29.1	114	6	US-08-425-	Sequence 9, Applicati	1.61e-56
13	734	28.9	114	6	US-08-425-	Sequence 7, Applicati	5.77e-56
14	714	28.1	117	6	US-08-425-	Sequence 11, Applicati	4.01e-54
15	684	26.9	114	6	US-08-425-	Sequence 8, Applicati	2.31e-51
16	666	26.2	158	7	US-08-425-	Sequence 54, Applicati	1.04e-49
17	651	25.6	117	6	US-08-425-	Sequence 12, Applicati	2.47e-48
18	613	24.1	149	6	US-08-425-	Sequence 5, Applicati	7.49e-45
19	605	23.8	153	7	US-08-050-	Sequence 52, Applicati	4.04e-44
20	339	13.3	41	7	US-08-050-	Sequence 36, Applicatio	3.84e-20
21	324	12.8	40	7	US-08-050-	Sequence 26, Applicati	8.05e-19
22	318	12.5	43	7	US-08-050-	Sequence 31, Applicati	2.71e-18
23	298	11.7	39	7	US-08-050-	Sequence 40, Applicati	1.53e-16
24	296	11.6	45	1	5451527-1	Patent No. 5451527.	2.28e-16
25	287	11.3	111	6	US-08-425-	Sequence 4, Applicatio	1.39e-15
26	287	11.3	111	6	US-08-425-	Sequence 3, Applicatio	1.39e-15
27	282	11.1	112	6	US-08-425-	Sequence 6, Applicatio	3.77e-15
28	268	10.5	46	5	US-08-086-	Sequence 14, Applicati	6.14e-14
29	261	10.3	46	5	US-08-086-	Sequence 12, Applicati	2.47e-13
30	260	10.2	131	1	5177193-0	Patent No. 5177193.	3.01e-13
31	249	9.8	46	5	US-08-086-	Sequence 11, Applicati	2.65e-12
32	249	9.8	46	5	US-08-086-	Sequence 13, Applicati	2.65e-12
33	230	9.1	41	5	US-08-086-	Sequence 17, Applicati	1.10e-10
34	227	9.1	34	1	5451527-4	Patent No. 5451527.	1.98e-10
35	227	8.9	39	1	5451527-8	Patent No. 5451527.	1.98e-10
36	227	8.9	39	1	5451527-12	Patent No. 5451527.	1.98e-10
37	227	8.9	39	13	PCT-US94-0	Sequence 29, Applicatio	1.98e-10
38	225	8.9	325	0	PCT-US91-0	Sequence 2, Applicati	2.93e-10
39	225	8.9	326	0	PCT-US91-0	Sequence 2, Applicati	2.93e-10
40	221	8.7	326	5	US-08-292-	Sequence 4, Applicatio	6.38e-10
41	221	8.7	326	10	PCT-US91-0	Sequence 4, Applicatio	6.38e-10
42	212	8.3	355	5	US-08-086-	Sequence 15, Applicatio	3.65e-09
43	212	8.3	474	1	5395760-4	Patent No. 5395760.	5.38e-09
44	210	8.3	1	7	US-08-050-	Sequence 26, Applicatio	3.65e-09
45	209	8.2	36	1	5451527-5	Patent No. 5451527.	6.52e-09

ALIGNMENTS

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AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 2, Application US/08321668.
XX
Patent No. 5665859
CC   Sequence 2, Application US/08321668.
CC   GENERAL INFORMATION:
CC   APPLICANT: WALLACH, David
CC   APPLICANT: BRAKEBUSCH, Cord
CC   APPLICANT: VAROLOMEEV, Eugene
CC   APPLICANT: BATKIN, Michael
CC   TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
CC   TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
CC   NUMBER OF SEQUENCES: 42
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: BROWDY AND NEIMARK
CC   STREET: 419 Seventh Street, N.W., Suite 300
CC   CITY: Washington
CC   STATE: D.C.
CC   COUNTRY: USA
CC   ZIP: 20004
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: Patentin Release #1.0, Version #1.30
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/321,668
CC   FILING DATE: 12-OCT-1994
CC   CLASSIFICATION: 435
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: IL 107268
CC   FILING DATE: 12-OCT-1993
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: BROWDY, Roger L.
CC   REGISTRATION NUMBER: 25,618
CC   REFERENCE/DOCKET NUMBER: WALLACH-13
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: 202-628-5197
CC   TELEFAX: 202-737-3528
CC   TELEX: 248633
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CC  INFORMATION FOR SEQ ID NO: 2:
CC    SEQUENCE CHARACTERISTICS:
CC      LENGTH: 455 amino acids
CC      TYPE: amino acid
CC      TOPOLOGY: linear
CC    MOLECULE TYPE: protein
SQ  SEQUENCE 455 AA; 50494 MW; 1048031 CN;

Query Match             52.0%;  Score 1322;  DB 7;  Length 455;
Best Local Similarity 100.0%;  Pred. No. 1.11e-110;
Matches 171; Conservative  0; Mismatches  0; Indels  0; Gaps  0;

Qy   41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
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Db   23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Qy  101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
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Db   83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Qy  161 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 211
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Db  143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 193
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ID   US-08-050-319B-25   STANDARD;   PRT;   455 AA.
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AC   xxxxxx
XX
DT   01-JAN-1900
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DE   Sequence 25, Application US/08050319B.
XX
CC   Sequence 25, Application US/08050319B.
CC   Patent No. 5633145
CC   GENERAL INFORMATION:
CC     APPLICANT: M.Feldmann, P.W.Gray,
CC     APPLICANT: M.J.C. Turner, F.M Brennan
CC     TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC     TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC     NUMBER OF SEQUENCES: 57
CC     CORRESPONDENCE ADDRESS:
CC       ADDRESSEE: Reed & Robbins
CC       STREET: 635 Bryant Street
CC       CITY: Palo Alto
CC       STATE: California
CC       COUNTRY: USA
CC       ZIP: 94301
CC     COMPUTER READABLE FORM:
CC       MEDIUM TYPE: Floppy disk
CC       COMPUTER: IBM PC compatible
CC       OPERATING SYSTEM: PC-DOS/MS-DOS
CC       SOFTWARE: Patentin Release #1.0, version #1.25
CC     CURRENT APPLICATION DATA:
CC       APPLICATION NUMBER: US/08/050,319B
CC       FILING DATE: 10-May-1993
CC       CLASSIFICATION: 435
CC     ATTORNEY/AGENT INFORMATION:
CC       NAME: Robbins, Roberta L.
CC       REGISTRATION NUMBER: 33,208
CC       REFERENCE/DOCKET NUMBER: 5150-0030
CC     TELECOMMUNICATION INFORMATION:
CC       TELEPHONE: (415) 617-8999
CC       TELEFAX: (415) 327-3231
CC   INFORMATION FOR SEQ ID NO: 25:
CC     SEQUENCE CHARACTERISTICS:
CC       LENGTH: 455 amino acids
CC       TYPE: amino acid
CC       TOPOLOGY: linear
CC     MOLECULE TYPE: protein
SQ   SEQUENCE 455 AA; 50579 MW; 1048388 CN;
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AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 48, Application US/08050319B.
XX
CC   Sequence 48, Application US/08050319B.
CC   Patent No. 5633145
CC   GENERAL INFORMATION:
CC     APPLICANT: M.Feldmann, P.W.Gray,
CC     APPLICANT: M.J.C. Turner, F.M Brennan
CC     TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC     TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC     NUMBER OF SEQUENCES: 57
CC     CORRESPONDENCE ADDRESS:
CC       ADDRESSEE: Reed & Robbins
CC       STREET: 635 Bryant Street
CC       CITY: Palo Alto
CC       STATE: California
CC       COUNTRY: USA
CC       ZIP: 94301
CC     COMPUTER READABLE FORM:
CC       MEDIUM TYPE: Floppy disk
CC       COMPUTER: IBM PC compatible
CC       OPERATING SYSTEM: PC-DOS/MS-DOS
CC       SOFTWARE: Patentin Release #1.0, version #1.25
CC     CURRENT APPLICATION DATA:
CC       APPLICATION NUMBER: US/08/050,319B
CC       FILING DATE: 10-May-1993
CC       CLASSIFICATION: 435
CC     ATTORNEY/AGENT INFORMATION:
CC       NAME: Robbins, Roberta L.
CC       REGISTRATION NUMBER: 33,208
CC       REFERENCE/DOCKET NUMBER: 5150-0030
CC     TELECOMMUNICATION INFORMATION:
CC       TELEPHONE: (415) 617-8999
CC       TELEFAX: (415) 327-3231
CC   INFORMATION FOR SEQ ID NO: 48:
CC     SEQUENCE CHARACTERISTICS:
CC       LENGTH: 199 amino acids
CC       TYPE: amino acid
CC       TOPOLOGY: linear
CC     MOLECULE TYPE: protein
SQ   SEQUENCE 199 AA; 22186 MW; 195553 CN;

Query Match             48.9%;  Score 1243;  DB 7;  Length 199;
Best Local Similarity 99.4%;  Pred. No. 2.75e-103;
Matches 158; Conservative  0; Mismatches  1; Indels  0; Gaps  0;

Qy   41 DSVCPTGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
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Db   23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82
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Db  101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLLCLNGTVHLSCQE 160
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Qy   83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLLCLNGTVHLSCQE 142

Db  161 KONTVCTCHAGFFLRENECVSCSNCKKSLECTKICLPQI 199
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Qy  143 KONTVCTCHAGFFLRENECVSCSNCKKSLECTKICLPQI 181
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RESULT 4
ID US-08-425-673-2   STANDARD;   PRT;   145 AA.
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AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 2, Application US/08425673.
XX
CC Sequence 2, Application US/08425673.
CC Patent No. 5508261
CC GENERAL INFORMATION:
CC APPLICANT: Moyle, William R.
CC APPLICANT: Campbell, Robert K.
CC TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having
CC TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and
CC TITLE OF INVENTION: Methods For Preparing and Using Same
CC NUMBER OF SEQUENCES: 12
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Richard R. Muccino
CC STREET: P.O. Box 1267
CC CITY: Princeton
CC STATE: New Jersey
CC COUNTRY: USA
CC ZIP: 08551
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/425,673
CC FILING DATE:
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/717,151
CC FILING DATE: 18-JUN-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Muccino, Richard R.
CC REGISTRATION NUMBER: 32,538
CC REFERENCE/DOCKET NUMBER: UMD 1.0-004
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (609) 466-3407
CC TELEFAX: (609) 466-2760
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 145 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
SQ SEQUENCE 145 AA; 15544 MW; 114662 CN;

Query Match 40.3%; Score 1025; DB 6; Length 145;
Best Local Similarity 99.3%; Pred. No. 6.14e-83;
Matches 138; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db   67 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSSKAPP 126
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Qy  258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSSKAPP 317
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Qy  258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSSKAPP 317

Db  127 SLPSPSRLPGPSDTPILPQ 145
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Qy  318 SLPSPSRLPGPSDTPILPQ 336
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RESULT 5
ID US-08-425-673-1   STANDARD;   PRT;   145 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 1, Application US/08425673.
XX
CC Sequence 1, Application US/08425673.
CC Patent No. 5508261
CC GENERAL INFORMATION:
CC APPLICANT: Moyle, William R.
CC APPLICANT: Campbell, Robert K.
CC TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having
CC TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and
CC TITLE OF INVENTION: Methods For Preparing and Using Same
CC NUMBER OF SEQUENCES: 12
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Richard R. Muccino
CC STREET: P.O. Box 1267
CC CITY: Princeton
CC STATE: New Jersey
CC COUNTRY: USA
CC ZIP: 08551
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/425,673
CC FILING DATE:
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/717,151
CC FILING DATE: 18-JUN-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Muccino, Richard R.
CC REGISTRATION NUMBER: 32,538
CC REFERENCE/DOCKET NUMBER: UMD 1.0-004
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (609) 466-3407
CC TELEFAX: (609) 466-2760
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 145 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
SQ SEQUENCE 145 AA; 15544 MW; 114662 CN;

Query Match 40.3%; Score 1025; DB 6; Length 145;
Best Local Similarity 99.3%; Pred. No. 6.14e-83;
Matches 138; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db    7 PRCRPINATLAVEKEGCPVCITVNTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 66
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Qy  198 PRCRPINATLAVEKEGCPVCITVNTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Db   67 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSSKAPP 126
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Qy  258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSSKAPP 317
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Db 127 SLPSPSRLPGPSDTPILPQ 145
|||||||||||||||||||
Qy 318 SLPSPSRLPGPSDTPILPQ 336

RESULT 6
ID US-08-298-189B-1 STANDARD; PRT; 145 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 1, Application US/08298189B.
XX
CC Patent No. 5674727
CC GENERAL INFORMATION:
CC APPLICANT: Dr. Laurence A. Cole and Dr. Andrew Kardana
CC TITLE OF INVENTION: No. 5674727el Methods for Detecting Reproductive
CC TITLE OF INVENTION: Cancers or Tumors and Assay Products
CC TITLE OF INVENTION: Therefor
CC NUMBER OF SEQUENCES: 1
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Dr. Laurence A. Cole, c/o Dept. of Obstetrics and
CC STREET: 333 Cedar Street
CC CITY: New Haven
CC STATE: Connecticut
CC COUNTRY: USA
CC ZIP: 06510
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 3.5" diskette
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: Windows 95
CC SOFTWARE: Microsoft Word 7.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/298,189B
CC FILING DATE: 08/31/94
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Brian D. Voyce
CC REGISTRATION NUMBER: 28,917
CC REFERENCE/DOCKET NUMBER: DSI1
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 919-638-3939 or 803-272-1471
CC TELEFAX: 919-638-3939 or 803-272-1471
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 145 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: NO. 5674727 applicable
CC TOPOLOGY: Unknown
CC MOLECULE TYPE: subunit of hormone, specifically the
CC MOLECULE TYPE: beta(subunit of hCG
CC ORIGINAL SOURCE: human urine
CC FEATURE:
CC NAME/KEY: beta subunit of hCG that is nicked by GBNE
CC LOCATION: hCG
CC IDENTIFICATION METHOD: N-terminal sequence analysis
CC PUBLICATION INFORMATION:
CC AUTHORS: Keutmann et al a
CC TITLE: "A Receptor-binding Region in Human
CC Choriogonadotrophin/Lutropr
CC JOURNAL: Proc Nat'l Acad Sci USA
CC VOLUME: 84
CC ISSUE: NO. 5674727 applicable
CC PAGES: 2038-2042
CC DATE: 1987
SQ SEQUENCE 145 AA; 15476 MW; 116769 CN;

Query Match 40.1%; Score 1020; DB 7; Length 145;
Best Local Similarity 98.6%; Pred. No. 1.79e-82;
Matches 137; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 7 PRCRPINATLAVEKEGCPVCITVNTICAGYCPTMRVLQGVLPALPQVVCNYRDVRFES 66

Qy 198 PRCRPINATLAVEKEGCPVCITVNTICAGYCPTMRVLQGVLPALPQVVCNYRDVRFES 257
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 67 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKRAPP 126

Qy 258 IRLPGCPRGVNPVVSYAVALSCQCALCKKSTTDCGGPKDHPLTCDDPRFQDSSSSKRAPP 317
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 127 SLPSPSRLPGPSDTPILPQ 145
|||||||||||||||||||
Qy 318 SLPSPSRLPGPSDTPILPQ 336

RESULT 7
ID US-08-425-673-10 STANDARD; PRT; 145 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 10, Application US/08425673.
XX
CC Patent No. 5508261
CC GENERAL INFORMATION:
CC APPLICANT: Moyle, William R.
CC APPLICANT: Campbell, Robert K.
CC TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having
CC TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and
CC TITLE OF INVENTION: Methods For Preparing and Using Same
CC NUMBER OF SEQUENCES: 12
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Richard R. Muccino
CC STREET: P.O. Box 1267
CC CITY: Princeton
CC STATE: New Jersey
CC COUNTRY: USA
CC ZIP: 08551
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/425,673
CC FILING DATE:
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/717,151
CC FILING DATE: 18-JUN-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Muccino, Richard R.
CC REGISTRATION NUMBER: 32,538
CC REFERENCE/DOCKET NUMBER: UMD 1.0-004
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (609) 466-3407
CC TELEFAX: (609) 466-2760
CC INFORMATION FOR SEQ ID NO: 10:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 145 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
SQ SEQUENCE 145 AA; 15448 MW; 114931 CN;

Query Match 39.2%; Score 995; DB 6; Length 145;
Best Local Similarity 96.4%; Pred. No. 3.81e-80;
Matches 134; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Db 7 PRCRPINATLAVEKEGCPVCITVNTICAGYCPTMRVLQGVLPALPQVVCNYRDVRFES 66
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 198 PRCRPINATLAVEKEGCPVCITVNTICAGYCPTMRVLQGVLPALPQVVCNYRDVRFES 257

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Db   67  IRLPGCPRGVNPVVSYAVALSCOCALCDSDSTDCGGPKDHPLICDDPRFQDSSSKAPP 126
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   258 IRLPGCPRGVNPVVSYAVALSCOCALCRRSTTDCGGRKDHPLICDDPRFQDSSSSSKAPP 317

Db   127 SLPSPSRLPGPSDTPILPQ 145
         ||||||||||||||||||
Qy   318 SLPSPSRLPGPSDTPILPQ 336
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RESULT   8
ID   US-08-050-319B-57   STANDARD;   PRT;   167 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 57, Application US/0805019B.
XX
CC   Patent No. 5633145
CC   GENERAL INFORMATION:
CC   APPLICANT: M.Feldmann, P.W. Gray,
CC   APPLICANT: M.J.C. Turner, F.M Brennan
CC   TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC   TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC   NUMBER OF SEQUENCES: 57
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Reed & Robbins
CC   STREET: 635 Bryant Street
CC   CITY: Palo Alto
CC   STATE: California
CC   COUNTRY: USA
CC   ZIP: 94301
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: Patentin Release #1.0, version #1.25
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/050,319B
CC   FILING DATE: 10-May-1993
CC   CLASSIFICATION: 435
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Robbins, Roberta L.
CC   REGISTRATION NUMBER: 33,208
CC   REFERENCE/DOCKET NUMBER: 5150-0030
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (415) 617-8999
CC   TELEFAX: (415) 327-3231
CC   INFORMATION FOR SEQ ID NO: 57:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 167 amino acids
CC   TYPE: amino acid
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: protein
SQ   SEQUENCE 167 AA; 18626 MW; 139513 CN;

Query Match   39.2%; Score 996; DB 7; Length 167;
Best Local Similarity 100.0%; Pred. No. 3.07e-80;
Matches 127; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Db   41  DSVCPQGKYIHPQNNSICCTKCHGTYLYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   23  DSVCPQGKYIHPQNNSICCTKCHGTYLYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db   101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   83  SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db   161 KONTVCT 167
         |||||||
Qy   143 KONTVCT 149
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RESULT   9
ID   US-08-050-319B-2   STANDARD;   PRT;   167 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 2, Application US/0805019B.
XX
CC   Patent No. 5633145
CC   GENERAL INFORMATION:
CC   APPLICANT: M.Feldmann, P.W. Gray,
CC   APPLICANT: M.J.C. Turner, F.M Brennan
CC   TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC   TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC   NUMBER OF SEQUENCES: 57
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Reed & Robbins
CC   STREET: 635 Bryant Street
CC   CITY: Palo Alto
CC   STATE: California
CC   COUNTRY: USA
CC   ZIP: 94301
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: Patentin Release #1.0, version #1.25
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/050,319B
CC   FILING DATE: 10-May-1993
CC   CLASSIFICATION: 435
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Robbins, Roberta L.
CC   REGISTRATION NUMBER: 33,208
CC   REFERENCE/DOCKET NUMBER: 5150-0030
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (415) 617-8999
CC   TELEFAX: (415) 327-3231
CC   INFORMATION FOR SEQ ID NO: 2:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 167 amino acids
CC   TYPE: amino acid
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: protein
SQ   SEQUENCE 167 AA; 18626 MW; 139513 CN;

Query Match   39.2%; Score 996; DB 7; Length 167;
Best Local Similarity 100.0%; Pred. No. 3.07e-80;
Matches 127; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Db   41  DSVCPQGKYIHPQNNSICCTKCHGTYLYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   23  DSVCPQGKYIHPQNNSICCTKCHGTYLYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db   101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   83  SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db   161 KONTVCT 167
         |||||||
Qy   143 KONTVCT 149
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RESULT   10
ID   US-08-050-319B-4   STANDARD;   PRT;   124 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900

XX
DE   Sequence 4, Application US/08050319B.
XX   Patent No. 5633145
CC   GENERAL INFORMATION:
CC   APPLICANT: M.Feldmann, P.W. Gray,
CC   APPLICANT: M.J.C. Turner, F.M Brennan
CC   TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC   TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC   NUMBER OF SEQUENCES: 57
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Reed & Robbins
CC   STREET: 635 Bryant Street
CC   CITY: Palo Alto
CC   STATE: California
CC   COUNTRY: USA
CC   ZIP: 94301
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: Patentin Release #1.0, version #1.25
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/050,319B
CC   FILING DATE: 10-May-1993
CC   CLASSIFICATION: 435
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Robbins, Roberta L.
CC   REGISTRATION NUMBER: 33,208
CC   REFERENCE/DOCKET NUMBER: 5150-0030
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (415) 327-3231
CC   TELEFAX: (415) 327-3231
CC   INFORMATION FOR SEQ ID NO: 4:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 124 amino acids
CC   TYPE: amino acid
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: protein
SQ   SEQUENCE 124 AA; 14047 MW; 75840 CN;

Query Match   38.6%; Score 981; DB 7; Length 124;
Best Local Similarity 100.0%; Pred. No. 7.64e-79;
Matches 124; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db   1 VCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC 60
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   25 VCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC 84

Db   61 SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQ 120
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   85 SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQ 144

Db   121 NTVC 124
             |||
Qy   145 NTVC 148

RESULT 11
ID   US-08-050-319B-50   STANDARD;   PRT; 157 AA.
XX
AC   xxxxxx
DT   01-JAN-1900
XX
DE   Sequence 50, Application US/08050319B.
XX   Patent No. 5633145
CC   GENERAL INFORMATION:
CC   APPLICANT: M.Feldmann, P.W. Gray,
CC   APPLICANT: M.J.C. Turner, F.M Brennan

CC   TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC   TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC   NUMBER OF SEQUENCES: 57
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Reed & Robbins
CC   STREET: 635 Bryant Street
CC   CITY: Palo Alto
CC   STATE: California
CC   COUNTRY: USA
CC   ZIP: 94301
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: Patentin Release #1.0, version #1.25
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/050,319B
CC   FILING DATE: 10-May-1993
CC   CLASSIFICATION: 435
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Robbins, Roberta L.
CC   REGISTRATION NUMBER: 33,208
CC   REFERENCE/DOCKET NUMBER: 5150-0030
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (415) 327-3231
CC   TELEFAX: (415) 327-3231
CC   INFORMATION FOR SEQ ID NO: 50:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 157 amino acids
CC   TYPE: amino acid
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: protein
SQ   SEQUENCE 157 AA; 17570 MW; 122247 CN;

Query Match   36.5%; Score 928; DB 7; Length 157;
Best Local Similarity 97.5%; Pred. No. 6.44e-74;
Matches 119; Conservative   1; Mismatches   2; Indels   0; Gaps   0;

Db   36 DREKRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWS 95
             ||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   60 DIDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWS 119

Db   96 ENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLP 155
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   120 ENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLP 179

Db   156 QI 157
             ||
Qy   180 QI 181

RESULT 12
ID   US-08-425-673-9   STANDARD;   PRT; 114 AA.
XX
AC   xxxxxx
DT   01-JAN-1900
XX
DE   Sequence 9, Application US/08425673.
XX   Patent No. 5508261
CC   GENERAL INFORMATION:
CC   APPLICANT: Moyle, William R.
CC   APPLICANT: Campbell, Robert K.
CC   TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having
CC   TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and
CC   TITLE OF INVENTION: Methods For Preparing and Using Same
CC   NUMBER OF SEQUENCES: 12
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Richard R. Muccino
CC   STREET: P.O. Box 1267
CC   CITY: Princeton

```
CC   STATE: New Jersey
CC   COUNTRY: USA
CC   ZIP: 08551
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: PatentIn Release #1.0, Version #1.25
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/425,673
CC   FILING DATE:
CC   CLASSIFICATION: 514
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: US 07/717,151
CC   FILING DATE: 18-JUN-1991
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Muccino, Richard R.
CC   REGISTRATION NUMBER: 32,538
CC   REFERENCE/DOCKET NUMBER: UMD 1.0-004
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (609) 466-3407
CC   TELEFAX: (609) 466-2760
CC   INFORMATION FOR SEQ ID NO: 9:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 114 amino acids
CC   TYPE: amino acid
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: peptide
CC   HYPOTHETICAL: NO
CC   ANTI-SENSE: NO
SQ   SEQUENCE 114 AA; 12250 MW; 68564 CN;

     Query Match    29.18%;  Score 740;  DB 6;  Length 114;
     Best Local Similarity   93.3%;  Pred. No. 1.61e-56;
     Matches  97;  Conservative  1;  Mismatches 6;  Indels 0;  Gaps 0;

Qy    7 PRCRPINATLAVEKEGCPVCITVNIICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 66
         ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db  198 PRCRPINATLAVEKEGCPVCITVNTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Qy   67 IRLPGCPRGVNPVVSYAVALSCQCALCDSDSTDCGGPKDHPSYC 110
         |||||||||||||||||||||| :|||||||||||||  |
Db  258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTC 301

RESULT  13
ID   US-08-425-673-7       STANDARD;     PRT;    114 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 7, Application US/08425673.
XX
CC   Sequence 7, Application US/08425673.
CC   Patent No. 5508261
CC   GENERAL INFORMATION:
CC   APPLICANT: Moyle, William R.
CC   APPLICANT: Campbell, Robert K.
CC   TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having
CC   TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and
CC   TITLE OF INVENTION: Methods For Preparing and Using Same
CC   NUMBER OF SEQUENCES: 12
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Richard R. Muccino
CC   STREET: P.O. Box 1267
CC   CITY: Princeton
CC   STATE: New Jersey
CC   COUNTRY: USA
CC   ZIP: 08551
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC compatible
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CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: PatentIn Release #1.0, Version #1.25
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/425,673
CC   FILING DATE:
CC   CLASSIFICATION: 514
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: US 07/717,151
CC   FILING DATE: 18-JUN-1991
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Muccino, Richard R.
CC   REGISTRATION NUMBER: 32,538
CC   REFERENCE/DOCKET NUMBER: UMD 1.0-004
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (609) 466-3407
CC   TELEFAX: (609) 466-2760
CC   INFORMATION FOR SEQ ID NO: 7:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 114 amino acids
CC   TYPE: amino acid
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: peptide
CC   HYPOTHETICAL: NO
CC   ANTI-SENSE: NO
SQ   SEQUENCE 114 AA; 12401 MW; 67071 CN;

     Query Match    28.9%;  Score 734;  DB 6;  Length 114;
     Best Local Similarity   91.7%;  Pred. No. 5.77e-56;
     Matches  99;  Conservative  0;  Mismatches 9;  Indels 0;  Gaps 0;

Qy    7 PRCRPINATLAVEKEGCPVCITVNIICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 66
         ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db  198 PRCRPINATLAVEKEGCPVCITVNTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Qy   67 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCTVRGLGPSYCDDPR 114
         ||||||||||||||||||||||||||||||||||  | ||||
Db  258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPR 305

RESULT  14
ID   US-08-425-673-11      STANDARD;     PRT;    117 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 11, Application US/08425673.
XX
CC   Sequence 11, Application US/08425673.
CC   Patent No. 5508261
CC   GENERAL INFORMATION:
CC   APPLICANT: Moyle, William R.
CC   APPLICANT: Campbell, Robert K.
CC   TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having
CC   TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and
CC   TITLE OF INVENTION: Methods For Preparing and Using Same
CC   NUMBER OF SEQUENCES: 12
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Richard R. Muccino
CC   STREET: P.O. Box 1267
CC   CITY: Princeton
CC   STATE: New Jersey
CC   COUNTRY: USA
CC   ZIP: 08551
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: PatentIn Release #1.0, Version #1.25
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/425,673
CC   FILING DATE:
CC   CLASSIFICATION: 514
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CC   PRIOR APPLICATION DATA:
CC     APPLICATION NUMBER: US 07/717,151
CC     FILING DATE: 18-JUN-1991
CC   ATTORNEY/AGENT INFORMATION:
CC     NAME: Muccino, Richard R.
CC     REGISTRATION NUMBER: 32,538
CC     REFERENCE/DOCKET NUMBER: UMD 1.0-004
CC   TELECOMMUNICATION INFORMATION:
CC     TELEPHONE: (609) 466-3407
CC     TELEFAX: (609) 466-2760
CC   INFORMATION FOR SEQ ID NO: 11:
CC   SEQUENCE CHARACTERISTICS:
CC     LENGTH: 117 amino acids
CC     TYPE: amino acid
CC     TOPOLOGY: linear
CC     MOLECULE TYPE: peptide
CC     HYPOTHETICAL: NO
CC     ANTI-SENSE: NO
SQ   SEQUENCE 117 AA; 12890 MW; 72412 CN;

Query Match     28.1%;  Score 714;  DB 6;  Length 117;
Best Local Similarity  98.9%;  Pred. No. 4.01e-54;
Matches   93;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Db    7 PRCRPINATLAVEKEGCPVCITVNITICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 66
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Qy  198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Db   67 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDC 100
         ||||||||||||||||||||||||||||||||||
Qy  258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDC 291
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RESULT 15
ID   US-08-425-673-8      STANDARD;     PRT;   114 AA.
AC   xxxxxx
DT   01-JAN-1900
DE   Sequence 8, Application US/08425673.
CC   Sequence 8, Application US/0842567.
CC   Patent No. 550826;
CC   GENERAL INFORMATION:
CC     APPLICANT: Moyle, William R.
CC     APPLICANT: Campbell, Robert K.
CC     TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having
CC     TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and
CC     TITLE OF INVENTION: Methods For Preparing and Using Same
CC     NUMBER OF SEQUENCES: 12
CC   CORRESPONDENCE ADDRESS:
CC     ADDRESSEE: Richard R. Muccino
CC     STREET: P.O. Box 1267
CC     CITY: Princeton
CC     STATE: New Jersey
CC     COUNTRY: USA
CC     ZIP: 08551
CC   COMPUTER READABLE FORM:
CC     MEDIUM TYPE: Floppy disk
CC     COMPUTER: IBM PC compatible
CC     OPERATING SYSTEM: PC-DOS/MS-DOS
CC     SOFTWARE: PatentIn Release #1.0, Version #1.25
CC   CURRENT APPLICATION DATA:
CC     APPLICATION NUMBER: US/08/425,673
CC     FILING DATE:
CC     CLASSIFICATION: 514
CC   PRIOR APPLICATION DATA:
CC     APPLICATION NUMBER: US 07/717,151
CC     FILING DATE: 18-JUN-1991
CC   ATTORNEY/AGENT INFORMATION:
CC     NAME: Muccino, Richard R.
CC     REGISTRATION NUMBER: 32,538
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CC     REFERENCE/DOCKET NUMBER: UMD 1.0-004
CC   TELECOMMUNICATION INFORMATION:
CC     TELEPHONE: (609) 466-3407
CC     TELEFAX: (609) 466-2760
CC   INFORMATION FOR SEQ ID NO: 8:
CC   SEQUENCE CHARACTERISTICS:
CC     LENGTH: 114 amino acids
CC     TYPE: amino acid
CC     TOPOLOGY: linear
CC     MOLECULE TYPE: peptide
CC     HYPOTHETICAL: NO
CC     ANTI-SENSE: NO
SQ   SEQUENCE 114 AA; 12242 MW; 69571 CN;

Query Match     26.9%;  Score 684;  DB 6;  Length 114;
Best Local Similarity  94.7%;  Pred. No. 2.31e-51;
Matches   89;  Conservative  1;  Mismatches  4;  Indels  0;  Gaps  0;

Db    7 PRCRPINATLAVEKEGCPVCITVNITICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 66
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Qy  198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Db   67 IRLPGCPRGVNPVVSYAVALSCQCALCDSDSTDC 100
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Qy  258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDC 291
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Search completed: Wed May 6 08:27:26 1998
Job time : 26 secs.

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************************************************************************
*                                                                      *
*                         M P S R C H  (TM)                            *
*                                                                      *
*      Release 3.0.5AA  John F. Collins, Biocomputing Research Unit.    *
*           Copyright (c) 1993-1997 University of Edinburgh, U.K.       *
*                 Distribution rights by Oxford Molecular Ltd          *
*                                                                      *
************************************************************************
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MPsrch_nn   n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed May 6 11:17:48 1998;   MasPar time 73.35 Seconds
                                             934.882 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-7
Description: (1-1301) from US08804166.seq
Perfect Score: 1301
N.A. Sequence: 1 CTCGAGATGGCTACAGGTAA...........CACAATAAGGATCCCTCGAG 1301
Comp: GAGCTCTACCGATGTCCATT...........GTGTTATTCCTAGGGAGCTC

Scoring table: TABLE default
                 Gap 6

Nmatch STD :   Dbase 0; Query 0

Match :   Gap 6

Searched: 102136 seqs, 26354296 bases x 2

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database: n-issued
                 1:back1 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:PCT90
                 10:PCT91 11:PCT92 12:PCT93 13:PCT94 14:PCT95 15:PCT96

Statistics: Mean 8.845; Variance 4.678; scale 1.891

                 Pred. No. is the number of results predicted by chance to have a
                 score greater than or equal to the score of the result being printed,
                 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	514	39.5	2062	7	US-08-050-	Sequence 24, Applicati	0.00e+00
2	514	39.5	2175	7	US-08-321-	Sequence 1, Applicatio	0.00e+00
3	514	39.5	6889	6	US-08-286-	Sequence 2, Applicatio	0.00e+00
4	514	39.5	6889	14	PCT-US95-0	Sequence 47, Applicati	0.00e+00
5	474	36.4	600	7	US-08-050-	Sequence 2, Applicatio	0.00e+00
6	383	29.4	504	7	US-08-050-	Sequence 1, Applicatio	6.44e-278
7	381	29.3	501	7	US-08-050-	Sequence 56, Applicati	2.60e-276
8	372	28.6	372	7	US-08-050-	Sequence 1, Applicatio	2.60e-276
9	354	27.2	474	7	US-08-050-	Sequence 49, Applicati	4.39e-269
10	304	23.4	2771	7	US-08-273-	Sequence 1, Applicatio	1.27e-254
11	303	23.3	4283	7	US-08-343-	Sequence 3, Applicatio	7.97e-214
12	303	23.3	4283	7	US-08-445-	Sequence 1, Applicatio	7.97e-214
13	257	19.8	477	7	US-08-050-	Sequence 53, Applicati	3.56e-177
14	221	17.0	462	7	US-08-050-	Sequence 51, Applicati	1.21e-148
15	103	7.9	138	5	US-08-086-	Sequence 2, Applicatio	6.08e-57
16	99	7.6	138	5	US-08-086-	Sequence 1, Applicatio	6.30e-54
17	84	6.5	7218	7	US-08-232-	Sequence 14, Applicati	1.00e-42
18	69	5.3	534	7	US-08-187-	Sequence 3, Applicatio	9.66e-32
19	69	5.3	654	6	US-08-187-	Sequence 1, Applicatio	9.66e-32
20	59	4.5	321	4	US-07-920-	Sequence 23, Applicati	1.37e-24
21	59	4.5	321	6	US-08-314-	Sequence 23, Applicati	1.37e-24
22	59	4.5	2248	7	US-08-187-	Sequence 1, Applicatio	1.37e-24
23	52	4.0	597	6	US-08-636-	Sequence 1, Applicatio	1.08e-19
24	52	4.0	2248	7	US-08-780-	Sequence 1, Applicatio	1.08e-19
25	52	4.0	2248	6	US-08-369-	Sequence 2, Applicatio	1.08e-19
26	52	4.0	215	6	US-08-475-	Sequence 1, Applicatio	1.08e-19
27	42	3.2	7218	7	US-08-232-	Sequence 5, Applicatio	6.38e-13
28	41	3.2	633	7	US-08-238-	Sequence 14, Applicati	2.91e-12
29	38	2.9	633	7	US-08-388-	Sequence 7, Applicatio	2.61e-10
30	36	2.8	4810	7	US-08-453-	Sequence 7, Applicatio	4.97e-09
31	36	2.8	4810	13	PCT-US94-0	Sequence 7, Applicatio	4.97e-09
32	36	2.8	4810	12	PCT-US93-0	Sequence 3, Applicatio	4.97e-09
33	36	2.8	4810	14	PCT-US95-0	Sequence 3, Applicatio	4.97e-09
34	36	2.8	5125	7	US-08-188-	Sequence 11, Applicati	4.97e-09
35	36	2.8	5125	12	PCT-US93-0	Sequence 11, Applicati	4.97e-09
36	36	2.8	5323	7	US-08-453-	Sequence 9, Applicatio	4.97e-09
37	36	2.8	5323	12	PCT-US93-0	Sequence 9, Applicatio	4.97e-09
38	36	2.8	196	1	5171193.	Patent No. 5171193.	1.56e-06
39	32	2.5	196	1	5177193.	Patent No. 517193.	1.56e-06
40	32	2.5	215	6	US-08-239-	Sequence 1, Applicatio	1.56e-06
41	32	2.5	1006	7	US-08-050-	Sequence 14, Applicati	1.56e-05
42	30	2.3	33	7	US-08-050-	Sequence 94, Applicati	2.53e-05
43	26	2.0	74	14	PCT-US95-1	Sequence 13, Applicati	5.44e-03
44	26	2.0	105	5	US-07-865-	Sequence 13, Applicati	5.44e-03
45	26	2.0	242	7	US-08-273-	Sequence 1, Applicatio	5.44e-03

ALIGNMENTS

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ID   US-08-050-319B-24 STANDARD; DNA; UNC; 2062 BP.
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AC   xxxxxx
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DT   01-JAN-1900
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DE   Sequence 24, Application US/08050319B.
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CC   Patent No. 5633145
CC   Sequence 24, Application US/08050319B.
CC   GENERAL INFORMATION:
CC     APPLICANT: M.Feldmann, P.W. Gray,
CC     APPLICANT: M.J.C. Turner, F.M Brennan
CC     TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC     TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC     NUMBER OF SEQUENCES: 57
CC     CORRESPONDENCE ADDRESS:
CC       ADDRESSEE: Reed & Robbins
CC       STREET: 635 Bryant Street
CC       CITY: Palo Alto
CC       STATE: California
CC       COUNTRY: USA
CC       ZIP: 94301
CC     COMPUTER READABLE FORM:
CC       MEDIUM TYPE: Floppy disk
CC       COMPUTER: IBM PC compatible
CC       OPERATING SYSTEM: PC-DOS/MS-DOS
CC       SOFTWARE: Patentin Release #1.0, version #1.25
CC     CURRENT APPLICATION DATA:
CC       APPLICATION NUMBER: US/08/050,319B
CC       FILING DATE: 10-May-1993
CC       CLASSIFICATION: 435
CC     ATTORNEY/AGENT INFORMATION:
CC       NAME: Robbins, Roberta L.
CC       REGISTRATION NUMBER: 33,208
CC       REFERENCE/DOCKET NUMBER: 5150-0030
CC     TELECOMMUNICATION INFORMATION:
CC       TELEPHONE: (415) 617-8999
CC       TELEFAX: (415) 327-3231
CC   INFORMATION FOR SEQ ID NO: 24:
CC     SEQUENCE CHARACTERISTICS:
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CC   LENGTH: 2062 base pairs
CC   TYPE: nucleic acid
CC   STRANDEDNESS: double
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: cDNA to mRNA
CC   FEATURE:
CC   NAME/KEY: CDS
CC   LOCATION: 155..1519
SO   Sequence 2062 BP; 429 A; 617 C; 573 G; 443 T; 0 other;

Query Match   39.5%; Score 514; DB 7; Length 2062;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db   275 GATAGTGTGTGTCCCCAAGGAAAAATATATCCACCCTCAAAATAATAATTCGATTTGCTGTACC 334
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Qy   345 GATAGTGTGTGTCCCCAAGGAAAAATATATCCACCCTCAAAATAATAATTCGATTTGCTGTACC 404

Db   335 AAGTGCCACAAAGGAAACCTACTTGTACAATGACTGTCCAGGCCCGGGGGCAGGATACGGAC 394
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Qy   405 AAGTGCCACAAAGGAAACCTACTTGTACAATGACTGTCCAGGCCCGGGGGCAGGATACGGAC 464

Db   395 TGCAGGGAGTGTGAGAGCGGGCGGTCCTTCACCCGCTTCAGAAAAACCACCTCAGACACTGCCTC 454
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Qy   465 TGCAGGGAGTGTGAGAGCGGGCGGTCCTTCACCCGCTTCAGAAAAACCACCTCAGACACTGCCTC 524

Db   455 AGCTGCTCCAAATGCCGAAAAGGAAAATGGGTCAGGTGGGAGATCTCTTCTTCTTGCACAGTGGAC 514
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Qy   525 AGCTGCTCCAAATGCCGAAAAGGAAAATGGGTCAGGTGGGAGATCTCTTCTTCTTGCACAGTGGAC 584

Db   515 CGGGACACCGTGTGGCCTGCAGGAAGAACCAGTACCGGACGTATGTGAAAACCTT 574
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Db   575 TTCCAGTGCTTCAATTGCAGCCTCTCCCTCAATGGGAGACCGGTGCCACCTCTCTGCTGTGCCAGGAG 634
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   645 TTCCAGTGCTTCAATTGCAGCCTCTCCCTCAATGGGAGACCGGTGCCACCTCTCTGCTGTGCCAGGAG 704

Db   635 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTCTTCTTAAGAGAAAACGAGTGTGTC 694
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Qy   705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTCTTCTTAAGAGAAAACGAGTGTGTC 764

Db   695 TCCTGTAGTAACTGTAAGAAAAAGCCTGGAGTGTGCTACACCCGAGATTGAG 754
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Qy   765 TCCTGTAGTAACTGTAAGAAAAAGCCTGGAGTGTGCTACACCCGAGATTGAG 824

Db   755 AATGTTAAGGCCACTGAGGACTCAGGCACCACAG 788
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Qy   825 AATGTTAAGGCCACTGAGGACTCAGGCACCACAG 858

RESULT 2
ID   US-08-321-668-1 STANDARD; DNA; UNC; 2175 BP.

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AC   xxxxxx
XX
DT   01-JAN-1900
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DE   Sequence 1, Application US/08321668.
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GENERAL INFORMATION:
Patent No. 5665859
Sequence 1, Application US/08321668
APPLICANT: WALLACH, David
APPLICANT: BRAKEBUSCH, Cord
APPLICANT: VARFOLOMEEV, Eugene
APPLICANT: BATKIN, Michael
TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: BRODY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/321,668
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107268
FILING DATE: 12-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BRODY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH-13
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2175 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 256..1620
SQ   Sequence 2175 BP; 474 A; 641 C; 604 G; 456 T; 0 other;

Query Match   39.5%; Score 514; DB 7; Length 2175;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db   376 GATAGTGTGTGTCCCCAAGGAAAAATATATCCACCCTCAAAATAATAATTCGATTTGCTGTACC 435
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Qy   345 GATAGTGTGTGTCCCCAAGGAAAAATATATCCACCCTCAAAATAATAATTCGATTTGCTGTACC 404

Db   436 AAGTGCCACAAAGGAAACCTACTTGTACAATGACTGTCCAGGCCCGGGGGCAGGATACGGAC 495
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Qy   405 AAGTGCCACAAAGGAAACCTACTTGTACAATGACTGTCCAGGCCCGGGGGCAGGATACGGAC 464

Db   496 TGCAGGGAGTGTGAGAGCGGGCGGTCCTTCACCCGCTTCAGAAAAACCACCTCAGACACTGCCTC 555
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   465 TGCAGGGAGTGTGAGAGCGGGCGGTCCTTCACCCGCTTCAGAAAAACCACCTCAGACACTGCCTC 524

Db   556 AGCTGCTCCAAATGCCGAAAAGGAAAATGGGTCAGGTGGGAGATCTCTTCTTCTTGCACAGTGGAC 615
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Qy   525 AGCTGCTCCAAATGCCGAAAAGGAAAATGGGTCAGGTGGGAGATCTCTTCTTCTTGCACAGTGGAC 584

Db   616 CGGGACACCGTGTGGCCTGCAGGAAGAACCAGTACCGGACGTATGTGAAAACCTT 675
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Qy   585 CGGGACACCGTGTGGCCTGCAGGAAGAACCAGTACCGGACGTATGTGAAAACCTT 644

Db   676 TTCCAGTGCTTCAATTGCAGCCTCTCCCTCAATGGGAGACCGGTGCCACCTCTCTGCTGTGCCAGGAG 735
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   645 TTCCAGTGCTTCAATTGCAGCCTCTCCCTCAATGGGAGACCGGTGCCACCTCTCTGCTGTGCCAGGAG 704

Db   736 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTCTTCTTAAGAGAAAACGAGTGTGTC 795
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTCTTCTTAAGAGAAAACGAGTGTGTC 764

Db   796 TCCTGTAGTAACTGTAAGAAAAAGCCTGGAGTGTGCTACACCCGAGATTGAG 855
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   765 TCCTGTAGTAACTGTAAGAAAAAGCCTGGAGTGTGCTACACCCGAGATTGAG 824

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Db    856 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 889
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Qy    825 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 858


ID   US-08-286-740-2 STANDARD; DNA; UNC; 6889 BP.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 2, Application US/08286740.
XX
CC   Patent No. 5561053
CC   GENERAL INFORMATION:
CC   APPLICANT: Crowley, Craig W.
CC   TITLE OF INVENTION: METHOD FOR SELECTING HIGH-EXPRESSING
CC   TITLE OF INVENTION: HOST CELLS
CC   NUMBER OF SEQUENCES: 4
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Genentech, Inc.
CC   STREET: 460 Point San Bruno Blvd
CC   CITY: South San Francisco
CC   STATE: California
CC   COUNTRY: USA
CC   ZIP: 94080
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
CC   COMPUTER: IBM PC compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: patin (Genentech)
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/286,740
CC   FILING DATE: 05-AUG-1994
CC   CLASSIFICATION: 435
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER:
CC   FILING DATE:
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Lee, Wendy M.
CC   REGISTRATION NUMBER:
CC   REFERENCE/DOCKET NUMBER: 798
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: 415/225-1994
CC   TELEFAX: 415/952-9881
CC   TELEX: 910/371-7168
CC   INFORMATION FOR SEQ ID NO: 2:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 6889 bases
CC   TYPE: nucleic acid
CC   STRANDEDNESS: double
CC   TOPOLOGY: linear
SQ   Sequence 6889 BP; 1729 A; 1826 C; 1681 G; 1653 T; 0 other;

Query Match             39.5%;  Score 514;  DB 6;  Length 6889;
Best Local Similarity   100.0%;  Pred. No. 0.00e+00;
Matches  514;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Db   1725 GATAGTGTGTGTCCCAGGAGAAAATATATCCACCTCAAAATATATTCGATTTGCTGTACC 1784
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Qy    345 GATAGTGTGTGTCCCAGGAGAAAATATATCCACCTCAAAATATATTCGATTTGCTGTACC 404

Db   1785 AAGTGCCACAAAGGAACCTACTTGTACAATAGACTTGTCCAGGGCCCGGGGCAGGATTACGGAC 1844
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Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATAGACTTGTCCAGGGCCCGGGGCAGGATTACGGAC 464

Db   1845 TGCCAGGGAGTGTGAGAGCGGGCTCCTTCACCGCGCTTCAGAAAAACCACACTCAGACACTGCCTC 1904
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Qy    465 TGCCAGGGAGTGTGAGAGCGGGCTCCTTCACCGCGCTTCAGAAAAACCACACTCAGACACTGCCTC 524
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Qy    525 AGCTGCTTCCAAATGCCGAAAGGAAAATGGGTTCAGGTGGGAGAATCTCTTCTTCTTGCACAGTGGAC 584

Db   1965 CGGGACACCGTGTGTGGGCTGCAGGAAGAACCAGTACCGGCATTAATTGGAGTGAAAAACCTT 2024
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    585 CGGGACACCGTGTGTGGGCTGCAGGAAGAACCAGTACCGGCATTAATTGGAGTGAAAAACCTT 644

Db   2025 TTCCAGTGCTTCAATTGCACCCTCTGCCCTCAAATGGGACCGTGCACCTCTCCTGCCAGGAG 2084
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Qy    645 TTCCAGTGCTTCAATTGCACCCTCTGCCCTCAAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db   2085 AAACAGACACCGTGTGCACCTGCCATGCAGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 2144
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    705 AAACAGACACCGTGTGCACCTGCCATGCAGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Db   2145 TCCTGTAGTTAACTGTTAAGAAAAAGCCTGGAGTGCACGGAAGTTGTGCCTACCCCAGAGTTGAG 2204
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    765 TCCTGTAGTTAACTGTTAAGAAAAAGCCTGGAGTGCACGGAAGTTGTGCCTACCCCAGAGTTGAG 824

Db   2205 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 2238
          ||||||||||||||||||||||||||||||||||
Qy    825 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 858


ID   PCT-US95-09576-2 STANDARD; DNA; UNC; 6889 BP.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 2, Application PCT/US9509576.
XX
CC   GENERAL INFORMATION:
CC   APPLICANT: GENENTECH, INC.
CC   TITLE OF INVENTION: METHOD FOR SELECTING HIGH-EXPRESSING
CC   TITLE OF INVENTION: HOST CELLS
CC   NUMBER OF SEQUENCES: 4
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Genentech, Inc.
CC   STREET: 460 Point San Bruno Blvd
CC   CITY: South San Francisco
CC   STATE: California
CC   COUNTRY: USA
CC   ZIP: 94080
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
CC   COMPUTER: IBM PC compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: patin (Genentech)
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: PCT/US95/09576
CC   FILING DATE:
CC   CLASSIFICATION:
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 08/286740
CC   FILING DATE: 05-AUG-1994
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Lee, Wendy M.
CC   REGISTRATION NUMBER: 00.000
CC   REFERENCE/DOCKET NUMBER: 798PCT
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: 415/225-1994
CC   TELEFAX: 415/952-9881
CC   TELEX: 910/371-7168
CC   INFORMATION FOR SEQ ID NO: 2:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 6889 bases
CC   TYPE: nucleic acid
CC   STRANDEDNESS: double
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RESULT 3

RESULT 4

Left column:

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CC   TOPOLOGY: linear
SQ   Sequence 6889 BP; 1729 A; 1826 C; 1681 G; 1653 T; 0 other;
CC
CC   Query Match          39.5%;  Score 514;  DB 14;  Length 6889;
CC   Best Local Similarity   100.0%;  Pred. No. 0.00e+00;
CC   Matches  514;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
CC

Db  1725 GATAGTGTGTGTCCCACAAGGAAAAATATATCCACCCTCAAAATAATTAATTCGATTTGCTGTACC 1784
           ||||||||||||||||    ||||||||||||||||||||||||||||||||||||||||||||
Qy   345 GATAGTGTGTGTCCCAAGGAAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC      404

Db  1785 AAGTGCCACAAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGGCGCAGGATACGGAC 1844
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   405 AAGTGCCACAAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGGCGCAGGATACGGAC 464

Db  1845 TGCAGGGAGTGTGAGAGCGGGCCTCCTTCACCGCCTTCAGAAAACCACCTCAGACACTGCCTC 1904
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   465 TGCAGGGAGTGTGAGAGCGGGCCTCCTTCACCGCCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db  1905 AGCTGCTCCAAATGCCGAAAAGGAAATGGGTCAGGTGGGAGATCTCTTCTTCTTGCACAGTGGAC 1964
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   525 AGCTGCTCCAAATGCCGAAAAGGAAATGGGTCAGGTGGGAGATCTCTTCTTCTTGCACAGTGGAC 584

Db  1965 CGGGACACCGTGTGTGGGCTGCAGGAAGAAACCAGTACCGGGCATTATTGGGAGTGAAAAACCTT 2024
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   585 CGGGACACCGTGTGTGGGCTGCAGGAAGAAACCAGTACCGGGCATTATTGGGAGTGAAAAACCTT 644

Db  2025 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTCCTGCCAGGAG 2084
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTCCTGCCAGGAG 704

Db  2085 AAACAGAACACCGTGTGCACCGTGTTTCTTTCTTCTTCTAAGAGAAAAACGAGTGTGTC 2144
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   705 AAACAGAACACCGTGTGCACCGTGTTTCTTTCTTCTTCTAAGAGAAAAACGAGTGTGTC 764

Db  2145 TCCTGTGTAGTTAACTGTTAAGAAAAGCCTGGAGTGCACGAAGGTTGTGCCTACCCCCAGATTGAG 2204
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   765 TCCTGTGTAGTTAACTGTTAAGAAAAGCCTGGAGTGCACGAAGGTTGTGCCTACCCCCAGATTGAG 824

Db  2205 AATGTTAAGGGCACTGAGGACTCAGGCCACCACAG 2238
           ||||||||||||||||||||||||||
Qy   825 AATGTTAAGGGCACTGAGGACTCAGGCCACCACAG 858

RESULT  5
ID   US-08-050-319B-47 STANDARD; DNA; UNC; 600 BP.

XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 47, Application US/08050319B.
CC   Patent No. 5633145.
CC   GENERAL INFORMATION:
CC     APPLICANT:  M.Feldmann, P.W. Gray,
CC     APPLICANT:  M.J.C. Turner, F.M Brennan
CC   TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC   TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC   NUMBER OF SEQUENCES:  57
CC   CORRESPONDENCE ADDRESS:
CC     ADDRESSEE:  Reed & Robbins
CC     STREET:  635 Bryant Street
CC     CITY:  Palo Alto
CC     STATE:  California
CC     COUNTRY:  USA
CC     ZIP:  94301
CC   COMPUTER READABLE FORM:
CC     MEDIUM TYPE:  Floppy disk
CC     COMPUTER:  IBM PC compatible
CC     OPERATING SYSTEM:  PC-DOS/MS-DOS
```

Right column:

```
CC   SOFTWARE: PatentIn Release #1.0, version #1.25
CC   CURRENT APPLICATION DATA:
CC     APPLICATION NUMBER:  US/08/050,319B
CC     FILING DATE:  10-May-1993
CC     CLASSIFICATION:  435
CC   ATTORNEY/AGENT INFORMATION:
CC     NAME:  Robbins, Roberta L.
CC     REGISTRATION NUMBER:  33,208
CC     REFERENCE/DOCKET NUMBER:  5150-0030
CC   TELECOMMUNICATION INFORMATION:
CC     TELEPHONE:  (415) 617-8999
CC     TELEFAX:  (415) 327-3231
CC   INFORMATION FOR SEQ ID NO:  47:
CC     SEQUENCE CHARACTERISTICS:
CC       LENGTH:  600 base pairs
CC       TYPE:  nucleic acid
CC       STRANDEDNESS:  double
CC       TOPOLOGY:  linear
CC     MOLECULE TYPE:  cDNA to mRNA
CC     FEATURE:
CC       NAME/KEY:  CDS
CC       LOCATION:  1..597
SQ   Sequence 600 BP; 148 A; 157 C; 162 G; 133 T; 0 other;

CC   Query Match          36.4%;  Score 474;  DB 7;  Length 600;
CC   Best Local Similarity   99.4%;  Pred. No. 0.00e+00;
CC   Matches  477;  Conservative  0;  Mismatches  3;  Indels  0;  Gaps  0;

Db   121 GATAGTGTGTGTCCCACAAGGAAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   345 GATAGTGTGTGTCCCAAGGAAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC    404

Db   181 AAGTGCCACAAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGGCGCAGGATACGGAC 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   405 AAGTGCCACAAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGGCGCAGGATACGGAC 464

Db   241 TGCAGGGAGTGTGAGAGCGGGCCTCCTTCACCGCCTTCAGAAAACCACCTCAGACACTGCCTC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   465 TGCAGGGAGTGTGAGAGCGGGCCTCCTTCACCGCCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db   301 AGCTGCTCCAAATGCCGAAAAGGAAATGGGTCAGGTGGGAGATCTCTTCTTCTTGCACAGTGGAC 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   525 AGCTGCTCCAAATGCCGAAAAGGAAATGGGTCAGGTGGGAGATCTCTTCTTCTTGCACAGTGGAC 584

Db   361 CGGGACACCGTGTGTGGGCTGCAGGAAGAAACCAGTACCGGGCATTATTGGGAGTGAAAAACCTT 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   585 CGGGACACCGTGTGTGGGCTGCAGGAAGAAACCAGTACCGGGCATTATTGGGAGTGAAAAACCTT 644

Db   421 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTCCTGCCAGGAG 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTCCTGCCAGGAG 704

Db   481 AAACAGAACACCGTGTGCACCGTGCCATGCAGGTTTCTTTCTTAAGAGAAAAACGAGTGTGTC 540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   705 AAACAGAACACCGTGTGCACCGTGCCATGCAGGTTTCTTTCTTAAGAGAAAAACGAGTGTGTC 764

Db   541 TCCTGTAGTTAACTGTTAAGAAAAGCCTGGAGTGCACGAAGGTTGTGCCTACCCCCAGATTTAG 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   765 TCCTGTAGTTAACTGTTAAGAAAAGCCTGGAGTGCACGAAGGTTGTGCCTACCCCCAGATTGAG 824

RESULT  6
ID   US-08-050-319B-56 STANDARD; DNA; UNC; 504 BP.

XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 56, Application US/08050319B.
CC   Patent No. 5633145
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CC GENERAL INFORMATION:
CC APPLICANT: M.Feldmann, P.W. Gray,
CC APPLICANT: M.J.C. Turner, F.M Brennan
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC NUMBER OF SEQUENCES: 57
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Reed & Robbins
CC STREET: 635 Bryant Street
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/050,319B
CC FILING DATE: 10-May-1993
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Robbins, Roberta L.
CC REGISTRATION NUMBER: 33,208
CC REFERENCE/DOCKET NUMBER: 5150-0030
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 617-8999
CC TELEFAX: (415) 327-3231
SQ INFORMATION FOR SEQ ID NO: 56:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 504 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: double
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA to mRNA
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 1..501
SQ Sequence 504 BP; 122 A; 137 C; 138 G; 107 T; 0 other;

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Query Match             29.4%;  Score 383;  DB 7;  Length 504;
Best Local Similarity   100.0%;  Pred. No. 6.44e-278;
Matches    383;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Db        121 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy        345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db        181 AAGTGCCACAAAAGGAACCTACTTGTACAATGACTGTCCAGGCCGCCGGGGGCCAGGATACGGAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy        405 AAGTGCCACAAAAGGAACCTACTTGTACAATGACTGTCCAGGCCGCCGGGGGCCAGGATACGGAC 464

Db        241 TGCAGGGAGTGTGAGAGCGGCGGCTCCTTCACCGCCGCTTCAGAAAACCACCTCAGACACTGCCTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy        465 TGCAGGGAGTGTGAGAGCGGCGGCTCCTTCACCGCCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db        301 AGCTGCTCCAAATGCCGAAAAGGAAAATGGGTGCAGGTGGAGAGATCTCTTCTTGCACAGTGGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy        525 AGCTGCTCCAAATGCCGAAAAGGAAAATGGGTGCAGGTGGAGAGATCTCTTCTTGCACAGTGGAC 584

Db        361 CGGGACAACCGTGTGTGGCCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy        585 CGGGACAACCGTGTGTGGCCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db        421 TTTCCAGTGCTTCAATTGCAGCCTCTGCCTCATGGGAACGGTGCACCTCTCCTGCCAGGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy        645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db        481 AAACAGAACACCGTGTGCACCTG 503
              |||||||||||||||||||||||
Qy        705 AAACAGAACACCGTGTGCACCTG 727
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RESULT 7
ID   US-08-050-319B-1 STANDARD; DNA; UNC; 501 BP.
XX
AC   US-08-050-319B-1;
XX
DT   01-JAN-1900
XX
DE   xxxxxx
XX
Sequence 1, Application US/08050319B.
Patent No. 5633145

CC GENERAL INFORMATION:
CC APPLICANT: M.Feldmann, P.W. Gray,
CC APPLICANT: M.J.C. Turner, F.M Brennan
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC NUMBER OF SEQUENCES: 57
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Reed & Robbins
CC STREET: 635 Bryant Street
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/050,319B
CC FILING DATE: 10-May-1993
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Robbins, Roberta L.
CC REGISTRATION NUMBER: 33,208
CC REFERENCE/DOCKET NUMBER: 5150-0030
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 617-8999
CC TELEFAX: (415) 327-3231
SQ INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 501 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: double
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 1..501
SQ Sequence 501 BP; 121 A; 137 C; 137 G; 106 T; 0 other;

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Query Match             29.3%;  Score 381;  DB 7;  Length 501;
Best Local Similarity   100.0%;  Pred. No. 2.60e-276;
Matches    381;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        121 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Qy        181 AAGTGCCACAAAAGGAACCTACTTGTACAATGACTGTCCAGGCCGCCGGGGGCCAGGATACGGAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AAGTGCCACAAAAGGAACCTACTTGTACAATGACTGTCCAGGCCGCCGGGGGCCAGGATACGGAC 464

Qy        241 TGCAGGGAGTGTGAGAGCGGCGGCTCCTTCACCGCCGCTTCAGAAAACCACCTCAGACACTGCCTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 TGCAGGGAGTGTGAGAGCGGCGGCTCCTTCACCGCCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Qy        301 AGCTGCTCCAAATGCCGAAAAGGAAAATGGGTGCAGGTGGAGAGATCTCTTCTTGCACAGTGGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 AGCTGCTCCAAATGCCGAAAAGGAAAATGGGTGCAGGTGGAGAGATCTCTTCTTGCACAGTGGAC 584
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RESULT 8
ID   US-08-050-319B-3 STANDARD; DNA; UNC; 372 BP.

XX

AC   xxxxxx

XX

DT   01-JAN-1900

XX

DE   Sequence 3, Application US/08050319B.

XX

Sequence 3, Application US/08050319B.
Patent No. 5633145
GENERAL INFORMATION:
 APPLICANT: M.Feldmann, P.W. Gray,
 APPLICANT: M.J.C. Turner, F.M Brennan
 TITLE OF INVENTION: Modified human TNFalpha (Tumor
 TITLE OF INVENTION: Necrosis Factor alpha) Receptor
 NUMBER OF SEQUENCES: 57
 CORRESPONDENCE ADDRESS:
  ADDRESSEE: Reed & Robbins
  STREET: 635 Bryant Street
  CITY: Palo Alto
  STATE: California
  COUNTRY: USA
  ZIP: 94301
 COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: Patentin Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/050,319B
  FILING DATE: 10-May-1993
  CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
  NAME: Robbins, Roberta L.
  REGISTRATION NUMBER: 33,208
  REFERENCE/DOCKET NUMBER: 5150-0030
 TELECOMMUNICATION INFORMATION:
  TELEPHONE: (415) 617-8999
  TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
  LENGTH: 372 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: double
  TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
  NAME/KEY: CDS
  LOCATION: 1..372

SQ   Sequence 372 BP; 98 A; 102 C; 95 G; 77 T; 0 other;

Query Match   28.6%; Score 372; DB 7; Length 372;
Best Local Similarity 100.0%; Pred. No. 4.39e-269;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 GTGTGTCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACCAAGTGC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db    361 CGGGACACCGTGTGTGGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 420
          ||||||||||||||||||||||||||||||||||||||||
Qy    585 CGGGACACCGTGTTGTGGGCTGCAGGAAGAACCAGTACCGGCCATTATTGGAGTGAAAACCTT 644
Db    421 TTCCAGTTGCTTCAATTGCAGCCTCTTGCCTCCTCCTGCCAGGAG 480
          ||||||||||||||||||||||||
Qy    645 TTCCAGTTGCTTCAATTGCAGCCTCTCGCCTCCTGCCTGCCAGGAG 704
Db    481 AAACAGAACACCGTGTGCACC 501
          |||||||||||||||||
Qy    705 AAACAGAACACCGTGTGCACC 725
```

RESULT 9
ID   US-08-050-319B-49 STANDARD; DNA; UNC; 474 BP.

XX

AC   xxxxxx

XX

DT   01-JAN-1900

XX

DE   Sequence 49, Application US/08050319B.

XX

Sequence 49, Application US/08050319B.
Patent No. 5633145
GENERAL INFORMATION:
 APPLICANT: M.Feldmann, P.W. Gray,
 APPLICANT: M.J.C. Turner, F.M Brennan
 TITLE OF INVENTION: Modified human TNFalpha (Tumor
 TITLE OF INVENTION: Necrosis Factor alpha) Receptor
 NUMBER OF SEQUENCES: 57
 CORRESPONDENCE ADDRESS:
  ADDRESSEE: Reed & Robbins
  STREET: 635 Bryant Street
  CITY: Palo Alto
  STATE: California
  COUNTRY: USA
  ZIP: 94301
 COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: Patentin Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/050,319B
  FILING DATE: 10-May-1993
  CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
  NAME: Robbins, Roberta L.
  REGISTRATION NUMBER: 33,208
  REFERENCE/DOCKET NUMBER: 5150-0030
 TELECOMMUNICATION INFORMATION:
  TELEPHONE: (415) 617-8999
  TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 49:
 SEQUENCE CHARACTERISTICS:
  LENGTH: 474 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: double

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Qy    351 GTGTGTCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACCAAGTGC 410
Qy    411 CACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGGGCAGGAATACGGACTGCAGG 470
Qy    471 GAGTGTGAGAGCGGGTCCTTCACCGCTTCAGAAAAACCACACTTCAGCTGC 530
Qy    531 TCCAAAATGCCGAAAAGGAAAATGGGTCAGGTGAGATCTTCTTGCACAGTGGACCGGGGAC 590
Qy    591 ACCGGTGTGCTGGCTGCAGGAGGAAGAACCAGTACCGGCCATTATTGGAGTGAAAAACCTTCCAG 650
Qy    651 TGCTTCAATTGCAGCCTCTGCCTCCTGCCAGGAGACCGTGCACCTCTCCTGCCAGGAGAAACAG 710
Qy    711 AACACCGTGTGCC 722
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CC   TOPOLOGY: linear
CC   MOLECULE TYPE: cDNA to mRNA
CC   FEATURE:
CC   NAME/KEY: CDS
CC   LOCATION: 1..471
SQ   Sequence 474 BP; 110 A; 126 C; 132 G; 106 T; 0 other;

Query Match   27.2%; Score 354; DB 7; Length 474;
Best Local Similarity 97.8%; Pred. No. 1.22e-254;
Matches 362; Conservative   0; Mismatches   8; Indels   0; Gaps   0;

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Db   105 GGACAGGAGGAGAGAGAGTGTGAGGAGCGGGGGCTTCCTTCACCGCTTCAGAAAACCACTCAG 164
         ||| |||||||||||||||||||||||||||||| || |||||||||||||||||||||||||
Qy   455 GGATACGGACGCTGCAGGGAGGTGTGAGGAGCGGGGGCTTCCTTCACCGCTTCAGAAAACCACTCAG 514

Db   165 ACACTGCCCTCAGCTCCTCCAAAATGCCGAAAGGAAAATGGGTGCAGGTGGGAGAATCTCTTCTTG 224
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   515 ACACTGCCCTCAGCTGCTCCAAAATGCCGAAAGGAAAATGGGTCAGGTGGGAGAATCTCTTCTTG 574

Db   225 CACAGTGGACCGGGGACACCGTGTGTGGCCGGCAGAGAACCAGTACCGGCATTATTGGGAG 284
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   575 CACAGTGGACCGGGGACACCGTGTGTGGCCGGCAGAGAACCAGTACCGGCATTATTGGGAG 634

Db   285 TGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTCTCGCCTCCCTCAAATGGACCGTGCACCTCTC 344
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   635 TGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTCTCGCCTCCCTCAAATGGACCGTGCACCTCTC 694

Db   345 CTGCCAGGAGAAAACAGAAACACCGTGTGCACCTGCCATGCAGGTTTCTTTTCTAAGAGAAAA 404
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   695 CTGCCAGGAGAAAACAGAAACACCGTGTGCACCTGCCATGCAGGTTTCTTTTCTAAGAGAAAA 754

Db   405 CGAGTGTGTCTCCCTGAGTAACTGTGTAAGAGAAAAGCCTGGAGTGCACGAAGTGTGTGCCCTACC 464
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   755 CGAGTGTGTCTCCCTGAGTAACTGTGTAAGAGAAAAGCCTGGAGTGCACGAAGTTGTGTGCCTACC 814

Db   465 CCAGATTAG 474
         ||||||| ||
Qy   815 CCAGATTGAG 824
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RESULT 10
ID   US-08-273-411-5 STANDARD; DNA; UNC; 2771 BP.

XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 5, Application US/08273411.
XX

Sequence 5, Application US/08273411
Patent No. 5625124
GENERAL INFORMATION:
APPLICANT: Falk, Per
APPLICANT: Gordon, Jeffrey I.
TITLE OF INVENTION: Animal Model for Gastro-Intestinal
TITLE OF INVENTION: Disease
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 1100 Peachtree Street, Suite 2800
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/273,411
FILING DATE:

CC   CLASSIFICATION: 435
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Pabst, Patrea L.
CC   REGISTRATION NUMBER: 31,284
CC   REFERENCE/DOCKET NUMBER: WU106
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (404) 815-6555
CC   TELEFAX: (404) 815-6508
CC   INFORMATION FOR SEQ ID NO: 5:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 2771 base pairs
CC   TYPE: nucleic acid
CC   STRANDEDNESS: double
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: DNA (genomic)
CC   HYPOTHETICAL: NO
CC   ANTI-SENSE: NO
CC   PUBLICATION INFORMATION:
CC   AUTHORS: Sweetser, et al.
CC   JOURNAL: Genes & Dev.
CC   VOLUME: 2
CC   PAGES: 1318-1332
CC   DATE: 1988
CC   RELEVANT RESIDUES IN SEQ ID NO: 5: FROM 561 TO 629
CC   PUBLICATION INFORMATION:
CC   AUTHORS: Seeburg, et al.
CC   JOURNAL: DNA
CC   VOLUME: 1
CC   PAGES: 239-249
CC   DATE: 1982
CC   RELEVANT RESIDUES IN SEQ ID NO: 5: FROM 620 TO 2771
CC   PUBLICATION INFORMATION:
CC   AUTHORS: Sweetser, et al.
CC   JOURNAL: J. Biol. Chem.
CC   VOLUME: 261
CC   PAGES: 5553-5561
CC   DATE: 1986
CC   RELEVANT RESIDUES IN SEQ ID NO: 5: FROM 1 TO 617
SQ   Sequence 2771 BP; 666 A; 718 C; 704 G; 683 T; 0 other;

Query Match   23.4%; Score 304; DB 7; Length 2771;
Best Local Similarity 97.9%; Conservative   0; Pred. No. 1.27e-214;
Matches 331; Conservative   0; Mismatches   3; Indels   4; Gaps   2;

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Db   680 ATGGCTACAGGTAAGCGCCCCCTAAAAATCCCTTTGGGCACAATGTGTCCTGAGGGGAGG 739
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Qy     7 ATGGCTACAGGTAAGCGCCCCCTAAAAATCCCTTTGGGCACAATGTGTCCTGAGGGGAGG 66

Db   740 CAGCGACCTGTAGATGGGACGGGGCGCACTAACCCTCAGGTTTGGGGGCTTCTGAATG--AG 797
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||
Qy    67 CAGCGACCTGTAGATGGGACGGGGCGCACTAACCCTCAGGTTTGGGGGCTTCTGAATGTGAG 126

Db   798 TATCGCCATGTAAGCCCAGTAT--GGCCAATCTCAGAAAAGCTCCCTGGGTGTCCTGACTG 855
         |||||||||||||||||||||  |||||||||||||||||||||||||||||||||||||
Qy   127 TATCGCCATGTAAGCCCAGTATTGGCCAATGTCAGAAAAGCTCCTGGTCCCCTGGAGGGAT 186

Db   856 GGAGGAGAAAAACAAACAGCCTCCTGGAGCAGGGAGAGTGCTGGCCTTCATTGCTCTCCGC 915
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   187 GGAGGAGAAAAACAAACAGCCTCCTGGAGCAGGGAGAGTGCTGGCCTTCATTGCTCTCCGC 246

Db   916 TCCCTCTGTTGCCCTCTGGTTTTCTCCCCAGGCTCCCCGACGTCCCTGCTCCTGGCTTTTG 975
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   247 TCCCTCTGTTGCCCTCTGGTTTTCTCCCCAGGCTCCCCGACGTCCCTGCTCCTGGCTTTTG 306

Db   976 GCCTGCTCTGCCTGCCCCTGGCTTCAACGAGGGCAGTGCC 1013
         |||||||||||||||||||||||||||||||||||||||||
Qy   307 GCCTGCTCTGCCTGCCCCTGGCTTCAACGAGGGCAGTGCC 344
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RESULT 11
ID   US-08-343-401A-3 STANDARD; DNA; UNC; 4283 BP.
XX

AC xxxxxx
XX
DT 01-JAN-1900
XX
XX
DE Sequence 3, Application US/08343401A.
   Patent No. 5661132
XX
XX
SQ Sequence 3, Application US/08343401A.
   GENERAL INFORMATION:
CC   APPLICANT: Swain, William F
CC   APPLICANT: Macklin, Michael D
CC   APPLICANT: Eriksson, Elof
CC   APPLICANT: Andree, Christophe
CC   TITLE OF INVENTION: Improved Wound Healing
CC   NUMBER OF SEQUENCES: 4
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Quarles & Brady
CC   STREET: PO Box 2113
CC   CITY: Madison
CC   STATE: WI
CC   COUNTRY: USA
CC   ZIP: 53701-2113
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC Compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: Patentin Release #1.0, Version #1.30
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/343,401A
CC   FILING DATE: 22-NOV-1994
CC   CLASSIFICATION: 514
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Seay, Nicholas J
CC   REGISTRATION NUMBER: 27,386
CC   REFERENCE/DOCKET NUMBER: 11-229-9103-9
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: 608-251-5000
CC   TELEFAX: 608-251-9166
CC INFORMATION FOR SEQ ID NO: 3:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 4283 base pairs
CC   TYPE: nucleic acid
CC   STRANDEDNESS: double
CC   TOPOLOGY: circular
CC   MOLECULE TYPE: DNA (genomic)
CC   IMMEDIATE SOURCE:
CC   CLONE: pWRG1630
CC   FEATURE:
CC   NAME/KEY: exon
CC   LOCATION: 713..721
CC   FEATURE:
CC   NAME/KEY: exon
CC   LOCATION: 981..1253
CC   FEATURE:
CC   NAME/KEY: CDS
CC   LOCATION: join(713..721, 981..1253)
CC   FEATURE:
CC   NAME/KEY: sig_peptide
CC   LOCATION: 713..1049
SQ Sequence 4283 BP; 1023 A; 1095 C; 1114 G; 1051 T; 0 other;

Query Match   23.3%; Score 303; DB 7; Length 4283;
Best Local Similarity 95.6%; Pred. No. 7.97e-214;
Matches 323; Conservative   0; Mismatches 14; Indels   1; Gaps   1;

Db   713 ATGGCTACAGGTAAGCGCGCCCTAAAATCCCTTGG-CACAATGTGTCCTGAGGGGGAGG 771
           |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Qy   7 ATGGCTACAGGTAAGCGCGCCCTAAAATCCCTTTGGGCACAATGTGTCCTGAGGGGGAGG 66

Db   772 CAGGGACCTGTAGAGTGGGGACGGGGGCACTAACCCTCAGGGTTTGGGGTTCTGAATGTGAG 831
           |||||||||||||| |||||||||||| |||||||||||||| ||||||| |||||||||||
Qy   67 CAGGGACCTGTAGAATGGGGACGGGGCACTAACCCTCAGTGTTTGGGGCTTCTGAATGTGAG 126

Db   832 TATCGGCCATCTAAGCCCAGTATTTGGCCAANTCTCAGAAAAGCTTCTTGGCTTCCCGGAGGAT 891
           ||||||||| |||||||||||||||||||||| | ||||||||| ||||||||||| ||| |||
Qy   127 TATCGGCCATGTAAGCCCAGTATTTGGCCAANTGTCAGAAAAGCTCCTTGGCTTCCCGGAGGAT 186

Db   892 GGAGAGAGAAAAACAAAACACCTCCTGGAGCAGGGAGAGTGTTGGGCCTTCCTCTCCGGGC 951
           |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||| |
Qy   187 GGAGAGAGAAAAACAAAACACCTCCTGGAGCAGGGAGAGTGTCGGGCCTTCCTCTCCGGC 246

Db   952 TCCCTCTGTTGCCCTCTGTTCTCCCCAGCCTCCGGGACGTCCCGGACGTCCCGGACGTGCCG 1011
           ||||||||||||||||| |||||||| |||||||||||||||||||||||||||||||| |||
Qy   247 TCCCTCTGTTGCCCTCTGGTTCTCCCAGCCTCCGGGACGTCCCGGACGTCCCGGACGTCCCGG 306

Db   1012 GCCTGCTTCTGCCTGCCCTGCCTTCAAGAGAGGGCAGTGCC 1049
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Qy   307 GCCTGCTTCTGCCTGCCCTGCCTTCAAGAGAGGGCAGTGCC 344

SQ Sequence 4283 BP; 1023 A; 1095 C; 1114 G; 1051 T; 0 other;

RESULT 12
ID US-08-445-265A-1 STANDARD; DNA; UNC; 4283 BP.
XX
AC xxxxxx
AC
XX
DT 01-JAN-1900
XX
XX
DE Sequence 1, Application US/08445265A.
   Patent No. 5697901
XX
XX
SQ Sequence 1, Application US/08445265A.
   GENERAL INFORMATION:
CC   APPLICANT: Eriksson, Elof
CC   TITLE OF INVENTION: GENE DELIVERY BY MICRONEEDLE INJECTION
CC   NUMBER OF SEQUENCES: 4
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Quarles & Brady
CC   STREET: 1 South Pinckney Street
CC   CITY: Madison
CC   STATE: WI
CC   COUNTRY: US
CC   ZIP: 53703
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC Compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: Patentin Release #1.0, Version #1.30
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/445,265A
CC   FILING DATE:
CC   CLASSIFICATION: 604
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Seay, Nicholas J
CC   REGISTRATION NUMBER: 27386
CC   REFERENCE/DOCKET NUMBER: 110229.91080
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: 608-251-5000
CC   TELEFAX: 608-251-9166
CC INFORMATION FOR SEQ ID NO: 1:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 4283 base pairs
CC   TYPE: nucleic acid
CC   STRANDEDNESS: double
CC   TOPOLOGY: circular
CC   MOLECULE TYPE: other nucleic acid
CC   DESCRIPTION: /desc = "Plasmid DNA"
CC   FEATURE:
CC   NAME/KEY: CDS
CC   LOCATION: join(713..721, 981..1250)
SQ Sequence 4283 BP; 1023 A; 1095 C; 1114 G; 1051 T; 0 other;

Query Match   23.3%; Score 303; DB 7; Length 4283;
Best Local Similarity 95.6%; Pred. No. 7.97e-214;
Matches 323; Conservative   0; Mismatches 14; Indels   1; Gaps   1;

Db 713 ATGGCTACAGGTAAGCCCCCTAAAAATCCCTTTGG-CACAATGTGTCTGAGGGAGG 771
        ||||||||||||||||| ||||||||||||||||| |||||||||||||||||||||
Qy   7 ATGGCTACAGGTAAGCGGCGCCCCTAAAAATCCCTTTGGGCACAATGTGTCTGAGGGAGAGG 66

Db 772 CAGCGACCTGTAGATGGGACGGGGGCGCACTAACCCTCACGGGTTGGAGGGTTCGAATGTGAG 831
        |||||||||||||||||||||||||||| ||||||||||||||||| ||||||||||||||
Qy   67 CAGCGACCTGTAGATGGGACGGGGGCGCACTAACCCTCACGGGTTGGGGCTTCGAATGTGAG 126

Db 832 TATCGGCCATCTAAGCCCAGTATTTGGGCCAAATCTTCAGAAAGCTCCTGGCTTCCCCTGGCC 891
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Qy 127 TATCGGCCATGTAAGCCCAGTATTTGGGCCAAATGTTCAGAAAGCTCCTGGCTTCCCCTGGGAT 186

Db 892 GGAGAGAGAGAAAACAAACAGCTCCTGAGCAGCAGGGAGGAGAGTGTTGGCCTCTTGCTCTCCGGC 951
        ||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Qy 187 GGAGAGAGAGAAAACAAACAAACCTCCTGGAGCAGCAGGGAGGAGAGTGCTGCTGCTCCTCCGGC 246

Db 952 TCCCTCGTGTGGCCCTCTGGTTTCTCCCCAGGCCTCCCGGACAGTGCCCTGCTCCTGGCTTTTG 1011
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Qy 247 TCCCTCGTTGCCCTCTGGTTTCTCCCCAGGCCTCCCGGACGTCCCTGCTCCTGGCTTTTG 306

Db 1012 GCTGCTCTGCCCTGCCCCCTGGGCTTCAAGAGGGCAGTGCC 1049
        |||||||||||||||||||||||||||||||||||||||||
Qy 307 GCTGCTCTGCCCTGGCCCCTGGGCTTCAAGAGGGCAGTGCC 344

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DT 01-JAN-1900

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DE Sequence 53, Application US/08050319B.

CC Patent No. 5633145

CC GENERAL INFORMATION:

CC   APPLICANT: M.Feldmann, P.W. Gray,

CC   APPLICANT: M.J.C. Turner, F.M Brennan

CC   TITLE OF INVENTION: Modified human TNFalpha (Tumor

CC   TITLE OF INVENTION: Necrosis Factor alpha) Receptor

CC   NUMBER OF SEQUENCES: 57

CC   CORRESPONDENCE ADDRESS:

CC   ADDRESSEE: Reed & Robbins

CC   STREET: 635 Bryant Street

CC   CITY: Palo Alto

CC   STATE: California

CC   COUNTRY: USA

CC   ZIP: 94301

CC   COMPUTER READABLE FORM:

CC   MEDIUM TYPE: Floppy disk

CC   COMPUTER: IBM PC compatible

CC   OPERATING SYSTEM: PC-DOS/MS-DOS

CC   SOFTWARE: Patentin Release #1.0, version #1.25

CC   CURRENT APPLICATION DATA:

CC   APPLICATION NUMBER: US/08/050,319B

CC   FILING DATE: 10-May-1993

CC   CLASSIFICATION: 435

CC   ATTORNEY/AGENT INFORMATION:

CC   NAME: Robbins, Roberta L.

CC   REGISTRATION NUMBER: 33,208

CC   REFERENCE/DOCKET NUMBER: 5150-0030

CC   TELECOMMUNICATION INFORMATION:

CC   TELEPHONE: (415) 617-8999

CC   TELEFAX: (415) 327-3231

CC   INFORMATION FOR SEQ ID NO: 53:

CC   SEQUENCE CHARACTERISTICS:

CC   LENGTH: 477 base pairs

CC   TYPE: nucleic acid

CC   STRANDEDNESS: double

CC   TOPOLOGY: linear

CC   MOLECULE TYPE: cDNA to mRNA

RESULT 13
ID US-08-050-319B-53 STANDARD; DNA; UNC; 477 BP.

CC   FEATURE:

CC   NAME/KEY: CDS

CC   LOCATION: 1..474

SQ Sequence 477 BP; 117 A; 122 C; 131 G; 107 T; 0 other;

CC Query Match   19.8%; Score 257; DB 7; Length 477;
CC Best Local Similarity 99.2%; Pred. No. 3.56e-177;
CC Matches 259; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

Db 121 GATAGTGTGTGTCCCCAAGGAAAAATATATATNCCACCCTCAAAATAATTCGATTTGTGTACC 180
        |||||||||||||||||||||||||||||||| ||||||||||||||||||||| |||||||
Qy 345 GATAGTGTGTGTCCCCAAGGAAAAATATATCCCCAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db 181 AAGTGCCACAAAAGGAAACCTTACTTGTACAATGACTGTCCAGGCCCCGGGGGCCGGGATACGGAC 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 405 AAGTGCCACAAAAGGAAACCTTACTTGTACAATGACTGTCCAGGCCCCGGGGGCCGGGATACGGAC 464

Db 241 TGCAGGGAGTGTGAGAGCGCGCCTCTTCCACCGGCTTCAGAAAACCACCTCAGACACTGCCCTC 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 465 TGCAGGGAGTGTGAGAGCGCGCCTCTTCCACCGGCTTCAGAAAACCACCTCAGACACTGCCCTC 524

Db 301 AGCTGCTCCAAATGCCGAAAAGGAAAATGGGTCAGGTGGGAGATCTCTTCTTGCACAGTGGGAC 360
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Qy 525 AGCTGCTCCAAATGCCGAAAAGGAAAATGGGTCAGGTGGGAGATCTCTTCTTGCACAGTGGGAC 584

Db 361 CGGGACACCGTGTGTACCTGC 381
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Qy 585 CGGGACACCGTGTGTGGCTGC 605

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AC

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DT 01-JAN-1900

XX

DE Sequence 51, Application US/08050319B.

CC Patent No. 5633145

CC GENERAL INFORMATION:

CC   APPLICANT: M.Feldmann, P.W. Gray,

CC   APPLICANT: M.J.C. Turner, F.M Brennan

CC   TITLE OF INVENTION: Modified human TNFalpha (Tumor

CC   TITLE OF INVENTION: Necrosis Factor alpha) Receptor

CC   NUMBER OF SEQUENCES: 57

CC   CORRESPONDENCE ADDRESS:

CC   ADDRESSEE: Reed & Robbins

CC   STREET: 635 Bryant Street

CC   CITY: Palo Alto

CC   STATE: California

CC   COUNTRY: USA

CC   ZIP: 94301

CC   COMPUTER READABLE FORM:

CC   MEDIUM TYPE: Floppy disk

CC   COMPUTER: IBM PC compatible

CC   OPERATING SYSTEM: PC-DOS/MS-DOS

CC   SOFTWARE: Patentin Release #1.0, version #1.25

CC   CURRENT APPLICATION DATA:

CC   APPLICATION NUMBER: US/08/050,319B

CC   FILING DATE: 10-May-1993

CC   CLASSIFICATION: 435

CC   ATTORNEY/AGENT INFORMATION:

CC   NAME: Robbins, Roberta L.

CC   REGISTRATION NUMBER: 33,208

CC   REFERENCE/DOCKET NUMBER: 5150-0030

CC   TELECOMMUNICATION INFORMATION:

CC   TELEPHONE: (415) 617-8999

CC   TELEFAX: (415) 327-3231

CC   INFORMATION FOR SEQ ID NO: 51:

CC   SEQUENCE CHARACTERISTICS:

RESULT 14
ID US-08-050-319B-51 STANDARD; DNA; UNC; 462 BP.

CC   LENGTH: 462 base pairs
CC   TYPE: nucleic acid
CC   STRANDEDNESS: double
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: cDNA to mRNA
CC   FEATURE:
CC   NAME/KEY: CDS
CC   LOCATION: 1..459
SQ   Sequence 462 BP; 116 A; 119 C; 121 G; 106 T; 0 other;

Query Match   17.0%; Score 221; DB 7; Length 462;
Best Local Similarity 99.6%; Pred. No. 1.21e-148;
Matches 222; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Db   240 CTGCAGGAAGAAACCAGTACCGGCCATTATTGGAGTGAAAAACCTTTTTCCAGTGCTTCAATTG 299
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Qy   602 CTGCAGGAAGAACCAGTACCGGCCATTATTGGAGTGAAAAACCTTTTTCCAGTGCTTCAATTG 661

Db   300 CAGGCTCTGCCTCAATGGGACCGTGCGACCTTCTCCTGCCAGGAGAAACAGAACACACCGTGTG 359
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Qy   662 CAGCCTCTGCCTCAATGGGACCGTGCGACCTTCTCCTGCCAGGAGAAACAGAACACACCGTGTG 721

Db   360 CACCTGCCATCCAGGTTTCTTTTCTAAGAGAAAAACGAGTGTGTCTCCTGTAGTAACTGTAA 419
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   722 CACCTGCCATGCAGGTTTCTTTCTAAGAGAAAAACGAGTGTGTCTCCCGTAGTAACTGTAA 781

Db   420 CACCTGCCATGCAGGTTTCTTTCTAAGAGAAAAACGAGTGTGTCTCCCGTAGTAACTGTAA 462
         |||||||||||||||||||||||||||||||||||||||||||
Qy   782 GAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 824

CC   TYPE: nucleic acid
CC   STRANDEDNESS: double
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: DNA (genomic)
CC   ANTI-SENSE: NO
CC   HYPOTHETICAL: NO
CC   ORIGINAL SOURCE:
CC   ORGANISM: Homo sapiens
CC   DEVELOPMENTAL STAGE: Adult
SQ   Sequence 138 BP; 24 A; 51 C; 42 G; 21 T; 0 other;

Query Match   7.9%; Score 103; DB 5; Length 138;
Best Local Similarity 99.0%; Pred. No. 6.08e-57;
Matches 104; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Db   34 CCACGGTGCCACCCCATCAATGCCACCCTGGCGTGGGAGAAGGAGGGCTGCCCCGGTGTGC 93
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Qy   870 CCACGGTGCCGCGCCCCATCAATGCCACCCTGGCGTGTGGGAGAAGGAGGGCTGCCCCGGTGTGC 929

Db   94 ATCACCGTCAACACACCACCATCTGTGCCGGCTTACTGCCCACCATG 138
         ||||||||||||||||||||||||||||||||||||||||||||||
Qy   930 ATCACCGTCAACACACCACCATCTGTGCCGGCTTACTGCCCACCATG 974

Search completed: Wed May 6 11:19:13 1998
Job time : 85 secs.

RESULT   15
ID   US-08-086-915-2 STANDARD; DNA; UNC; 138 BP.
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AC   xxxxxx
XX
DT   01-JAN-1900
XX
XX
DE   Sequence 2, Application US/08086915.
XX
Patent No. 5444167
Sequence 2, Application US/08086915.
GENERAL INFORMATION:
APPLICANT: Pettersson, Kim SI
TITLE OF INVENTION: Variant Luteinizing Hormone Encoding DNA
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Adduci, Mastriani, Schaumberg & Schill
STREET: 1140 Connecticut Avenue, N.W., Suite 250
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/086,915
FILING DATE: 07-JUL-1993
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kubovcik, Ronald J.
REGISTRATION NUMBER: 25,401
REFERENCE/DOCKET NUMBER: 15873005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-466-2006
TELEFAX: 202-467-6300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 base pairs

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*****************************************************************
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Release 3.0.5Aa John F. Collins, Biocomputing Research Unit,
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Distribution rights by Oxford Molecular Ltd

MPsrch_pp   protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May   6 08:23:57 1998;   MasPar time 4.43 seconds
                                368.292 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-6
Description: (1-285) from US08804166.pep
Perfect Score: 2183
Sequence: 1 SRTSLLAFGLLCLPWLQEG..........GFKVENHTACHCSTCYYHKS 285

Scoring table: PAM 150
               Gap 11

Searched: 62627 seqs, 5720858 residues

Post-processing: Minimum Match 0%
                Listing first 45 summaries

Database: a-issued
            1:back1 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:PCT90
            10:PCT91 11:PCT92 12:PCT93 13:PCT94 14:PCT95 15:PCT96

Statistics: Mean 30.064; Variance 126.027; scale 0.239

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query % Match	Length	DB	ID	Description	Pred. No.
1	1306	59.8	455	7	US-08-321-	Sequence 2, Applicatio	7.75e-119
2	1306	59.8	455	7	US-08-050-	Sequence 25, Applicati	7.75e-119
3	1227	56.2	199	7	US-08-050-	Sequence 48, Applicati	8.08e-111
4	994	45.5	167	7	US-08-050-	Sequence 2, Applicati	3.05e-87
5	979	44.8	167	7	US-08-050-	Sequence 57, Applicati	3.05e-87
6	979	44.8	124	7	US-08-050-	Sequence 2, Applicatio	9.96e-86
7	912	41.8	157	7	US-08-050-	Sequence 4, Applicatio	5.63e-79
8	666	30.5	158	7	US-08-050-	Sequence 50, Applicatio	2.50e-54
9	589	27.0	153	7	US-08-050-	Sequence 54, Applicatio	1.12e-46
10	337	15.4	41	7	US-08-050-	Sequence 52, Applicatio	4.74e-22
11	324	14.8	40	7	US-08-050-	Sequence 36, Applicati	8.28e-21
12	318	14.6	43	7	US-08-050-	Sequence 26, Applicati	3.09e-20
13	284	13.0	39	7	US-08-050-	Sequence 31, Applicati	5.18e-17
14	225	10.3	325	10	US-08-292-	Sequence 40, Applicati	1.64e-11
15	225	10.3	325	10	US-08-292-	Sequence 2, Applicatio	1.64e-11
16	225	10.3	326	5	PCT-US91-0	Sequence 4, Applicatio	1.81e-11
17	221	10.1	326	5	PCT-US91-0	Sequence 2, Applicatio	1.81e-11
18	212	9.7	474	1	5395760-4	Patent No. 5395760.	2.54e-10
19	210	9.6	355	5	US-08-292-	Sequence 6, Applicatio	3.86e-10
20	183	8.4	283	15	PCT-US96-1	Sequence 2, Applicatio	1.06e-07
21	183	8.4	595	7	US-08-570-	Sequence 2, Applicatio	1.06e-07
22	183	8.4	595	5	US-08-225-	Sequence 2, Applicatio	1.06e-07
23	181	8.3	228	12	PCT-US93-0	Sequence 8, Applicatio	1.59e-07
24	181	8.3	228	7	US-08-188-	Sequence 4, Applicatio	1.59e-07
25	181	8.3	228	7	US-08-453-	Sequence 8, Applicatio	1.59e-07
26	181	8.3	228	13	PCT-US94-0	Sequence 8, Applicatio	1.59e-07
27	181	8.3	228	14	PCT-US95-0	Sequence 4, Applicatio	1.59e-07
28	180	8.2	461	7	US-08-385-	Sequence 2, Applicatio	1.96e-07
29	180	8.2	461	7	5395760-2	Patent No. 5395760.	1.96e-07
30	180	8.2	486	7	US-08-243-	Sequence 1, Applicatio	1.96e-07
31	180	8.2	518	7	US-08-385-	Sequence 4, Applicatio	1.96e-07
32	167	7.7	70	4	US-07-920-	Sequence 24, Applicati	2.77e-06
33	167	7.7	71	6	US-08-314-	Sequence 24, Applicati	2.77e-06
34	167	7.7	93	7	US-08-445-	Sequence 4, Applicatio	2.77e-06
35	167	7.7	93	7	US-08-343-	Sequence 12, Applicati	2.77e-06
36	169	7.7	333	7	US-08-453-	Sequence 12, Applicati	1.85e-06
37	169	7.7	333	12	PCT-US93-0	Sequence 12, Applicati	1.85e-06
38	169	7.7	399	7	US-08-453-	Sequence 10, Applicati	1.85e-06
39	169	7.7	399	12	PCT-US93-0	Sequence 10, Applicati	1.85e-06
40	165	7.6	186	4	US-08-089-	Sequence 6, Applicatio	4.16e-06
41	160	7.3	198	6	US-08-187-	Sequence 5, Applicatio	1.14e-05
42	160	7.3	461	7	US-08-187-	Sequence 6, Applicatio	1.14e-05
43	160	7.3	217	6	US-08-187-	Sequence 4, Applicatio	1.14e-05
44	160	7.3	206	5	US-08-097-	Sequence 7, Applicatio	3.10e-05
45	155	7.1	438	5	US-08-097-	Sequence 11, Applicati	3.10e-05
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ALIGNMENTS

RESULT   1
ID   US-08-321-668-2      STANDARD;     PRT;     455 AA.
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AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 2, Application US/08321668.
XX
CC
CC   Patent No. 5665859
CC   Sequence 2, Application US/08321668.
CC   GENERAL INFORMATION:
CC    APPLICANT: WALLACH, David
CC    APPLICANT: BRAKEBUSCH, Cord
CC    APPLICANT: VARFOLOMEEV, Eugene
CC    APPLICANT: BAIKIN, Michael
CC    TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
CC    TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
CC    NUMBER OF SEQUENCES: 42
CC    CORRESPONDENCE ADDRESS:
CC     ADDRESSEE: BROWDY AND NEIMARK
CC     STREET: 419 Seventh Street, N.W., Suite 300
CC     CITY: Washington
CC     STATE: D.C.
CC     COUNTRY: USA
CC     ZIP: 20004
CC    COMPUTER READABLE FORM:
CC     MEDIUM TYPE: Floppy disk
CC     COMPUTER: IBM PC compatible
CC     OPERATING SYSTEM: PC-DOS/MS-DOS
CC     SOFTWARE: PatentIn Release #1.0, Version #1.30
CC    CURRENT APPLICATION DATA:
CC     APPLICATION NUMBER: US/08/321,668
CC     FILING DATE: 12-OCT-1994
CC    PRIOR APPLICATION DATA:
CC     APPLICATION NUMBER: 435
CC     CLASSIFICATION:
CC     APPLICATION NUMBER: IL 107268
CC     FILING DATE: 12-OCT-1993
CC    ATTORNEY/AGENT INFORMATION:
CC     NAME: BROWDY, Roger L.
CC     REGISTRATION NUMBER: 25,618
CC     REFERENCE/DOCKET NUMBER: WALLACH-13
CC    TELECOMMUNICATION INFORMATION:
CC     TELEPHONE: 202-628-5197
CC     TELEFAX: 202-737-3528
CC     TELEX: 248633

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CC   INFORMATION FOR SEQ ID NO: 2:
CC     SEQUENCE CHARACTERISTICS:
CC       LENGTH: 455 amino acids
CC       TYPE: amino acid
CC       TOPOLOGY: linear
CC     MOLECULE TYPE: protein
SQ   SEQUENCE 455 AA; 50494 MW; 1048031 CN;

Query Match       59.8%;  Score 1306;  DB 7;  Length 455;
Best Local Similarity  98.8%;  Pred. No. 7.75e-119;
Matches  169;  Conservative  1;  Mismatches  1;  Indels   0;  Gaps   0;

Qy    1  DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
         ||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||
Db   23  DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db   41  KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 193
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  161  KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 211

Db   83  SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  101  SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160

RESULT 2
ID   US-08-050-319B-25               STANDARD;       PRT;      455 AA.

XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 25, Application US/08050319B.
CC   Patent No. 5633145
CC   GENERAL INFORMATION:
CC     APPLICANT: M.Feldmann, P.W. Gray,
CC     APPLICANT: M.J.C. Turner, F.M Brennan
CC     TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC     TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC     NUMBER OF SEQUENCES: 57
CC     CORRESPONDENCE ADDRESS:
CC       ADDRESSEE: Reed & Robbins
CC       STREET: 635 Bryant Street
CC       CITY: Palo Alto
CC       STATE: California
CC       COUNTRY: USA
CC       ZIP: 94301
CC     COMPUTER READABLE FORM:
CC       MEDIUM TYPE: Floppy disk
CC       COMPUTER: IBM PC Compatible
CC       OPERATING SYSTEM: PC-DOS/MS-DOS
CC       SOFTWARE: PatentIn Release #1.0, version #1.25
CC     CURRENT APPLICATION DATA:
CC       APPLICATION NUMBER: US/08/050,319B
CC       FILING DATE: 10-May-1993
CC       CLASSIFICATION: 435
CC     ATTORNEY/AGENT INFORMATION:
CC       NAME: Robbins, Roberta L.
CC       REGISTRATION NUMBER: 33,208
CC       REFERENCE/DOCKET NUMBER: 5150-0030
CC     TELECOMMUNICATION INFORMATION:
CC       TELEPHONE: (415) 617-8999
CC       TELEFAX: (415) 327-3231
CC   INFORMATION FOR SEQ ID NO: 25:
CC     SEQUENCE CHARACTERISTICS:
CC       LENGTH: 455 amino acids
CC       TYPE: amino acid
CC       TOPOLOGY: linear
CC     MOLECULE TYPE: protein
SQ   SEQUENCE 455 AA; 50579 MW; 1048388 CN;
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Query Match       59.8%;  Score 1306;  DB 7;  Length 455;
Best Local Similarity  98.8%;  Pred. No. 7.75e-119;
Matches  169;  Conservative  1;  Mismatches  1;  Indels   0;  Gaps   0;

Qy    1  DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
         ||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||
Db   23  DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db   41  KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 193
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  161  KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 211

Db   83  SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  101  SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160

RESULT 3
ID   US-08-050-319B-48               STANDARD;       PRT;      199 AA.

XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 48, Application US/08050319B.
CC   Patent No. 5633145
CC   GENERAL INFORMATION:
CC     APPLICANT: M.Feldmann, P.W. Gray,
CC     APPLICANT: M.J.C. Turner, F.M Brennan
CC     TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC     TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC     NUMBER OF SEQUENCES: 57
CC     CORRESPONDENCE ADDRESS:
CC       ADDRESSEE: Reed & Robbins
CC       STREET: 635 Bryant Street
CC       CITY: Palo Alto
CC       STATE: California
CC       COUNTRY: USA
CC       ZIP: 94301
CC     COMPUTER READABLE FORM:
CC       MEDIUM TYPE: Floppy disk
CC       COMPUTER: IBM PC Compatible
CC       OPERATING SYSTEM: PC-DOS/MS-DOS
CC       SOFTWARE: PatentIn Release #1.0, version #1.25
CC     CURRENT APPLICATION DATA:
CC       APPLICATION NUMBER: US/08/050,319B
CC       FILING DATE: 10-May-1993
CC       CLASSIFICATION: 435
CC     ATTORNEY/AGENT INFORMATION:
CC       NAME: Robbins, Roberta L.
CC       REGISTRATION NUMBER: 33,208
CC       REFERENCE/DOCKET NUMBER: 5150-0030
CC     TELECOMMUNICATION INFORMATION:
CC       TELEPHONE: (415) 617-8999
CC       TELEFAX: (415) 327-3231
CC   INFORMATION FOR SEQ ID NO: 48:
CC     SEQUENCE CHARACTERISTICS:
CC       LENGTH: 199 amino acids
CC       TYPE: amino acid
CC       TOPOLOGY: linear
CC     MOLECULE TYPE: protein
SQ   SEQUENCE 199 AA; 22186 MW; 195553 CN;

Query Match       56.2%;  Score 1227;  DB 7;  Length 199;
Best Local Similarity  99.1%;  Pred. No. 8.08e-111;
Matches  156;  Conservative  1;  Mismatches  2;  Indels   0;  Gaps   0;

Db   41  DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
         ||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||
Qy   23  DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82
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Db    101  SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     83  SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQE 142

Db    161  KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQI 199
           ||||||||||||||||||||||||||||||| ||||||||
Qy    143  KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQI 181
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RESULT 4

ID   US-08-050-319B-2   STANDARD;   PRT;   167 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 2, Application US/08050319B.
XX
CC   Patent No. 5633145
CC   GENERAL INFORMATION:
CC   APPLICANT: M.Feldmann, P.W. Gray,
CC   APPLICANT: M.J.C. Turner, F.M Brennan
CC   TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC   TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC   NUMBER OF SEQUENCES: 57
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Reed & Robbins
CC   STREET: 635 Bryant Street
CC   CITY: Palo Alto
CC   STATE: California
CC   COUNTRY: USA
CC   ZIP: 94301
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: Patentin Release #1.0, version #1.25
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/050,319B
CC   FILING DATE: 10-May-1993
CC   CLASSIFICATION: 435
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Robbins, Roberta L.
CC   REGISTRATION NUMBER: 33,208
CC   REFERENCE/DOCKET NUMBER: 5150-0030
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (415) 617-8999
CC   TELEFAX: (415) 327-3231
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 167 amino acids
CC   TYPE: amino acid
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: protein
SQ   SEQUENCE 167 AA; 18626 MW; 139513 CN;

Query Match   45.5%; Score 994; DB 7; Length 167;
Best Local Similarity 99.2%; Pred. No. 3.05e-87;
Matches 126; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db     41  DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23  DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101  SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
           |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Qy     83  SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQE 142

Db    161  KQNTVCT 167
           |||||||
Qy    143  KQNTVCT 149
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RESULT 5

ID   US-08-050-319B-57   STANDARD;   PRT;   167 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 57, Application US/08050319B.
XX
CC   Patent No. 5633145
CC   GENERAL INFORMATION:
CC   APPLICANT: M.Feldmann, P.W. Gray,
CC   APPLICANT: M.J.C. Turner, F.M Brennan
CC   TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC   TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC   NUMBER OF SEQUENCES: 57
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Reed & Robbins
CC   STREET: 635 Bryant Street
CC   CITY: Palo Alto
CC   STATE: California
CC   COUNTRY: USA
CC   ZIP: 94301
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: Patentin Release #1.0, version #1.25
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/050,319B
CC   FILING DATE: 10-May-1993
CC   CLASSIFICATION: 435
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Robbins, Roberta L.
CC   REGISTRATION NUMBER: 33,208
CC   REFERENCE/DOCKET NUMBER: 5150-0030
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (415) 617-8999
CC   TELEFAX: (415) 327-3231
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 167 amino acids
CC   TYPE: amino acid
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: protein
SQ   SEQUENCE 167 AA; 18626 MW; 139513 CN;

Query Match   45.5%; Score 994; DB 7; Length 167;
Best Local Similarity 99.2%; Pred. No. 3.05e-87;
Matches 126; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db     41  DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23  DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db    101  SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
           |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Qy     83  SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQE 142

Db    161  KQNTVCT 167
           |||||||
Qy    143  KQNTVCT 149
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RESULT 6

ID   US-08-050-319B-4   STANDARD;   PRT;   124 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX

Sequence 4, Application US/0805031 9B.
CC
XX Patent No. 5633145
CC GENERAL INFORMATION:
CC APPLICANT: M.Feldmann, P.W. Gray,
CC APPLICANT: M.J.C. Turner, F.M Brennan
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC NUMBER OF SEQUENCES: 57
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Reed & Robbins
CC STREET: 635 Bryant Street
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/050,319B
CC FILING DATE: 10-May-1993
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Robbins, Roberta L.
CC REGISTRATION NUMBER: 33,208
CC REFERENCE/DOCKET NUMBER: 5150-0030
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 617-8999
CC TELEFAX: (415) 327-3231
CC INFORMATION FOR SEQ ID NO: 4:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 124 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 124 AA; 14047 MW; 75840 CN;

Query Match
Best Local Similarity   44.8%;   Score 979; DB 7; Length 124;
Matches 123; Conservative 1; Pred. No. 9.96e-86; Mismatches 0; Indels 0; Gaps 0;

Db   1 VCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGCQDTDCRECESGSFTASENHLRHCLSC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   25 VCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGCQDTDCRECESGSFTASENHLRHCLSC 84

Db   61 SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQ 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   85 SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHWSENLFQCFNCTLCLNGTVHLSCQEKQ 144

DE Sequence 50, Application US/0805031 9B.
XX Patent No. 5633145
CC GENERAL INFORMATION:
DE Sequence 50, Application US/0805031 9B.
DT 01-JAN-1900
XX
AC xxxxxx
XX
ID US-08-050-319B-50   STANDARD;   PRT;   157 AA.
RESULT   7

Qy   145 NTVC 148

Db   121 NTVC 124

Qy   85 SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHWSENLFQCFNCTLCLNGTVHLSCQEKQ 144

Db   61 SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQ 120

Qy   25 VCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGCQDTDCRECESGSFTASENHLRHCLSC 84

Db   1 VCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGCQDTDCRECESGSFTASENHLRHCLSC 60

Matches 123; Conservative 1; Pred. No. 9.96e-86; Mismatches 0; Indels 0; Gaps 0;
Best Local Similarity   44.8%;   Score 979; DB 7; Length 124;
Query Match

SQ SEQUENCE 124 AA; 14047 MW; 75840 CN;
CC MOLECULE TYPE: protein
CC TOPOLOGY: linear
CC TYPE: amino acid
CC LENGTH: 124 amino acids
CC SEQUENCE CHARACTERISTICS:
CC INFORMATION FOR SEQ ID NO: 4:
CC TELEFAX: (415) 327-3231
CC TELEPHONE: (415) 617-8999
CC TELECOMMUNICATION INFORMATION:
CC REFERENCE/DOCKET NUMBER: 5150-0030
CC REGISTRATION NUMBER: 33,208
CC NAME: Robbins, Roberta L.
CC ATTORNEY/AGENT INFORMATION:
CC CLASSIFICATION: 435
CC FILING DATE: 10-May-1993
CC APPLICATION NUMBER: US/08/050,319B
CC CURRENT APPLICATION DATA:
CC SOFTWARE: Patentin Release #1.0, version #1.25
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC COMPUTER: IBM PC compatible
CC MEDIUM TYPE: Floppy disk
CC COMPUTER READABLE FORM:
CC ZIP: 94301
CC COUNTRY: USA
CC STATE: California
CC CITY: Palo Alto
CC STREET: 635 Bryant Street
CC ADDRESSEE: Reed & Robbins
CC CORRESPONDENCE ADDRESS:
CC NUMBER OF SEQUENCES: 57
CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC APPLICANT: M.J.C. Turner, F.M Brennan
CC APPLICANT: M.Feldmann, P.W. Gray,

CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC NUMBER OF SEQUENCES: 57
CC CORRESPONDENCE ADDRESS:
CC STREET: 635 Bryant Street
CC ADDRESSEE: Reed & Robbins
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/050,319B
CC FILING DATE: 10-May-1993
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Robbins, Roberta L.
CC REGISTRATION NUMBER: 33,208
CC REFERENCE/DOCKET NUMBER: 5150-0030
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 617-8999
CC TELEFAX: (415) 327-3231
CC INFORMATION FOR SEQ ID NO: 50:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 157 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 157 AA; 17570 MW; 122247 CN;

Query Match
Best Local Similarity   41.8%;   Score 912; DB 7; Length 157;
Matches 117; Conservative 2; Pred. No. 5.63e-79; Mismatches 3; Indels 0; Gaps 0;

Db   36 DREKRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWS 95
           :·||||||||||||||||||||||·||||||||||||||||||||||||||||||||||
Qy   60 DTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWS 119

Db   96 ENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLP 155
           ||||||||·||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   120 ENLFQCFNCTLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLP 179

Db   156 QI 157
           ||
Qy   180 QI 181

DE Sequence 54, Application US/0805031 9B.
XX
DT 01-JAN-1900
XX
AC xxxxxx
XX
ID US-08-050-319B-54   STANDARD;   PRT;   158 AA.
RESULT   8

CC APPLICANT: M.Feldmann, P.W. Gray,
CC APPLICANT: M.J.C. Turner, F.M Brennan
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC NUMBER OF SEQUENCES: 57
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Reed & Robbins
CC STREET: 635 Bryant Street
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: USA

RESULT 9
ID   US-08-050-319B-52   STANDARD;   PRT;   153 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 52, Application US/08050319B.
XX
CC   Patent No. 5633145
CC   GENERAL INFORMATION:
CC   APPLICANT: M.Feldmann, P.W. Gray,
CC   APPLICANT: M.J.C. Turner, F.M Brennan
CC   TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC   TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC   NUMBER OF SEQUENCES: 57
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Reed & Robbins
CC   STREET: 635 Bryant Street
CC   CITY: Palo Alto
CC   STATE: California
CC   COUNTRY: USA
CC   ZIP: 94301
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: Patentin Release #1.0, version #1.25
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/050,319B
CC   FILING DATE: 10-May-1993
CC   CLASSIFICATION: 435
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Robbins, Roberta L.
CC   REGISTRATION NUMBER: 33,208
CC   REFERENCE/DOCKET NUMBER: 5150-0030
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (415) 617-8999
CC   TELEFAX: (415) 327-3231
CC   INFORMATION FOR SEQ ID NO: 54:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 158 amino acids
CC   TYPE: amino acid
CC   TOPOLOGY: linear
SQ   MOLECULE TYPE: protein
SQ   SEQUENCE 158 AA; 17375 MW; 124033 CN;

Query Match
Best Local Similarity 97.7%;
Matches 86; Conservative 30.5%; Score 666; DB 7; Length 158;
Pred. No. 2.50e-54; Mismatches 1; Indels 0; Gaps 0;

Db 41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYLNDCPGPGQODTDCRECESGSGSFTASENHLRHCL 100
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYLNDCPGPGQODTDCRECESGSGSFTASENHLRHCL 82

Db 101 SCSKCRKEMGQVEISSCTVDRDTVCTCH 128
        |||||||||||||||||||||||||||
Qy 83 SCSKCRKEMGQVEISSCTVDRDTVCGCR 110

RESULT 10
ID   US-08-050-319B-36   STANDARD;   PRT;   41 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 36, Application US/08050319B.
XX
CC   Patent No. 5633145
CC   GENERAL INFORMATION:
CC   APPLICANT: M.Feldmann, P.W. Gray,
CC   APPLICANT: M.J.C. Turner, F.M Brennan
CC   TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC   TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC   NUMBER OF SEQUENCES: 57
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Reed & Robbins
CC   STREET: 635 Bryant Street
CC   CITY: Palo Alto
CC   STATE: California
CC   COUNTRY: USA
CC   ZIP: 94301
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: Patentin Release #1.0, version #1.25
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/050,319B
CC   FILING DATE: 10-May-1993
CC   CLASSIFICATION: 435
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Robbins, Roberta L.
CC   REGISTRATION NUMBER: 33,208
CC   REFERENCE/DOCKET NUMBER: 5150-0030
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (415) 617-8999
CC   TELEFAX: (415) 327-3231
CC   INFORMATION FOR SEQ ID NO: 52:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 153 amino acids
CC   TYPE: amino acid
CC   TOPOLOGY: linear
SQ   MOLECULE TYPE: protein
SQ   SEQUENCE 153 AA; 17148 MW; 116104 CN;

Query Match
Best Local Similarity 69.8%;
Matches 81; Conservative 27.0%; Score 589; DB 7; Length 153;
Pred. No. 1.12e-46; Mismatches 20; Indels 6; Gaps 4;

Db 44 CPQGKYIHPQNN-SIC--CTKCHK--GTYLYLNDCPGPGQDT-DCRKNQYRHYWSENLFQC 97
        |::|:|||:|:|| |:|: ||:|:| |||:|||||||||||| |||||||||||||||||
Qy 66 CESGGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC 125

Db 98 FNCSLCLNGTVHLSCQEKQNTVCTCHAGFEFLRENECVSCSNCKKSLECTKLCLPQI 153
        |||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 126 FNCTLCLNGTVHLSCOEKQNTVCTCHAGFEFLRENECVSCSNCKKSLECTKLSLPQI 181

RESULT 11

ID US-08-050-319B-26   STANDARD;   PRT;   40 AA.
XX
AC xxxxxx
XX
DE Sequence 26, Application US/08050319B.
XX
DT 01-JAN-1900
XX
SQ SEQUENCE   41 AA; 4856 MW; 8601 CN;

Query Match
Best Local Similarity   15.4%;   Score 337; DB 7; Length 41;
                         97.6%;   Pred. No. 4.74e-22;
Matches   40; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Db   1 GCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVC 41
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Qy   108 GCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQEKQNTVC 148

CC Sequence 26, Application US/08050319B.
CC Patent No. 5633145
CC GENERAL INFORMATION:
CC   APPLICANT: M.Feldmann, P.W. Gray,
CC   APPLICANT: M.J.C. Turner, F.M Brennan
CC   TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC   TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC   NUMBER OF SEQUENCES: 57
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Reed & Robbins
CC   STREET: 635 Bryant Street
CC   CITY: Palo Alto
CC   STATE: California
CC   COUNTRY: USA
CC   ZIP: 94301
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: Patentin Release #1.0, version #1.25
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/050,319B
CC   FILING DATE: 10-May-1993
CC   CLASSIFICATION: 435
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Robbins, Roberta L.
CC   REGISTRATION NUMBER: 33,208
CC   REFERENCE/DOCKET NUMBER: 5150-0030
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (415) 617-8999
CC   TELEFAX: (415) 327-3231
CC INFORMATION FOR SEQ ID NO: 26:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 40 amino acids
CC   TYPE: amino acid
CC   STRANDEDNESS: single
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: protein
SQ SEQUENCE   40 AA; 4459 MW; 7536 CN;

RESULT 12

ID US-08-050-319B-31   STANDARD;   PRT;   43 AA.
XX
AC xxxxxxx
XX

Query Match
Best Local Similarity   14.8%;   Score 324; DB 7; Length 40;
                        100.0%;   Pred. No. 8.28e-21;
Matches   40; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db   1 VCPQGKYIHPQNNSICCTKCHKGTVLYNDCPGQDTDCR 40
          ||||||||||||||||||||||||||||||||||||||
Qy   25 VCPQGKYIHPQNNSICCTKCHKGTVLYNDCPGQDTDCR 64

RESULT 13

ID US-08-050-319B-40   STANDARD;   PRT;   39 AA.
XX
AC xxxxxx
XX
DE Sequence 40, Application US/08050319B.
XX
DT 01-JAN-1900
XX
SQ SEQUENCE   43 AA; 4767 MW; 9758 CN;

Query Match
Best Local Similarity   14.0%;   Score 318; DB 7; Length 43;
                        100.0%;   Pred. No. 3.09e-20;
Matches   43; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db   1 ECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVC 43
          |||||||||||||||||||||||||||||||||||||||||||
Qy   65 ECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVC 107

CC Sequence 31, Application US/08050319B.
CC Patent No. 5633145
CC GENERAL INFORMATION:
CC   APPLICANT: M.Feldmann, P.W. Gray,
CC   APPLICANT: M.J.C. Turner, F.M Brennan
CC   TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC   TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC   NUMBER OF SEQUENCES: 57
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Reed & Robbins
CC   STREET: 635 Bryant Street
CC   CITY: Palo Alto
CC   STATE: California
CC   COUNTRY: USA
CC   ZIP: 94301
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: Patentin Release #1.0, version #1.25
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/050,319B
CC   FILING DATE: 10-May-1993
CC   CLASSIFICATION: 435
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Robbins, Roberta L.
CC   REGISTRATION NUMBER: 33,208
CC   REFERENCE/DOCKET NUMBER: 5150-0030
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (415) 617-8999
CC   TELEFAX: (415) 327-3231
CC INFORMATION FOR SEQ ID NO: 31:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 43 amino acids
CC   TYPE: amino acid
CC   STRANDEDNESS: single
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: protein
SQ SEQUENCE   43 AA; 4767 MW; 9758 CN;

CC   STREET: 635 Bryant Street
CC   CITY: Palo Alto
CC   STATE: California
CC   COUNTRY: USA
CC   ZIP: 94301
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: PatentIn Release #1.0, version #1.25
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/050,319B
CC   FILING DATE: 10-May-1993
CC   CLASSIFICATION: 435
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Robbins, Roberta L.
CC   REGISTRATION NUMBER: 33,208
CC   REFERENCE/DOCKET NUMBER: 5150-0030
CC   TELECOMMUNICATION INFORMATION:
CC   TELEFAX: (415) 327-3231
CC   TELEPHONE: (415) 617-8999
CC   INFORMATION FOR SEQ ID NO: 40:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 39 amino acids
CC   TYPE: amino acid
CC   STRANDEDNESS: single
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: protein
SQ   SEQUENCE 39 AA; 4335 MW; 8059 CN;

Query Match   13.0%; Score 284; DB 7; Length 39;
Best Local Similarity   97.4%; Pred. No. 5.18e-17;
Matches 38; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db   1 TCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGT 39
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Qy 149 TCHAGFFLRENECVSCSNCKKSLECTKLSLPQIENVKGT 187

RESULT 14
ID US-08-292-549-2   STANDARD;   PRT;   325 AA.
AC Patent No. 5464938
AC xxxxxx
DT 01-JAN-1900
DE Sequence 2, Application US/08292549.
XX
XX Sequence 2, Application US/0829254 9.
CC GENERAL INFORMATION:
CC APPLICANT: Smith, Craig A.
CC APPLICANT: Goodwin, Raymond G.
CC TITLE OF INVENTION: Isolated Viral Protein TNF Antagonists
CC NUMBER OF SEQUENCES: 10
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Immunex Corporation
CC STREET: 51 University Street
CC CITY: Seattle
CC STATE: Washington
CC COUNTRY: USA
CC ZIP: 98101
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/292,549
CC FILING DATE:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/963,330

CC   FILING DATE: 10/19/92
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Perkins, Patricia A.
CC   REGISTRATION NUMBER: 34,693
CC   REFERENCE/DOCKET NUMBER: 2602-A
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (206) 587-0430
CC   TELEFAX: (206) 233-0644
CC   INFORMATION FOR SEQ ID NO: 2:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 325 amino acids
CC   TYPE: amino acid
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: protein
SQ   SEQUENCE 325 AA; 35132 MW; 591446 CN;

Query Match   10.3%; Score 225; DB 5; Length 325;
Best Local Similarity   34.8%; Pred. No. 1.64e-11;
Matches 39; Conservative 21; Mismatches 45; Indels 7; Gaps 6;

Db   4 LIAL-LVCVYVYVGDDVPYSSNQGKCGGHDYEKDGLCCASCHPGFYASRLC-GPGSNTVC 61
        |:|: |:|: |||||| |:::|:::||:|| |:||| | |||:|:|
Qy   6 LLAFGLLCLPWLQEGSADSVCPQGKYI-RP-QNNSICCTRCHKGTYLYNDCPGPGQGQDTDC 63

Db 62 SPCEDGTFTASTNHAPACVSCRGPCTGHLSESQ--PCDRTHDRVCNCSTGNY 111
        ||:|:||| || || :|||| || | |
Qy 64 RECESGSFFTASENHLRHCLSC-SKCRKEMGQVEISSCTVDRDTVCGCRKNQY 114

RESULT 15
ID PCT-US91-02207-2   STANDARD;   PRT;   325 AA.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 2, Application PC/TUS9102207.
XX
XX Sequence 2, Application PC/TUS9102207.
CC GENERAL INFORMATION:
CC APPLICANT: Smith, Craig A.
CC APPLICANT: Goodwin, Raymond G.
CC TITLE OF INVENTION: Isolated Viral Protein Cytokine Antagonists
CC NUMBER OF SEQUENCES: 4
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Immunex Corporation
CC STREET: 51 University Street
CC CITY: Seattle
CC STATE: Washington
CC COUNTRY: USA
CC ZIP: 98101
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.24
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US91/02207
CC FILING DATE: 19910329
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Wight, Christopher L.
CC REGISTRATION NUMBER: 31,680
CC REFERENCE/DOCKET NUMBER: 2602
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206) 587-0606
CC TELEFAX: (206) 587-0430
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 325 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein

SQ   SEQUENCE   325 AA; 35132 MW; 591446 CN;

Query Match   10.3%;   Score 225;   DB 10;   Length 325;
Best Local Similarity   34.8%;   Pred. No. 1.64e-11;
Matches 39; Conservative 21; Mismatches 45; Indels 7; Gaps 6;

Db   4 LIAL-LVCVVTVYGDDVPYSSNQGKCGGGHDYEKDGLCCASCHPGFYASRLC-GPGSNTVC 61
         |:|: |:|: : ||| | :::::||||:||:| | ||| :|| :|
Qy   6 LLAFGLLCLPWLQEGSADSVCPQGKYI-HP-QNNSICCTKCHKGTYLYNDCPGPGQDTDC   63

Db   62 SPCEDGTFTASTNHAPACVSCRGPCTGHLSESQ--PCDRTHDRVCNCSTGNY 111
         |:|:||||| | :|| | | | :||| | | | | :| | |
Qy   64 RECESGSFTASENHLRHCLSC-SKCRKEMGQVEISSCTVDRDTVCGCRKNQY 114

Search completed: Wed May 6 08:24:12 1998
Job time : 15 secs.

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 M P S R C H
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(TM)

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*********************************************************************
*********************************************************************
         Release 3.0.5AA John F. Collins, Biocomputing Research Unit.
                  Copyright (c) 1993-1997 University of Edinburgh, U.K.
                     Distribution rights by Oxford Molecular Ltd
*********************************************************************
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```

MPsrch.nn   n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed May 6 10:56:07 1998;   MasPar time 65.66 Seconds
                                            920.693 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-5
Description: (1-1147) from US08804166.seq
Perfect Score: 1147
N.A. Sequence: 1 TCGAGATGGCTACAGGTAAG.......................AATCTTAGGATCCCTCGAG 1147
Comp: AGCTCTACCGATGTCCATTC....................TTAGAATTCCTAGGAGCTC

Scoring table: TABLE default
                Gap 6

Nmatch STD :   Dbase 0; Query 0

Searched: 102136 seqs, 26354296 bases x 2

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database: n-issued
                 1:back1 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:PCT90
                 10:PCT91 11:PCT92 12:PCT93 13:PCT94 14:PCT95 15:PCT96

Statistics: Mean 8.727; Variance 4.288; scale 2.035

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	506	44.1	2062	7	US-08-050-	Sequence 24, Applicatio	3.87e-20
2	506	44.1	2175	7	US-08-321-	Sequence 1, Applicatio	3.87e-20
3	504	43.9	6889	13	PCT-US95-0	Sequence 1, Applicatio	3.87e-20
4	504	43.9	6889	14	US-08-286-	Sequence 2, Applicatio	3.87e-20
5	464	40.5	600	7	US-08-050-	Sequence 47, Applicatio	0.00e+00
6	375	32.7	504	7	US-08-050-	Sequence 2, Applicatio	7.03e-21
7	373	32.5	501	7	US-08-050-	Sequence 14, Applicatio	1.67e-11
8	364	31.7	372	7	US-08-050-	Sequence 1, Applicatio	1.67e-11
9	345	30.1	474	7	US-08-050-	Sequence 3, Applicatio	4.58e-291
10	288	25.1	2771	7	US-08-273-	Sequence 49, Applicatio	2.74e-283
11	288	25.1	474	7	US-08-050-	Sequence 5, Applicatio	6.94e-267
12	287	25.0	4283	7	US-08-343-	Sequence 3, Applicatio	8.12e-218
13	287	25.0	4283	7	US-08-445-	Sequence 1, Applicatio	8.12e-217
14	255	22.2	477	7	US-08-050-	Sequence 53, Applicatio	5.86e-189
15	213	18.6	462	7	US-08-050-	Sequence 51, Applicatio	1.56e-189
16	67	5.8	534	6	US-08-187-	Sequence 1, Applicatio	1.02e-153
17	67	5.8	654	6	US-08-187-	Sequence 23, Applicatio	4.70e-33
18	58	5.1	321	6	US-07-920-	Sequence 23, Applicati	3.86e-26
19	57	5.0	597	6	US-08-187-	Sequence 2, Applicatio	2.21e-25
20	50	4.4	2248	7	US-08-475-	Sequence 1, Applicatio	3.87e-20
21	50	4.4	2248	7	US-08-780-	Sequence 1, Applicatio	3.87e-20
22	50	4.4	2248	7	US-08-636-	Sequence 1, Applicatio	3.87e-20
23	50	4.4	2248	6	US-08-369-	Sequence 3, Applicatio	3.87e-20
24	51	4.4	7218	7	US-08-232-	Sequence 14, Applicatio	1.67e-11
25	38	3.3	633	7	US-08-388-	Sequence 14, Applicatio	1.67e-11
26	38	3.3	7218	7	US-08-232-	Sequence 14, Applicatio	1.67e-11
27	34	3.0	215	6	US-08-238-	Sequence 5, Applicatio	1.77e-05
28	34	3.0	215	6	US-08-238-	Sequence 14, Applicati	7.63e-05
29	34	3.0	4810	13	PCT-US93-0	Sequence 5, Applicatio	1.33e-03
30	34	3.0	4810	17	US-08-453-	Sequence 3, Applicatio	9.19e-09
31	34	3.0	4810	12	PCT-US93-0	Sequence 3, Applicatio	9.19e-09
32	34	3.0	4810	14	US-08-050-	Sequence 7, Applicatio	9.19e-09
33	34	3.0	5125	7	PCT-US94-0	Sequence 3, Applicatio	9.19e-09
34	34	3.0	5125	12	US-08-188-	Sequence 3, Applicatio	9.19e-09
35	34	3.0	5323	12	PCT-US93-0	Sequence 11, Applicati	9.19e-09
36	34	3.0	5323	0	PCT-US95-1	Sequence 9, Applicatio	9.19e-09
37	34	2.5	215	6	US-08-453-	Sequence 100, Applicat	5.37e-03
38	29	2.5	33	7	US-08-050-	Sequence 9, Applicatio	5.37e-03
39	28	2.4	81	14	PCT-US95-1	Sequence 98, Applicatio	5.37e-03
40	26	2.3	81	14	PCT-US95-1	Sequence 94, Applicati	5.37e-03
41	25	2.2	74	14	PCT-US95-1	Sequence 9, Applicatio	5.37e-03
42	25	2.2	81	14	PCT-US95-1	Sequence 14, Applicati	7.63e-05
43	25	2.2	82	14	PCT-US94-0	Sequence 7, Applicatio	2.11e-02
44	24	2.1	57	7	US-08-050-	Sequence 6, Applicatio	2.11e-02
45	24	2.1	82	14	PCT-US95-1	Sequence 97, Applicati	2.11e-02

ALIGNMENTS

RESULT   1
ID US-08-050-3198-24 STANDARD; DNA; UNC; 2062 BP.

XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 24, Application US/08050319B
XX
Patent No. 5633145
Sequence 24, Application US/08050319B.
GENERAL INFORMATION:
   APPLICANT: M.Feldmann, P.W. Gray,
   APPLICANT: M.J.C. Turner, F.M Brennan
   TITLE OF INVENTION: Modified human TNFalpha (Tumor
   TITLE OF INVENTION: Necrosis Factor alpha) Receptor
   NUMBER OF SEQUENCES: 57
   CORRESPONDENCE ADDRESS:
      ADDRESSEE: Reed & Robbins
      STREET: 635 Bryant Street
      CITY: Palo Alto
      STATE: California
      COUNTRY: USA
      ZIP: 94301
   COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: PatentIn Release #1.0, version #1.25
   CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/050,319B
      FILING DATE: 10-May-1993
      CLASSIFICATION: 435
   ATTORNEY/AGENT INFORMATION:
      NAME: Robbins, Roberta L.
      REGISTRATION NUMBER: 33,208
      REFERENCE/DOCKET NUMBER: 5150-0030
   TELECOMMUNICATION INFORMATION:
      TELEPHONE: (415) 617-8899
      TELEFAX: (415) 327-3231
   INFORMATION FOR SEQ ID NO: 24:
      SEQUENCE CHARACTERISTICS:

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CC   LENGTH: 2062 base pairs
CC   TYPE: nucleic acid
CC   STRANDEDNESS: double
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: cDNA to mRNA
CC   FEATURE:
CC     NAME/KEY: CDS
CC     LOCATION: 155..1519
SQ   Sequence 2062 BP; 429 A; 617 C; 573 G; 443 T; 0 other;

Query Match         44.1%;  Score 506;  DB 7;  Length 2062;
Best Local Similarity   98.1%;  Pred. No. 0.00e+00;
Matches   521;  Conservative    0;  Mismatches    9;  Indels    1;  Gaps    1;

Db    275 GATAGTGTGTGTCCCCAAGGAAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 334
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Db    335 AAGTGCCACAAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGCAGGATACGGAC 394
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Qy    404 AAGTGCCACAAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGCAGGATACCGAC 463

Db    395 TGCAGGGAGTGTGAGAGCGGCGCTCCTTCCTTCACCGGTTCAGAAAAACCACCTCAGCGCCTC 454
          ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Qy    464 TGCAGGGAGTGTGAGAGCGGCGCTCCTTCCTTCAGAAAAACCACCTCAGACACTGCCCTC 523

Db    455 AGCTGCTCCAAATGCCGAAAGGAAAATGGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 514
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    524 AGCTGCTCCAAATGCCGAAAGGAAAATGGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    515 CGGGACACCGTGTGTGGCCTCCAGGAAGAACCAGTACCGGACGATTATTGGGAGTGAAAACCTT 574
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    584 CGGGACACCGTGTGTGGCCTCCAGGAAGAACCAGTACCGGACGATTATTGGGAGTGAAAACCTT 643

Db    575 TTCCAGTGCTTCAAATGCACCCTCTGCCTCCTCAAATGGGACCGGTGCACCCTCTCCTGCTGCGTC 634
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    644 TTCCAGTGCTTCAAATGCACCCTCTGCCTCCTCAAATGGGACCGGTGCACCCTCTCCTGCTGCGTC 703

Db    635 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTTAAGAGAAAAACGAGTGTGTC 694
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    704 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTTAAGAGAAAAACGAGTGTGTC 763

Db    695 TCCTGTAGTAACTGTAAGAAAAGACCTGGAGTGCACGAAGAGTTGTGCCTACCCCAGATTGAG 754
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    764 TCCTGTAGTAACTGTAAGAAAAGACCTGGAGTGCACGAAGAGTTGTGCCTACCCCAGATTGAG 823

Db    755 AATGTTAAGGCACTGAGGACTCAGGCACCACACAGT-GCTGTTGCCCCTGGT 804
          ||||||||||||||||||||||||||||||||||| |||||||||||||||
Qy    824 AATGTTAAGGCACTGAGGACTCAGGCACCACACAGCCGGGTGCTGCCCCAGGT 874
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CC   STREET: 419 Seventh Street, N.W., Suite 300
CC   CITY: Washington
CC   STATE: D.C.
CC   COUNTRY: USA
CC   ZIP: 20004
CC   COMPUTER READABLE FORM:
CC     MEDIUM TYPE: Floppy disk
CC     COMPUTER: IBM PC compatible
CC     OPERATING SYSTEM: PC-DOS/MS-DOS
CC     SOFTWARE: Patentin Release #1.0, Version #1.30
CC   CURRENT APPLICATION DATA:
CC     APPLICATION NUMBER: US/08/321,668
CC     FILING DATE: 12-OCT-1994
CC     CLASSIFICATION: 435
CC   PRIOR APPLICATION DATA:
CC     APPLICATION NUMBER: IL 107268
CC     FILING DATE: 12-OCT-1993
CC   ATTORNEY/AGENT INFORMATION:
CC     NAME: BROWDY, Roger L.
CC     REGISTRATION NUMBER: 25,618
CC     REFERENCE/DOCKET NUMBER: WALLACH-13
CC   TELECOMMUNICATION INFORMATION:
CC     TELEPHONE: 202-628-5197
CC     TELEFAX: 202-737-3528
CC     TELEX: 248633
CC   INFORMATION FOR SEQ ID NO:  1:
CC     SEQUENCE CHARACTERISTICS:
CC     LENGTH: 2175 base pairs
CC     TYPE: nucleic acid
CC     STRANDEDNESS: single
CC     TOPOLOGY: linear
CC   MOLECULE TYPE: cDNA
CC   FEATURE:
CC     NAME/KEY: CDS
CC     LOCATION: 256..1620
SQ   Sequence 2175 BP; 474 A; 641 C; 604 G; 456 T; 0 other;

Query Match         44.1%;  Score 506;  DB 7;  Length 2175;
Best Local Similarity   98.1%;  Pred. No. 0.00e+00;
Matches   521;  Conservative    0;  Mismatches    9;  Indels    1;  Gaps    1;

Db    376 GATAGTGTGTGTCCCCAAGGAAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 435
          ||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Qy    344 GATAGTGTGTGTCCCCAAGGAAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403

Db    436 AAGTGCCACAAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGCAGGATACGGAC 495
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Qy    404 AAGTGCCACAAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGCAGGATACCGAC 463

Db    496 TGCAGGGAGTGTGAGAGCGGCGCTCCTTCCTTCACCGGTTCAGAAAAACCACCTCAGCGCCTC 555
          ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Qy    464 TGCAGGGAGTGTGAGAGCGGCGCTCCTTCCTTCAGAAAAACCACCTCAGACACTGCCCTC 523

Db    556 AGCTGCTCCAAATGCCGAAAGGAAAATGGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 615
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    524 AGCTGCTCCAAATGCCGAAAGGAAAATGGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db    616 CGGGACACCGTGTGTGGCCTCCAGGAAGAACCAGTACCGGACGATTATTGGGAGTGAAAACCTT 675
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    584 CGGGACACCGTGTGTGGCCTGCAGGAAGAACCAGTACCGGACGATTATTGGGAGTGAAAACCTT 643

Db    676 TTCCAGTGCTTCAAATGCACCCTCTGCCTCCTCAAATGGGACCGGTGCACCCTCTCCTGCCGGAG 735
          |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Qy    644 TTCCAGTGCTTCAAATGCACCCTCTGCCTCCTCAAATGGGACCGGTGCACCCTCTCCTGCCGGAG 703

Db    736 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTTAAGAGAAAAACGAGTGTGTC 795
          ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    704 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTTAAGAGAAAAACGAGTGTGTC 763

Db    796 TCCTGTAGTAACTGTAAGAAAAGACCTGGAGTGCACGAAGAGTTGTGCCTACCCCAGATTGAG 855
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    764 TCCTGTAGTAACTGTAAGAAAAGACCTGGAGTGCACGAAGAGTTGTGCCTACCCCAGATTGAG 823
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RESULT         2
ID   US-08-321-668-1 STANDARD; DNA; UNC; 2175 BP.
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Db    856 AATGTTAAGGCGACTGAGGACTCAGGCACCACAGT-GCTGTTGCCGTCTGGT 905
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Qy    824 AATGTTAAGGCGACTGAGGACTCAGGCACCACAGCCGGTGCTTGCCCCAGGT 874
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RESULT 3
ID PCT-US95-09576-2 STANDARD; DNA; UNC; 6889 BP.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 2, Application PC/TUS9509576.
XX
CC GENERAL INFORMATION:
CC APPLICANT: GENENTECH, INC.
CC TITLE OF INVENTION: METHOD FOR SELECTING HIGH-EXPRESSING
CC TITLE OF INVENTION: HOST CELLS
CC NUMBER OF SEQUENCES: 4
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Genentech, Inc.
CC STREET: 460 Point San Bruno Blvd
CC CITY: South San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94080
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patin (Genentech)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/09576
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/286740
CC FILING DATE: 05-AUG-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Lee, Wendy M.
CC REGISTRATION NUMBER: 00,000
CC REFERENCE/DOCKET NUMBER: 798PCT
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415/225-1994
CC TELEFAX: 415/952-9881
CC TELEX: 910/371-7168
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 6889 bases
CC TYPE: nucleic acid
CC STRANDEDNESS: double
CC TOPOLOGY: linear
SQ Sequence 6889 BP; 1729 A; 1826 C; 1681 G; 1653 T; 0 other;

Query Match   43.9%; Score 504; DB 14; Length 6889;
Best Local Similarity 99.0%; Pred. No. 0.00e+00;
Matches 509; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db   1725 GATAGTGTGTGTCCCAAGGAGAAATATATCCACCCTCAAAATAATAATTGATTTGCTGTACC 1784
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    344 GATAGTGTGTCTCCCAAGGAGAAATATATCCACCCTCAAAATAATAATTCGATTTGCTGTACC 403

Db   1785 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGCGCCCCGGGGCAGGATACGGAC 1844
          ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Qy    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGCGCCCGGGGCAGGATACCGAC 463

Db   1845 TGCAGGGAGTGTGTGAGAGCGGCGTCCCTTCACCGTTCAGAAAAACCACCTCCAGNCACTGCCTC 1904
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    464 TGCAGGGAGTGTGAGACGGCGGTCCTTCACCCGTTCAGAAAAAACCACCTCAGACACTGCCTC 523

Db   1905 AGCTGCTCCAAATGCCGAAAAGGAAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 1964
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    524 AGCTGCTCCAAATGCCGAAAAGGAAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db   1965 CGGGAACACCGTGTTGTGGCTGCGAGGAAGAAACCAGTACCGGCACATTATTGGAGTGAAAAACCTT 2024
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    584 CGGGACACCGTGTTGTGGCCTGCAGGAAGAAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db   2025 TTCCAGTGCTTCAAATTGCAGCCTCTGCCTCAATGGACGTGCCACGGAAGTGTTGTGCCTAC 2084
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    644 TTCCAGTGCTTCAAATTGCACCCTCTGCCTCAATGGACGTGCCACGGAAGTGTTGTGCC 703

Db   2085 AAACAGAACACCGTGTGCACCCTGCCACCTCCATGCAGGTTTCTTTTCTAAGAGAAAAACGAGTGTGTC 2144
          |||||||||||||||||||||||||||||||||||||||||||||||||
Qy    704 AAACAGAACACCGTGTGCACCCTGCCACCTCCATGCAGGTTTCTTTTCTAAGAGAAAAACGAGTGTGTC 763

Db   2145 TCCTGTAGTAACTGTAAGAAAAAGCCTGGAGTGCCACGGAAGTGTTGCCTACACCCAGCCAGATTGAG 2204
          ||||||||||||||||||||||||||||||||||||||||||||||
Qy    764 TCCTGTAGTAACTGTAAGAAAAACCCTGAGTGCCACGGAAGTTGTGCCTACACCCAGCCAGATTGAG 823

Db   2205 AATGTTAAGGCGACTGAGGACTCAGGCACCACAG 2238
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Qy    824 AATGTTAAGGCGACTGAGGACTCAGGCACCACAG 857
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RESULT 4
ID US-08-286-740-2 STANDARD; DNA; UNC; 6889 BP.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 2, Application US/08286740.
XX
Patent No. 5561053
CC GENERAL INFORMATION:
CC APPLICANT: Crowley, Craig W.
CC TITLE OF INVENTION: METHOD FOR SELECTING HIGH-EXPRESSING
CC TITLE OF INVENTION: HOST CELLS
CC NUMBER OF SEQUENCES: 4
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Genentech, Inc.
CC STREET: 460 Point San Bruno Blvd
CC CITY: South San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94080
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patin (Genentech)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/286,740
CC FILING DATE: 05-AUG-1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER:
CC FILING DATE:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Lee, Wendy M.
CC REGISTRATION NUMBER:
CC REFERENCE/DOCKET NUMBER: 798
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415/225-1994
CC TELEFAX: 415/952-9881
CC TELEX: 910/371-7168
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 6889 bases
CC TYPE: nucleic acid
CC STRANDEDNESS: double

Left column

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CC
SQ  Sequence 6889 BP; 1729 A; 1826 C; 1681 G; 1653 T; 0 other;
CC  TOPOLOGY: linear

Query Match      43.9%;   Score 504;  DB 6;  Length 6889;
Best Local Similarity  99.0%;  Pred. No. 0.00e+00;
Matches 509;  Conservative  0;  Mismatches  5;  Indels  0;  Gaps  0;

Db 1725 GATAGTGTGTGTCCCCACAGGAGAAAATATATCCACACCTCAAAATAATTAATTCGATTTGCTGTACC 1784
        |||||||||||||||||    ||||||||||||||||||||||||||||||||||||||||||||||
Qy  344 GATAGTGTGTGTCCCAAGGAAAATATATCCACACCTCAAAATAATTAATTCGATTTGCTGTACC 403

Db 1785 AAGTGCCACAAAAGGAAACCTACTTGTTACAATGACTGTCTCCAGGCCCGGGGCCAGGATACGGAC 1844
        |||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||| |||
Qy  404 AAGTGCCACAAAGGAAACCTACTTGTTACAATGACTGTCTCCAGGCCCGGGGCCAGGATACCGAC 463

Db 1845 TGCAGGGAGTGTGAGAGCGGCGGCTCCTTCACCGGCTTCAGAAAACCACCTCAGACACTGCCTC 1904
        |||||||||||||||||||   |||||||||||||||||||||||||||||||||||||||||||
Qy  464 TGCAGGGAGTGTGAGAGCGGGGGCTCCTTCACCGGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db 1905 AGCTGCTCCAAATGCCGAAAAGGAAAATGGGTCAGGTGGGAGGAGATCTCTTCTTCTTGCACAGTGGAC 1964
        ||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||
Qy  524 AGCTGCTCCAAATGCCGAAAAGGAAAATGGGTCAGGTGGGAGATCTCTTCTTCTTGCACAGTGGAC 583

Db 1965 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAAACCTT 2024
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAAACCTT 643

Db 2025 TTCCAGTGCTTCAATTGCAGCCCTTGCCCTCAAATGGGACCGTGCACCTCTCCTGCGCAGGAG 2084
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||||
Qy  644 TTCCAGTGCTTCAATTGCAGCCCTTGCCCTCAAATGGGACCGTGCACCTCTCCTGTGTCAGGAG 703

Db 2085 AAACAGAACACCGTGCCACCTGCCATGCAGGTTTCTTTTCTTAAGAGAAAACGAGTGTGTGTC 2144
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  704 AAACAGAACACCGTGCCACCTGCCATGCAGGTTTCTTTTCTTAAGAGAAAACGAGTGTGTGTC 763

Db 2145 TCCTGTAGTAACTGTAAGAAAAAGCCTGGAGTGCACGAAGAGTGTGTCGCCTACCCAGATTGAG 2204
        ||||||||||||||||||||||||||||||||||||||||||||||||   |||||||||||||
Qy  764 TCCTGTAGTAACTGTAAGAAAAAGCCTGGAGTGCACGAAGAGTGTGTCCCTACCCAGATTGAG 823

Db 2205 AATGTTAAGGGCACTGAGGACTCAGGCACCACACAG 2238
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Qy  824 AATGTTAAGGGCACTGAGGACTCAGGCACCACACAG 857

RESULT 5
ID US-08-050-319B-47 STANDARD; DNA; UNC; 600 BP.

Sequence 47, Application US/08050319B.

01-JAN-1900

xxxxxx
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DE
XX
DT 01-JAN-1900
XX
AC xxxxxx
XX
Sequence 47, Application US/08050319B.
Patent NO. 5633145

GENERAL INFORMATION:
- APPLICANT: M.Feldmann, P.W. Gray,
- APPLICANT: M.J.C. Turner, F.M Brennan
- TITLE OF INVENTION:
- TITLE OF INVENTION: Modified human TNFalpha (Tumor Necrosis Factor alpha) Receptor
- NUMBER OF SEQUENCES: 57
- CORRESPONDENCE ADDRESS:
- ADDRESSEE: Reed & Robbins
- STREET: 635 Bryant Street
- CITY: Palo Alto
- STATE: California
- COUNTRY: USA
- ZIP: 94301
- COMPUTER READABLE FORM:
- MEDIUM TYPE: Floppy disk
- COMPUTER: IBM PC compatible
- OPERATING SYSTEM: PC-DOS/MS-DOS

Right column

SOFTWARE: Patentin Release #1.0, version #1.25
- CURRENT APPLICATION DATA:
- CURRENT APPLICATION NUMBER: US/08/050,319B
- APPLICATION NUMBER: US/08/050,319B
- FILING DATE: 10-May-1993
- CLASSIFICATION: 435
- ATTORNEY/AGENT INFORMATION:
  - NAME: Robbins, Roberta L.
  - REGISTRATION NUMBER: 33,208
  - REFERENCE/DOCKET NUMBER: 5150-0030
- TELECOMMUNICATION INFORMATION:
  - TELEPHONE: (415) 617-8999
  - TELEFAX: (415) 327-3231
- INFORMATION FOR SEQ ID NO: 47:
- SEQUENCE CHARACTERISTICS:
  - LENGTH: 600 base pairs
  - TYPE: nucleic acid
  - STRANDEDNESS: double
  - TOPOLOGY: linear
- MOLECULE TYPE: cDNA to mRNA
- FEATURE:
  - NAME/KEY: CDS
  - LOCATION: 1..597

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SQ  Sequence 600 BP; 148 A; 157 C; 162 G; 133 T; 0 other;

Query Match      40.5%;   Score 464;  DB 7;  Length 600;
Best Local Similarity  98.3%;  Pred. No. 0.00e+00;
Matches 472;  Conservative  0;  Mismatches  8;  Indels  0;  Gaps  0;

Db  121 GATAGTGTGTGTCCCCACAGGAGAAAATATATCCACACCTCAAAATAATTAATTCGATTTGCTGTACC 180
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Qy  344 GATAGTGTGTGTCCCAAGGAAAATATATCCACACCTCAAAATAATTAATTCGATTTGCTGTACC 403

Db  181 AAGTGCCACAAAGGAAACCTACTTGTACAATGACTGTCTCCAGGCCCGGGGCCAGGATACCGAC 240
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Qy  404 AAGTGCCACAAAGGAAACCTACTTGTTACAATGACTGTCTCCAGGCCCGGGGCCAGGATACCGAC 463

Db  241 TGCAGGGAGTGTGAGAGCGGCGGCTCCTTCACCGGCTTCAGAAAACCACCTCAGACACTGCCTC 300
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Qy  464 TGCAGGGAGTGTGAGAGCGGGGGCTCCTTCACCGGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db  301 AGCTGCTCCAAATGCCGAAAAGGAAAATGGGTCAGGTGGGAGGAGATCTCTTCTTCTTGCACAGTGGAC 360
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Qy  524 AGCTGCTCCAAATGCCGAAAAGGAAAATGGGTCAGGTGGGAGATCTCTTCTTCTTGCACAGTGGAC 583

Db  361 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAAACCTT 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAAACCTT 643

Db  421 TTCCAGTGCTTCAATTGCAGCCCTTGCCCTCAAATGGGACCGTGCACCTCTCCTGCGCAGGAG 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||||
Qy  644 TTCCAGTGCTTCAATTGCAGCCCTTGCCCTCAAATGGGACCGTGCACCTCTCCTGTGTCAGGAG 703

Db  481 AAACAGAACACCGTGCCACCTGCCATGCAGGTTTCTTTTCTTAAGAGAAAACGAGTGTGTC 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  704 AAACAGAACACCGTGCCACCTGCCATGCAGGTTTCTTTTCTTAAGAGAAAACGAGTGTGTC 763

Db  541 TCCTGTAGTAACTGTAAGAAAAAGCCTGGAGTGCACGAAGAGTGTGTCGCCTACCCAGATTTAG 600
        ||||||||||||||||||||||||||||||||||||||||||||||||   ||||||||||| ||
Qy  764 TCCTGTAGTAACTGTAAGAAAAAGCCTGGAGTGCACGAAGAGTGTGTCCCTACCCAGATTGAG 823

RESULT 6
ID US-08-050-319B-56 STANDARD; DNA; UNC; 504 BP.
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DE
XX
DT 01-JAN-1900
XX
AC xxxxxx
XX
Sequence 56, Application US/08050319B.
Patent NO. 5633145

Left column

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CC  GENERAL INFORMATION:
CC  APPLICANT: M.Feldmann, P.W. Gray,
CC  APPLICANT: M.J.C. Turner, F.M Brennan
CC  TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC  TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC  NUMBER OF SEQUENCES: 57
CC  CORRESPONDENCE ADDRESS:
CC  ADDRESSEE: Reed & Robbins
CC  STREET: 635 Bryant Street
CC  CITY: Palo Alto
CC  STATE: California
CC  COUNTRY: USA
CC  ZIP: 94301
CC  COMPUTER READABLE FORM:
CC  MEDIUM TYPE: Floppy disk
CC  COMPUTER: IBM PC compatible
CC  OPERATING SYSTEM: PC-DOS/MS-DOS
CC  SOFTWARE: Patentin Release #1.0, version #1.25
CC  CURRENT APPLICATION DATA:
CC  APPLICATION NUMBER: US/08/050,319B
CC  FILING DATE: 10-May-1993
CC  CLASSIFICATION: 435
CC  ATTORNEY/AGENT INFORMATION:
CC  NAME: Robbins, Roberta L.
CC  REGISTRATION NUMBER: 33,208
CC  REFERENCE/DOCKET NUMBER: 5150-0030
CC  TELECOMMUNICATION INFORMATION:
CC  TELEPHONE: (415) 617-8999
CC  TELEFAX: (415) 327-3231
CC  INFORMATION FOR SEQ ID NO: 56:
CC  SEQUENCE CHARACTERISTICS:
CC  LENGTH: 504 base pairs
CC  TYPE: nucleic acid
CC  STRANDEDNESS: double
CC  TOPOLOGY: linear
CC  MOLECULE TYPE: cDNA to mRNA
CC  FEATURE:
CC  NAME/KEY: CDS
CC  LOCATION: 1..501
SQ  Sequence 504 BP; 122 A; 137 C; 138 G; 107 T; 0 other;

Query Match            32.7%;    Score 375;  DB 7;  Length 504;
Best Local Similarity  99.0%;    Pred. No. 8.54e-293;
Matches   379;   Conservative   0;   Mismatches   4;   Indels   0;   Gaps   0;

Qy  121  GATAGTGTGTGTCCCCAAGGAGAAAATATATCCACCCTCAAAATAATTAATTCGATTTGCTGTTACC  180
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Db  344  GATAGTGTGTGTCCCCAAGGAAAATAATATATTCCACCCTCAAAATAATTAATTCGATTTGCTGTTACC  403
Qy  181  AAGTGCCACAAAGGAACCTACTTGTACAAATGACTGTCCAGGCCCCGGGCAGGATACGGAC  240
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Db  404  AAGTGCCACAAAGGAACCTACTTGTACAAATGACTGTCCAGGCCCCGGGCAGGATACGGAC  463
Qy  241  TGCAGGGAGTGTTGAGAGCGGCTCCTTCACCGCTTCAGAAAAACCACCTCAGACACTGCCTC  300
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Db  464  TGCAGGGAGTGTTGAGAGCGGCTCCTTCACCGCTTCAGAAAAACCACCTCAGACACTGCCTC  523
Qy  301  AGCTGCTCCAAATGCCGAAAGGAAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC  360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  524  AGCTGCTCCAAATGCCGAAAGGAAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC  583
Qy  361  CGGGACACCGGTGTGTGGTGCGCAGGAGAGACAACACAGTACCGGC...  420
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Db  584  CGGGACACCGGTGTGTGGTGCGCAGGAGAAGAACCAGTACCGGC...  643
Qy  421  TTCCAGTGCTTCAATTGCCAGCCTCTGGCCTCAACCGTCACCTCT...  480
         |||||||||||||||||||||||||||||||||||||||||||||
Db  644  TTCCAGTGCTTCAATTGCCAGCCTCTGGCCTCAACCGTCACCTCTCAATGGGACCGGTGCCACCTCTCAGGAG  703
Qy  481  AAACAGAACACCGTGTCGCACCTG  503
         ||||||||||||||||||||||||
Db  704  AAACAGAACACCGTGTCGCACCTG  726
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Right column

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RESULT  7
ID   US-08-050-319B-1 STANDARD; DNA; UNC; 501 BP.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 1, Application US/08050319B.
     Patent No. 5633145
CC   GENERAL INFORMATION:
CC   APPLICANT: M.Feldmann, P.W. Gray,
CC   APPLICANT: M.J.C. Turner, F.M Brennan
CC   TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC   TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC   NUMBER OF SEQUENCES: 57
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Reed & Robbins
CC   STREET: 635 Bryant Street
CC   CITY: Palo Alto
CC   STATE: California
CC   COUNTRY: USA
CC   ZIP: 94301
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: Patentin Release #1.0, version #1.25
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/050,319B
CC   FILING DATE: 10-May-1993
CC   CLASSIFICATION: 435
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Robbins, Roberta L.
CC   REGISTRATION NUMBER: 33,208
CC   REFERENCE/DOCKET NUMBER: 5150-0030
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (415) 617-8999
CC   TELEFAX: (415) 327-3231
CC   INFORMATION FOR SEQ ID NO: 1:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 501 base pairs
CC   TYPE: nucleic acid
CC   STRANDEDNESS: double
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: DNA (genomic)
CC   FEATURE:
CC   NAME/KEY: CDS
CC   LOCATION: 1..501
SQ   Sequence 501 BP; 121 A; 137 C; 137 G; 106 T; 0 other;

Query Match            32.5%;    Score 373;  DB 7;  Length 501;
Best Local Similarity  99.0%;    Pred. No. 4.58e-291;
Matches   377;   Conservative   0;   Mismatches   4;   Indels   0;   Gaps   0;

Qy  121  GATAGTGTGTGTCCCCAAGGAGAAAATATATCCACCCTCAAAATAATTAATTCGATTTGCTGTTACC  180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  344  GATAGTGTGTGTCCCCAAGGAAAATAATATATTCCACCCTCAAAATAATTAATTCGATTTGCTGTTACC  403
Qy  181  AAGTGCCACAAAGGAACCTACTTGTACAAATGACTGTCCAGGCCCCGGGCAGGATACGGAC  240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db  404  AAGTGCCACAAAGGAACCTACTTGTACAAATGACTGTCCAGGCCCCGGGCAGGATACGGAC  463
Qy  241  TGCAGGGAGTGTTGAGAGCGGCTCCTTCACCGCTTCAGAAAAACCACCTCAGACACTGCCTC  300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  464  TGCAGGGAGTGTTGAGAGCGGCTCCTTCACCGCTTCAGAAAAACCACCTCAGACACTGCCTC  523
Qy  301  AGCTGCTCCAAATGCCGAAAGGAAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC  360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  524  AGCTGCTCCAAATGCCGAAAGGAAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC  583
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Qy 361 CGGGACACCGTGTGTGGCTGCCAGGAAGAACCAGTACCGGCATTATTGGGAGTGAAAACCTT 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 584 CGGGACACCGTGTGTGGCTGCCAGGAAGAACCAGTACCGGCATTATTGGGAGTGAAAACCTT 643

Qy 421 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCCGTGCACCTCTTCCTGTGCCAGGAG 480
        |||||||||||||||||||| |||||||||||||||||||| || |||| |||||
Db 644 TTCCAGTGCTTCAATTGCACCCTCTGCCTCCGTGCACCCTGCCACCTCTCCTGTGTCAGGAG 703

Qy 481 AAACAGAACACCGTGTGCACC 501
        ||||||||||||| |||||||
Db 704 AAACAGAACACCGTCTGCACC 724

DE Sequence 3, Application US/08050319B.
XX
DT 01-JAN-1900
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AC xxxxxx
XX
ID US-08-050-319B-3 STANDARD; DNA; UNC; 372 BP.

RESULT 8

Patent No. 5633145
Sequence 3, Application US/08050319B

CC GENERAL INFORMATION:
CC APPLICANT: M.Feldmann, P.W.Gray,
CC APPLICANT: M.J.C. Turner, F.M Brennan
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC NUMBER OF SEQUENCES: 57
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Reed & Robbins
CC STREET: 635 Bryant Street
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/050,319B
CC FILING DATE: 10-May-1993
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Robbins, Roberta L.
CC REGISTRATION NUMBER: 33,208
CC REFERENCE/DOCKET NUMBER: 5150-0030
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 327-3231
CC TELEFAX: (415) 617-8999
CC INFORMATION FOR SEQ ID NO: 3:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 372 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: double
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 1..372
SQ Sequence 372 BP; 98 A; 102 C; 95 G; 77 T; 0 other;

Query Match   31.7%; Score 364; DB 7; Length 372;
Best Local Similarity   98.9%; Pred. No. 2.74e-283;
Matches   368; Conservative   0; Mismatches   4; Indels   0; Gaps   0;

Db 1 GTGTGTCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACCAAGTGC 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 350 GTGTGTCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACCAAGTGC 409
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CACAAAGGAACCTACTTGTACAATGACTGTCCAGCCCGGGGGGCCAGGATACGAGCGCAGG 120

Qy 410 CACAAAGGAACCTACTTGTACAATGACTGTCCAGCCCGGGGGGCCAGGATACGAGCGCAGG 469
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 GAGTGTGAGAGACGGCGTCCTTCACCGCCTTCAGAAAACCACCTCAGAGACACTGCCTCAGCTGC 180

Qy 470 GAGTGTGAGAGCGGCGTCCTTCAGGAGTGTTCAGAAAACCACCTCAGAGACACTGCCTCAGCTGC 529
        ||||||| |||||||||| ||||| |||| ||||||||||||||||||||||||||||||||||
Db 181 TCCAAATGCCGAAAAGGAAAATGGGTCAGGTGGCAGGTGGAGATCTTCTTCTTGCACAGTG 240

Qy 530 TCCAAATGCCGAAAAGGAAAATGGGTCAGGTGGCAGGTGGAGATCTTCTTCTTGCACAGTG 589
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 ACCGGTGTGGCCTGCAGGAAGAACCAGTACCGGCATTATTGGGAGTGAAAACCTTTTCCAG 300

Qy 590 ACCGGTGTGGCCTGCAGGAAGAACCAGTACCGGCATTATTGGGAGTGAAAACCTTTTCCAG 649
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 TGCTTCAATTGCAGCCTCTGCCTCCGTGCACCTCTTCCTGTGCCAGGAGAAAACAG 360

Qy 650 TGCTTCAATTGCACCCTCTGCCTCCGTGCACCCTGCCACCTCTCCTGTGTCAGGAGAAAACAG 709
        |||||||||||| ||||||||||||||||||| || |||| ||| ||||||||||||
Db 361 AACACCGTGTGC 372

Qy 710 AACACCGTCTGC 721

DE Sequence 49, Application US/08050319B.
XX
DT 01-JAN-1900
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AC xxxxxx
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ID US-08-050-319B-49 STANDARD; DNA; UNC; 474 BP.

RESULT 9

Patent No. 5633145
Sequence 49, Application US/08050319B

CC GENERAL INFORMATION:
CC APPLICANT: M.Feldmann, P.W.Gray,
CC APPLICANT: M.J.C. Turner, F.M Brennan
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC NUMBER OF SEQUENCES: 57
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Reed & Robbins
CC STREET: 635 Bryant Street
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/050,319B
CC FILING DATE: 10-May-1993
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Robbins, Roberta L.
CC REGISTRATION NUMBER: 33,208
CC REFERENCE/DOCKET NUMBER: 5150-0030
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 327-3231
CC TELEFAX: (415) 617-8999
CC INFORMATION FOR SEQ ID NO: 49:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 474 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: double

CC
CC
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA to mRNA
CC FEATURE:
CC   NAME/KEY: CDS
CC   LOCATION: 1..471
SQ Sequence 474 BP; 126 A; 126 C; 132 G; 106 T; 0 other;

Query Match   30.1%; Score 345; DB 7; Length 474;
Best Local Similarity 98.3%; Pred. No. 6.94e-267;
Matches 351; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db   118 AGAGAGTGTGAGGAGCGGCTCCTTCACCCGTTCAGAAAAACCACCTCAGACACTGCCTCAGC 177
          | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   467 AGGGAGTGTGAGGAGCGGCGGCTCCTTCACCCGTTCAGAAAAACCACCTCAGACACTGCCTCAGC 526

Db   178 TGCTCCAAATGCCGAAAAGGAAAAATGGGGTCAGGTGGGAGAGTCTCTTCTTCCACACTGGACACGG 237
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   527 TGCTCCAAATGCCGAAAGGAAAAATGGGGTCAGGTGGGAGAGATCTCTTTTTCTTCGACACTGGACCGG 586

Db   238 GACACCGTGTGGCTGCCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAAACCTTTTC 297
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   587 GACACCGTGTGGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAAACCTTTTC 646

Db   298 CAGTGCTTCAATTGCACGCCTCTGCCCTCAAATGGGACCGTGCACCTCTCCTGCAGGAGAAA 357
          |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Qy   647 CAGTGCTTCAATTGCACCTCTGCCCTCAAATGGGACCGTGCACCTCTCCTGTCAGGAGAAA 706

Db   358 CAGAACACCGTGTGCACCTGCCATGCACAGTTTCTTTTCTTAAGAGAAAACGAGTGTGTCTCC 417
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   707 CAGAACACCGTGTGCACCTGCCATGCACAGTTTCTTTTCTTAAGAGAAAACGAGTGTGTCTCC 766

Db   418 TGTAGTAACTGTAAGAAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCCAGATTTAG 474
          ||||||||||||||||||||||||||||||||||||| |||| ||||||||||||| ||
Qy   767 TGTAGTAACTGTAAGAAAAAGCCTGGAGTGCACGAAGTTGTCCTACCCCCAGATTGAG 823

RESULT 10
ID US-08-273-411-5 STANDARD; DNA; UNC; 2771 BP.

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AC xxxxxx
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DT 01-JAN-1900
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DE Sequence 5, Application US/08273411.
XX
Patent No. 5625124
Sequence 5, Application US/08273411.
GENERAL INFORMATION:
    APPLICANT: Falk, Per
    APPLICANT: Gordon, Jeffrey I.
    TITLE OF INVENTION: Animal Model for Gastro-Intestinal
    TITLE OF INVENTION: Disease
    NUMBER OF SEQUENCES: 10
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Patrea L. Pabst
    STREET: 1100 Peachtree Street, Suite 2800
    CITY: Atlanta
    STATE: Georgia
    COUNTRY: USA
    ZIP: 30309-4530
    COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.25
    CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/273,411
    FILING DATE:
    CLASSIFICATION: 435
    ATTORNEY/AGENT INFORMATION:
    NAME: Pabst, Patrea L.
    REGISTRATION NUMBER: 31,284

CC REFERENCE/DOCKET NUMBER: WU106
CC TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (404) 815-6508
CC   TELEFAX: (404) 815-6555
CC INFORMATION FOR SEQ ID NO: 5:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 2771 base pairs
CC   TYPE: nucleic acid
CC   STRANDEDNESS: double
CC   TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
CC PUBLICATION INFORMATION:
CC   AUTHORS: Sweetser, et al.
CC   JOURNAL: Genes & Dev.
CC   VOLUME: 2
CC   PAGES: 1318-1332
CC   DATE: 1988
CC RELEVANT RESIDUES IN SEQ ID NO: 5: FROM 561 TO 629
CC PUBLICATION INFORMATION:
CC   AUTHORS: Seeburg, et al.
CC   JOURNAL: DNA
CC   VOLUME: 1
CC   PAGES: 239-249
CC   DATE: 1982
CC RELEVANT RESIDUES IN SEQ ID NO: 5: FROM 620 TO 2771
CC PUBLICATION INFORMATION:
CC   AUTHORS: Sweetser, et al.
CC   JOURNAL: J. Biol. Chem.
CC   VOLUME: 261
CC   PAGES: 5553-5561
CC   DATE: 1986
CC RELEVANT RESIDUES IN SEQ ID NO: 5: FROM 1 TO 617
SQ Sequence 2771 BP; 666 A; 718 C; 683 T; 704 G; 0 other;

Query Match   25.1%; Score 288; DB 7; Length 2771;
Best Local Similarity 95.6%; Pred. No. 8.12e-218;
Matches 323; Conservative 0; Mismatches 11; Indels 4; Gaps 3;

Db   680 ATGGCTACAGGTAAGCGCCCCTAAAATCCCTTTGGGCACAAATGTGTCCTGAGGGGAGAGG 739
          ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Qy   6 ATGGCTACAGGTAAGCGCCCCTAAAATCCCTTTGGGCACAAATGTGTCCTGAGGGGAGAGG 65

Db   740 CAGCGACCTGTAGATGGGACGGGGGCACTAACCCTCAGTTTGGGGCTTCTGAATG--AG 797
          |||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Qy   66 CAGCGACCTGTAGATGGGACGGGGGCACTAACCCTCAGTTTGGGGCTTTTGAATGTGAG 125

Db   798 TATCGCCATGTAAGCCCAGTATG-GCC-AATCTCAGAGAAAGCTCCTGGTCCCTGGAGGGAT 855
          ||| ||||||||||||||||||| ||| |||||||||||||||||||||||||||||||||
Qy   126 TATGGCCATGTAAGCCCAGTATTGCCCAATCTCAGAGAAAGCTCCTGGTCCCCTGGAGGGAT 185

Db   856 GGAGAGAGAAAAACAGAAACAGCTCCTGGACCAGGAGGAGAGTGCCGTGCCCTTTGCTCTCCGGC 915
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   186 GGAGAGAGAAAAACAGAAACAGCTCCTGGACCAGGAGCACTCCTGGCGCCTCTTGCTCTCGCGGC 245

Db   916 TCCCTCTCGTTGCCCCTCTCGGTTTCTCCCCAGGCTCCCGGACGGTCCCTGGCTTTTG 975
          ||| |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Qy   246 TCCCTGTGTTGCCCTGGGTTTTCTCCCCACGCTCCCGGACGGTCCCTGGCTTTTG 305

Db   976 GCCTGCCTCTGCCTGCCTCTGCCTTCAAGAGAGGGCAGTGCC 1013
          ||||||||||||||||||||||||||||||||||||||||||
Qy   306 GCCTGCCTCTGCCTGCCCTGGCCTTCAAGAGAGGGCAGTGCC 343

RESULT 11
ID US-08-343-401A-3 STANDARD; DNA; UNC; 4283 BP.

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AC xxxxxx
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DT 01-JAN-1900
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Sequence 3, Application US/08343401A.

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DE   Sequence 3, Application US/08343401A.
XX
     Patent No. 5661132
CC   GENERAL INFORMATION:
CC   APPLICANT:    Swain, William F
CC   APPLICANT:    Macklin, Michael D
CC   APPLICANT:    Eriksson, Elof
CC   APPLICANT:    Andree, Christophe
CC   TITLE OF INVENTION:  Improved Wound Healing
CC   NUMBER OF SEQUENCES:  4
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE:    Quarles & Brady
CC   STREET:       PO Box 2113
CC   CITY:         Madison
CC   STATE:        WI
CC   COUNTRY:      USA
CC   ZIP:          53701-2113
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE:  Floppy disk
CC   COMPUTER:     IBM PC compatible
CC   OPERATING SYSTEM:  PC-DOS/MS-DOS
CC   SOFTWARE:     PatentIn Release #1.0, Version #1.30
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER:  US/08/343,401A
CC   FILING DATE:  22-NOV-1994
CC   CLASSIFICATION:  514
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME:         Seay, Nicholas J
CC   REGISTRATION NUMBER:  27,386
CC   REFERENCE/DOCKET NUMBER:  11-229-9103-9
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE:    608-251-5000
CC   TELEFAX:      608-251-9166
CC   INFORMATION FOR SEQ ID NO: 3:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH:       4283 base pairs
CC   TYPE:         nucleic acid
CC   STRANDEDNESS:  double
CC   TOPOLOGY:     circular
CC   MOLECULE TYPE:  DNA (genomic)
CC   IMMEDIATE SOURCE:
CC   CLONE:        pWRG1630
CC   FEATURE:
CC   NAME/KEY:     exon
CC   LOCATION:     713..721
CC   FEATURE:
CC   NAME/KEY:     exon
CC   LOCATION:     981..1253
CC   FEATURE:
CC   NAME/KEY:     CDS
CC   LOCATION:     join(713..721, 981..1253)
CC   FEATURE:
CC   NAME/KEY:     sig_peptide
CC   LOCATION:     713..1049
SQ   Sequence 4283 BP; 1023 A; 1095 C; 1114 G; 1051 T; 0 other;
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Query Match   25.0%; Score 287; DB 7; Length 4283;
Best Local Similarity 93.2%; Pred. No. 5.86e-217;
Matches 315; Conservative   0; Mismatches 22; Indels 1; Gaps 1;

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Qy   713 ATGGCTACAGGTAAGCGCGCCCCTAAAATCCCTTTGG-CACAATGTGTCCTGAGGGGAGAGG 771
         ||||||||| ||||||||||||||||||||||||||||  |||||||||||||||||||||
Db     6 ATGGCTACAGGTAAGCGCCCTAAAAATCCCTTTGGGCACAATGTGTCCTGAGGGGAGAGG 65

Qy   772 CAGGCGACCTGTAGATGGAGGGGGCCACTAAACCCTCAGGGTTTGGGGTTCTGAAGTGAG 831
         ||||||| |||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    66 CAGGCGACCTGTAGATGGGACGGGGGCACTAACCCTCAGGGTTTGGGGTTCTGAAGTGAG 125

Qy   832 TATCGCCATCTAAGCCCCAGTATTTGCCCAATCTCAGAAAAGCTCCTCGGTCCCTGGAGGAT 891
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||||
Db   126 TATGGCCATGTAAGCCCCAGTATTTGCCCAATCTCAGAAAAGCTCCTCGGTCCCTGGAGGAT 185
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ID US-08-445-265A-1 STANDARD; DNA; UNC; 4283 BP.

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AC   xxxxxx
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DT   01-JAN-1900
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DE   Sequence 1, Application US/08445265A.
XX
CC   Patent No. 5697901
CC   GENERAL INFORMATION:
CC   APPLICANT:    Eriksson, Elof
CC   TITLE OF INVENTION:  GENE DELIVERY BY MICRONEEDLE INJECTION
CC   NUMBER OF SEQUENCES:  4
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE:    Quarles & Brady
CC   STREET:       1 South Pinckney Street
CC   CITY:         Madison
CC   STATE:        WI
CC   COUNTRY:      US
CC   ZIP:          53703
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE:  Floppy disk
CC   COMPUTER:     IBM PC compatible
CC   OPERATING SYSTEM:  PC-DOS/MS-DOS
CC   SOFTWARE:     PatentIn Release #1.0, Version #1.30
CC   CURRENT APPLICATION DATA:
CC   TELEPHONE:    608-251-5000
CC   TELEFAX:      608-251-9166
CC   INFORMATION FOR SEQ ID NO: 1:
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME:         Seay, Nicholas J
CC   REGISTRATION NUMBER:  27386
CC   REFERENCE/DOCKET NUMBER:  110229.91080
CC   TELECOMMUNICATION INFORMATION:
CC   CLASSIFICATION:  604
CC   FILING DATE:
CC   APPLICATION NUMBER:  US/08/445,265A
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH:       4283 base pairs
CC   TYPE:         nucleic acid
CC   STRANDEDNESS:  double
CC   TOPOLOGY:     circular
CC   MOLECULE TYPE:  other nucleic acid
CC   DESCRIPTION:  /desc = "Plasmid DNA"
CC   FEATURE:
CC   NAME/KEY:     CDS
CC   LOCATION:     join(713..721, 981..1250)
SQ   Sequence 4283 BP; 1023 A; 1095 C; 1114 G; 1051 T; 0 other;
```

Query Match   25.0%; Score 287; DB 7; Length 4283;
Best Local Similarity 93.2%; Pred. No. 5.86e-217;
Matches 315; Conservative   0; Mismatches 22; Indels 1; Gaps 1;

```
Qy   713 ATGGCTACAGGTAAGCGCGCCCCTAAAATCCCTTTGG-CACAATGTGTCCTGAGGGGAGAGG 771
         ||||||||| ||||||||||||||||||||||||||||  |||||||||||||||||||||
Db     6 ATGGCTACAGGTAAGCGCCCTAAAAATCCCTTTGGGCACAATGTGTCCTGAGGGGAGAGG 65
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Db   892 GGAGAGAGAAAAACAAACAGCTCCTGAGCAGGAGAGAGTGTTGGGCCTCTTGCTCTCCGGC 951
         |||||||||||||||||||||||||||||||||||| || | |||||||||||||| ||||
Qy   186 GGAGAGAGAAAAACAAACAGCTCCTGAGCAGCAGGGACAGCTCCTTGCCTTGCTCTGCGGGC 245

Db   952 TCCCTCTGTTGCCCTCTGGTTTCTCCCACAGGCGTCCCGGACGGTCCCCTCGTCCGGCTTTTG 1011
         ||| | |||||||  ||| ||| |||||||||||||||||||||||||||||||||||||||
Qy   246 TCCGTGTGTTGGCCCTGTGGTTTCTCCCACAGGTCCCGGACGGTCCCCTGCTCTCGGCTTTTG 305

Db  1012 GCCTGCTTCTGCCTGCCCTGGCTTCAAGAGGGCCAGTGCC 1049
         |||||||||||||||||||||||||||||||||||||
Qy   306 GCCTGCTTCTGCCTGCCCTGGCTTCAAGAGGGCAGTGCC 343
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RESULT 13
ID US-08-050-319B-53 STANDARD; DNA; UNC; 477 BP.

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DT 01-JAN-1900
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DE xxxxxx
XX
CC Sequence 53, Application US/0805031 9B.
CC Patent No. 5633145
CC GENERAL INFORMATION:
CC APPLICANT: M.Feldmann, P.W. Gray,
CC APPLICANT: M.J.C. Turner, F.M Brennan
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC NUMBER OF SEQUENCES: 57
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Reed & Robbins
CC STREET: 635 Bryant Street
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/050,319B
CC FILING DATE: 10-May-1993
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Robbins, Roberta L.
CC REGISTRATION NUMBER: 33,208
CC REFERENCE/DOCKET NUMBER: 5150-0030
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 617-8999
CC TELEFAX: (415) 327-3231
CC INFORMATION FOR SEQ ID NO: 53:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 477 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: double
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA to mRNA
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 1..474
SQ Sequence 477 BP; 117 A; 122 C; 131 G; 107 T; 0 other;

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Db  772 CAGCGACCTGTAGATGGGACGGGGGGGACTAACCCTCAGGGGTTTGGGGTTCTGAATGTGAG 831
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Qy   66 CAGCGACCTGTAGATGGGACGGGGGGCACTAACCCTCAGGTTTGGGGCTTTGAATGTGCAG 125
Db  832 TATCGCCATCTAAGCCCAGTATTTGGCCAATCTCAGAAAGCTCCTGCCTCCCTGGAGGGAT 891
        ||||| |||| ||||||||||||| |||||||||||||| ||||||| || ||||||||||| |||
Qy  126 TATGGCCATGTAAGCCCAGTATTTGCCCAATCTCAGAAAGCTCCTGTCCCTGGAGGGAT 125
Db  892 GGAGAGAGAAAACAAACAGCTCCTGGAGCAGGAGAGTGTTGGCCCTCTTGCTCTCCGGC 951
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Qy  186 GGAGAGAGAAAACAAACAGCTCCTGGAGCAGGAGCACTCCGGCCTTCTTGCTCTGGGGC 245
Db  952 TCCCTCTGTTGCCCCTCTCCTTGGTTTCTTCCCCAGCTCCCGTCCCTCCTCTCTGGGCTTTTTG 1011
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Qy  246 TCCGTGTGTTGCCCTGTGGTTTTCTCCCCACGTCCCTGCTCCTCGTCCTTTG 305
Db 1012 GCCTGCTCTGCCTGCCCTGGCTTCAAGAGGGCCAGTGCC 1049
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Qy  306 GCCTGCTCTGCCTGCCCTGGCTTCAAGAGGGCCAGTGCC 343
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Query Match 22.2%; Score 255; DB 7; Length 477;
Best Local Similarity 98.9%; Pred. No. 1.56e-189;
Matches 258; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 14
ID US-08-050-319B-51 STANDARD; DNA; UNC; 462 BP.

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AC
XX
DT 01-JAN-1900
XX
DE xxxxxx
XX
CC Sequence 51, Application US/0805031 9B.
CC Patent No. 5633145
CC GENERAL INFORMATION:
CC APPLICANT: M.Feldmann, P.W. Gray,
CC APPLICANT: M.J.C. Turner, F.M Brennan
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC NUMBER OF SEQUENCES: 57
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Reed & Robbins
CC STREET: 635 Bryant Street
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/050,319B
CC FILING DATE: 10-May-1993
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Robbins, Roberta L.
CC REGISTRATION NUMBER: 33,208
CC REFERENCE/DOCKET NUMBER: 5150-0030
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 617-8999
CC TELEFAX: (415) 327-3231
CC INFORMATION FOR SEQ ID NO: 51:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 462 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: double
CC TOPOLOGY: linear

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Db  121 GATAGTGTGTGTCCCCAGGAGAAAATATATCCACCCTCAAAATAATTCGAATTGCTGTACC 180
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Db  181 AACTGCCCACAAAGGAACCTACTTGTACAATGACTGTGTCCAGGCCCGGGGCCAGGATACGGAC 240
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Qy  404 AAGTGCCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCCAGGATACCGAC 463
Db  241 TGCAGGGAGTGTGAGAGGGCCTCCTTCACCGGCTTCAGAAAAACCACCTAGACACTGCCTC 300
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Qy  464 TGCAGGGAGTGTGAGAGCGGGTCCTTCACCGGCTTCAGAAAACCACCTCAGACACTGCCTC 523
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Qy  524 AGCTGCTCCAAAATCCCGAAAAGGAAAATGGGTCAGGTGGAGATCTCTTCTTTGCACAGTGGAC 583
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CC   MOLECULE TYPE: cDNA to mRNA
CC   FEATURE:
CC   NAME/KEY: CDS
CC   LOCATION: 1..459
SQ   Sequence 462 BP; 116 A; 119 C; 121 G; 106 T; 0 other;

Query Match   18.6%;   Score 213;   DB 7;   Length 462;
Best Local Similarity   97.8%;   Pred. No. 1.02e-153;
Matches   218;   Conservative   0;   Mismatches   5;   Indels   0;   Gaps   0;

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Db    240 CTGCAGGAGGAACCAGTACCGGCACMTTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTG 299
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Qy    661 CACCCTCTGCCTCAAATGGGACCGTGCACCTCTCCTGTCAGGAGAAACAGAACACCGTGTG 720

Db    360 CACCTGCCATGCAGGTTTCTTTTCTAAGAGAAAACGAGTGTGTCCCTGTGAGTAACTGTAA 419
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    721 CACCTGCCATGCAGGTTTCTTTTCTAAGAGAAAACGAGTGTGTCCCTGTGAGTAACTGTAA 780

Db    420 GAAAAGCCTGGAGTGCACCAAGTTGTGCCTACCCCAGATTTAG 462
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Qy    781 GAAAAGCCTGGAGTGCACCAAGTTGTCCCTACCCCAGATTGAG 823
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CC   TYPE: NUCLEIC ACID
CC   STRANDEDNESS: SINGLE
CC   TOPOLOGY: LINEAR
CC   MOLECULE TYPE: cDNA
SQ   Sequence 534 BP; 108 A; 166 C; 143 G; 117 T; 0 other;

Query Match   5.8%;   Score 67;   DB 6;   Length 534;
Best Local Similarity   97.2%;   Pred. No. 4.70e-33;
Matches   69;   Conservative   0;   Mismatches   2;   Indels   0;   Gaps   0;

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Qy    273 CACGCTCCCGGACGTCCCTCCTGGCTTTTGGCCTGTCGTCCTGGCTTCAAG 332

Db     68 AGGGCAGTGCC 78
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Qy    333 AGGGCAGTGCC 343
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Search completed: Wed May   6 10:57:34 1998
Job time : 87 secs.

RESULT   15
ID   US-08-187-756C-3 STANDARD; DNA; UNC; 534 BP.

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AC   xxxxxx

XX

DT   01-JAN-1900

XX

DE   Sequence 3, Application US/08187756C.
XX   Patent No. 5597709
XX   GENERAL INFORMATION:
XX   APPLICANT: ROSEN, ET AL.
XX   TITLE OF INVENTION: Human Growth Hormone
CC   NUMBER OF SEQUENCES: 7
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
CC   CECCHI, STEWART & OLSTEIN
CC   STREET: 6 BECKER FARM ROAD
CC   CITY: ROSELAND
CC   STATE: NEW JERSEY
CC   COUNTRY: USA
CC   ZIP: 07068
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: 3.5 INCH DISKETTE
CC   COMPUTER: IBM PS/2
CC   OPERATING SYSTEM: MS-DOS
CC   SOFTWARE: WORD PERFECT 5.1
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/187,756C
CC   FILING DATE: January 27, 1994
CC   CLASSIFICATION: 435
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER:
CC   FILING DATE:
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: FERRARO, GREGORY D.
CC   REGISTRATION NUMBER: 36,134
CC   REFERENCE/DOCKET NUMBER: 325800-55
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: 201-994-1700
CC   TELEFAX: 201-994-1744
CC   INFORMATION FOR SEQ ID NO: 3:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 534 BASE PAIRS

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**************************************************************
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 M P S R C H  (TM)

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**************************************************************

        Release 3.0.5AA John F. Collins, Biocomputing Research Unit.
        Copyright (c) 1993-1997 University of Edinburgh, U.K.
                Distribution rights by Oxford Molecular Ltd
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MPsrch.pp   protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 6 08:20:59 1998; MasPar time 4.78 Seconds
                                        367.559 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-4
Description: (1-307) from US08004166.pep
Perfect Score: 2341
Sequence: 1 SRTSLLIAFGLLCLPWLQEG............PSLPSPSRLPGPSDTPILPQ 307

Scoring table: PAM 150
               Gap 11

Searched: 62627 seqs, 5720858 residues

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database: a-issued
             1:back1 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:PCT90
             10:PCT91 11:PCT92 12:PCT93 13:PCT94 14:PCT95 15:PCT96

Statistics: Mean 30.606; Variance 140.802; scale 0.217

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description	Pred. No.
1	1124	48.0	455	7	US-08-321-	Sequence 2, Applicatio	4.13e-91
2	1124	48.0	455	7	US-08-050-	Sequence 25, Applicati	4.13e-91
3	1115	47.6	199	5	US-08-425-	Sequence 48, Applicatio	2.79e-90
4	1025	43.8	145	6	US-08-425-	Sequence 2, Applicatio	5.45e-82
5	1025	43.8	145	6	US-08-425-	Sequence 1, Applicatio	5.45e-82
6	1020	43.6	145	7	US-08-298-	Sequence 1, Applicatio	1.57e-81
7	995	42.5	145	7	US-08-425-	Sequence 10, Applicatio	3.13e-79
8	996	42.5	167	7	US-08-050-	Sequence 57, Applicatio	2.54e-79
9	996	42.5	167	7	US-08-050-	Sequence 2, Applicatio	2.54e-79
10	981	41.9	124	7	US-08-050-	Sequence 4, Applicatio	6.07e-78
11	800	34.2	157	7	US-08-050-	Sequence 50, Applicati	3.36e-61
12	740	31.6	114	6	US-08-425-	Sequence 9, Applicatio	7.01e-56
13	734	31.4	114	6	US-08-425-	Sequence 7, Applicatio	2.47e-55
14	714	30.5	117	6	US-08-425-	Sequence 11, Applicatio	1.63e-53
15	684	29.2	114	6	US-08-425-	Sequence 8, Applicatio	8.72e-51
16	666	28.4	158	7	US-08-050-	Sequence 54, Applicati	3.76e-49
17	651	27.8	117	6	US-08-425-	Sequence 12, Applicatio	8.62e-48
18	613	26.2	149	6	US-08-425-	Sequence 5, Applicatio	2.38e-44
19	477	20.4	153	7	US-08-050-	Sequence 52, Applicati	4.02e-32
20	339	14.5	41	7	US-08-050-	Sequence 36, Applicati	6.36e-20
21	324	13.8	40	7	US-08-050-	Sequence 26, Applicati	1.29e-18
22	318	13.6	43	7	US-08-050-	Sequence 31, Applicati	4.28e-18
23	296	12.6	45	1	5451527-	Patent No. 5451527.	3.43e-16
24	287	12.3	111	6	US-08-425-	Sequence 3, Applicatio	2.04e-15
25	287	12.3	111	6	US-08-425-	Sequence 4, Applicatio	2.04e-15
26	282	12.0	112	6	US-08-425-	Sequence 6, Applicatio	5.49e-15
27	268	11.4	46	5	US-08-086-	Sequence 12, Applicati	6.68e-14
28	261	11.1	46	5	US-08-086-	Sequence 14, Applicati	3.43e-13
29	260	11.1	131	7	5177193-3	Patent No. 5177193.	4.17e-13
30	249	10.6	46	5	US-08-086-	Sequence 11, Applicati	3.59e-12
31	249	10.6	46	5	US-08-086-	Sequence 13, Applicati	3.59e-12
32	230	9.8	41	5	5395760-4	Patent No. 5395760.	1.44e-10
33	227	9.7	34	1	5451527-4	Patent No. 5451527.	2.57e-10
34	227	9.7	39	1	5451527-8	Patent No. 5451527.	2.57e-10
35	227	9.7	39	1	5451527-12	PCT-US94-0	Sequence 29, Applicatio	2.57e-10
36	225	9.6	39	13	PCT-US91-0	Sequence 2, Applicatio	3.78e-10
37	225	9.6	325	10	PCT-US91-0	Sequence 4, Applicatio	3.78e-10
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43	210	9.0	355	5	US-08-292-	Sequence 6, Applicatio	6.72e-09
44	209	8.9	41	1	5451527-10	Patent No. 5451527.	8.14e-09
45	209	8.9	41	1	5451527-11	Patent No. 5451527.	8.14e-09
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AC   xxxxxx
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DT   01-JAN-1900
XX
DE   Sequence 2, Application US/08321668.

ALIGNMENTS

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CC   Sequence 2, Application US/08321668.
CC   Patent No. 5665859
CC   GENERAL INFORMATION:
CC   APPLICANT:  WALLACH, David
CC   APPLICANT:  BRAKEBUSCH, Cord
CC   APPLICANT:  VARFOLOMEEV, Eugene
CC   APPLICANT:  BATKIN, Michael
CC   TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
CC   TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
CC   NUMBER OF SEQUENCES: 42
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: BROWDY AND NEIMARK
CC   STREET: 419 Seventh Street, N.W., Suite 300
CC   CITY: Washington
CC   STATE: D.C
CC   COUNTRY: USA
CC   ZIP: 20004
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: PatentIn Release #1.0, Version #1.30
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/321,668
CC   FILING DATE: 12-OCT-1994
CC   PRIOR APPLICATION DATA:
CC   CLASSIFICATION: 435
CC   APPLICATION NUMBER: IL 107268
CC   FILING DATE: 12-OCT-1993
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: BROWDY, Roger L.
CC   REGISTRATION NUMBER: 25,618
CC   REFERENCE/DOCKET NUMBER: WALLACH-13
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: 202-628-5197
CC   TELEFAX: 202-737-3528
CC   TELEX: 248633
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CC   INFORMATION FOR SEQ ID NO: 2:
CC     SEQUENCE CHARACTERISTICS:
CC       LENGTH: 455 amino acids
CC       TYPE: amino acid
CC       TOPOLOGY: linear
CC     MOLECULE TYPE: protein
SQ   SEQUENCE 455 AA; 50494 MW; 1048031 CN;

     Query Match       48.0%;  Score 1124;  DB 7;  Length 455;
     Best Local Similarity   99.3%;  Pred. No. 4.13e-91;
     Matches 142;  Conservative 1;  Mismatches 0;  Indels 0;  Gaps 0;

Db   41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQQDTDCRECESGSFTASENHLRHCL 100
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AC   xxxxxx
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DT   01-JAN-1900
XX
     Sequence 25, Application US/08050319B.

CC   Sequence 25, Application US/08050319B.
CC   Patent No. 5633145
CC   GENERAL INFORMATION:
CC     APPLICANT: M.Feldmann, P.W. Gray,
CC     APPLICANT: M.J.C. Turner, F.M Brennan
CC     TITLE OF INVENTION: Modified human TNFalpha
CC     TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC     NUMBER OF SEQUENCES: 57
CC     CORRESPONDENCE ADDRESS:
CC       ADDRESSEE: Reed & Robbins
CC       STREET: 635 Bryant Street
CC       CITY: Palo Alto
CC       STATE: California
CC       COUNTRY: USA
CC       ZIP: 94301
CC     COMPUTER READABLE FORM:
CC       MEDIUM TYPE: Floppy disk
CC       COMPUTER: IBM PC compatible
CC       OPERATING SYSTEM: PC-DOS/MS-DOS
CC       SOFTWARE: Patentin Release #1.0, version #1.25
CC     CURRENT APPLICATION DATA:
CC       APPLICATION NUMBER: US/08/050,319B
CC       FILING DATE: 10-May-1993
CC       CLASSIFICATION: 435
CC     ATTORNEY/AGENT INFORMATION:
CC       NAME: Robbins, Roberta L.
CC       REGISTRATION NUMBER: 33,208
CC       REFERENCE/DOCKET NUMBER: 5150-0030
CC     TELECOMMUNICATION INFORMATION:
CC       TELEPHONE: (415) 617-8999
CC       TELEFAX: (415) 327-3231
CC   INFORMATION FOR SEQ ID NO: 25:
CC     SEQUENCE CHARACTERISTICS:
CC       LENGTH: 455 amino acids
CC       TYPE: amino acid
CC       TOPOLOGY: linear
CC     MOLECULE TYPE: protein
SEQUENCE 455 AA; 50579 MW; 1048388 CN;
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     Best Local Similarity   99.3%;  Pred. No. 4.13e-91;
     Matches 142;  Conservative 1;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy   83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db  161 KQNTVCTCHAGFFLRENECVSCS 183
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AC   xxxxxx
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DT   01-JAN-1900
XX
     Sequence 48, Application US/08050319B.

CC   Sequence 48, Application US/08050319B.
CC   Patent No. 5633145
CC   GENERAL INFORMATION:
CC     APPLICANT: M.Feldmann, P.W. Gray,
CC     APPLICANT: M.J.C. Turner, F.M Brennan
CC     TITLE OF INVENTION: Modified human TNFalpha
CC     TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC     NUMBER OF SEQUENCES: 57
CC     CORRESPONDENCE ADDRESS:
CC       ADDRESSEE: Reed & Robbins
CC       STREET: 635 Bryant Street
CC       CITY: Palo Alto
CC       STATE: California
CC       COUNTRY: USA
CC       ZIP: 94301
CC     COMPUTER READABLE FORM:
CC       MEDIUM TYPE: Floppy disk
CC       COMPUTER: IBM PC compatible
CC       OPERATING SYSTEM: PC-DOS/MS-DOS
CC       SOFTWARE: Patentin Release #1.0, version #1.25
CC     CURRENT APPLICATION DATA:
CC       APPLICATION NUMBER: US/08/050,319B
CC       FILING DATE: 10-May-1993
CC       CLASSIFICATION: 435
CC     ATTORNEY/AGENT INFORMATION:
CC       NAME: Robbins, Roberta L.
CC       REGISTRATION NUMBER: 33,208
CC       REFERENCE/DOCKET NUMBER: 5150-0030
CC     TELECOMMUNICATION INFORMATION:
CC       TELEPHONE: (415) 617-8999
CC       TELEFAX: (415) 327-3231
CC   INFORMATION FOR SEQ ID NO: 48:
CC     SEQUENCE CHARACTERISTICS:
CC       LENGTH: 199 amino acids
CC       TYPE: amino acid
CC       TOPOLOGY: linear
CC     MOLECULE TYPE: protein
SEQUENCE 199 AA; 22186 MW; 195553 CN;
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     Query Match       47.6%;  Score 1115;  DB 7;  Length 199;
     Best Local Similarity   98.6%;  Pred. No. 2.79e-90;
     Matches 141;  Conservative 1;  Mismatches 1;  Indels 0;  Gaps 0;

Db   41 DSVCPTGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQQDTDCRECESGSFTASENHLRHCL 100
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Qy   23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQQDTDCRECESGSFTASENHLRHCL 82
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Db
Qy 101 SCSKCKRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
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Db 161 KQNTVCTCHAGFFLRENECVSCS 183
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Qy 143 KQNTVCTCHAGFFLRENECVSCA 165

RESULT 4
ID   US-08-425-673-2   STANDARD;   PRT;   145 AA.
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AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE
XX
     Sequence 2, Application US/08425673.
     Patent No. 5508261
CC   GENERAL INFORMATION:
CC   APPLICANT: Moyle, William R.
CC   APPLICANT: Campbell, Robert K.
CC   TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having
CC   TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and
CC   TITLE OF INVENTION: Methods For Preparing and Using Same
CC   NUMBER OF SEQUENCES: 12
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Richard R. Muccino
CC   STREET: P.O. Box 1267
CC   CITY: Princeton
CC   STATE: New Jersey
CC   COUNTRY: USA
CC   ZIP: 08551
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: PatentIn Release #1.0, Version #1.25
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/425,673
CC   FILING DATE:
CC   CLASSIFICATION: 514
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: US 07/717,151
CC   FILING DATE: 18-JUN-1991
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Muccino, Richard R.
CC   REGISTRATION NUMBER: 32,538
CC   REFERENCE/DOCKET NUMBER: UMD 1.0-004
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (609) 466-3407
CC   TELEFAX: (609) 466-2760
CC   INFORMATION FOR SEQ ID NO: 2:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 145 amino acids
CC   TYPE: amino acid
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: peptide
CC   HYPOTHETICAL: NO
CC   ANTI-SENSE: NO
SQ   SEQUENCE 145 AA; 15544 MW; 114662 CN;

Query Match   43.8%; Score 1025; DB 6; Length 145;
Best Local Similarity 99.3%; Pred. No. 5.45e-82;
Matches 138; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Db   7 PRCRPINATLAVEKEGCPVCITVNITICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 66
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 169 PRCRPINATLAVEKEGCPVCITVNITICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

Db   67 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTDCGGPKDHPLTCDDPRFQDSSSSKAPP 126
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTDCGGPKDHPLTCDDPRFQDSSSSKAPP 288
        |||||||||||||||||||
Db 127 SLPSPSRLPGPSDTPILPQ 145

Qy 289 SLPSPSRLPGPSDTPILPQ 307

RESULT 5
ID   US-08-425-673-1   STANDARD;   PRT;   145 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE
XX
     Sequence 1, Application US/08425673.
     Patent No. 5508261
CC   GENERAL INFORMATION:
CC   APPLICANT: Moyle, William R.
CC   APPLICANT: Campbell, Robert K.
CC   TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having
CC   TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and
CC   TITLE OF INVENTION: Methods For Preparing and Using Same
CC   NUMBER OF SEQUENCES: 12
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Richard R. Muccino
CC   STREET: P.O. Box 1267
CC   CITY: Princeton
CC   STATE: New Jersey
CC   COUNTRY: USA
CC   ZIP: 08551
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: PatentIn Release #1.0, Version #1.25
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/425,673
CC   FILING DATE:
CC   CLASSIFICATION: 514
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: US 07/717,151
CC   FILING DATE: 18-JUN-1991
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Muccino, Richard R.
CC   REGISTRATION NUMBER: 32,538
CC   REFERENCE/DOCKET NUMBER: UMD 1.0-004
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (609) 466-3407
CC   TELEFAX: (609) 466-2760
CC   INFORMATION FOR SEQ ID NO: 1:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 145 amino acids
CC   TYPE: amino acid
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: peptide
CC   HYPOTHETICAL: NO
CC   ANTI-SENSE: NO
SQ   SEQUENCE 145 AA; 15544 MW; 114662 CN;

Query Match   43.8%; Score 1025; DB 6; Length 145;
Best Local Similarity 99.3%; Pred. No. 5.45e-82;
Matches 138; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Db   7 PRCRPINATLAVEKEGCPVCITVNITICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 66
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 169 PRCRPINATLAVEKEGCPVCITVNITICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

Db   67 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTDCGGPKDHPLTCDDPRFQDSSSSKAPP 126
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTDCGGPKDHPLTCDDPRFQDSSSSKAPP 288

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Db  127  SLPSPSRLPGPSDTPILPQ  145
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Qy  289  SLPSPSRLPGPSDTPILPQ  307
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RESULT 6
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ID  US-08-298-189B-1        STANDARD;        PRT;        145 AA.
XX
AC  xxxxx
XX
DT  01-JAN-1900
XX
DE  Sequence 1, Application US/08298189B.
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CC Patent No. 5674727
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: Dr. Laurence A. Cole and Dr. Andrew Kardana
CC TITLE OF INVENTION: No. 5674727el Methods for Detecting Reproductive
CC TITLE OF INVENTION: Cancers or Tumors and Assay Products
CC TITLE OF INVENTION: Therefor
CC NUMBER OF SEQUENCES: 1
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Dr. Laurence A. Cole , c/o Dept. of Obstetrics and
CC STREET: 333 Cedar Street
CC CITY: New Haven
CC STATE: Connecticut
CC COUNTRY: USA
CC ZIP: 06510
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 3.5" diskette
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: Windows 95
CC SOFTWARE: Microsoft Word 7.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/298,189B
CC FILING DATE: 08/31/94
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Brian D. Voyce
CC REGISTRATION NUMBER: 28,917
CC REFERENCE/DOCKET NUMBER: DSI1
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 919-638-3939 or 803-272-1471
CC TELEFAX: 919-638-3939 or 803-272-1471
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 145 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: No. 5674727 applicable
CC TOPOLOGY: Unknown
CC MOLECULE TYPE: subunit of hormone, specifically the
CC MOLECULE TYPE: beta\subunit of hCG
CC ORIGINAL SOURCE: human urine
CC FEATURE:
CC NAME/KEY: beta subunit of hCG that is nicked by GBNE
CC LOCATION: hCG
CC IDENTIFICATION METHOD: N-terminal sequence analysis
CC PUBLICATION INFORMATION:
CC AUTHORS: Keutmann et alia
CC TITLE: "A Receptor-binding Region in Human
CC JOURNAL: Proc Nat'l Acad Sci USA   Choriogonadotrophin/Lutropr
CC VOLUME: 84
CC ISSUE: No. 5674727 applicable
CC PAGES: 2038-2042
CC DATE: 1987
SQ SEQUENCE 145 AA; 15476 MW; 116769 CN;

Query Match   43.6%;   Score 1020;   DB 7;   Length 145;
Best Local Similarity 98.6%; Pred. No. 1.57e-81;
Matches 137;   Conservative   2;   Mismatches   0;   Indels   0;   Gaps   0;

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Db  7  PRCRPINATLAVEKEGCPVCITVNTICAGYCPTMRVLQGVLPALPQVVCNYRDVRFES  66
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  7  PRCRPINATLAVEKEGCPVCITVNTICAGYCPTMRVLQGVLPALPQVVCNYRDVRFES  66
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Qy  169  PRCRPINATLAVEKEGCPVCITVNTICAGYCPTMRVLQGVLPALPQVVCNYRDVRFES  228
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   67  IRLPGCPRGVNPVVSYAVALSCQCALCKKSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP  126
         ||||||||||||||||||||||||||| :|||||||||||||||||||||||||||||||
Qy  229  IRLPGCPRGVNPVVSTAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP  288

Db  127  SLPSPSRLPGPSDTPILPQ  145
         ||||||||||||||||||
Qy  289  SLPSPSRLPGPSDTPILPQ  307
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RESULT 7
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ID  US-08-425-673-10        STANDARD;        PRT;        145 AA.
XX
AC  xxxxxx
XX
DT  01-JAN-1900
Qy  Sequence 10, Application US/08425673.
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CC Patent No. 5502261
CC GENERAL INFORMATION:
CC APPLICANT: Moyle, William R.
CC APPLICANT: Campbell, Robert K.
CC TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having
CC TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and
CC TITLE OF INVENTION: Methods for Preparing and Using Same
CC NUMBER OF SEQUENCES: 12
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Richard R. Muccino
CC STREET: P.O. Box 1267
CC CITY: Princeton
CC STATE: New Jersey
CC COUNTRY: USA
CC ZIP: 08551
CC CLASSIFICATION: 514
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC Compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/425,673
CC FILING DATE:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/717,151
CC FILING DATE: 18-JUN-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Muccino, Richard R.
CC REGISTRATION NUMBER: 32,538
CC REFERENCE/DOCKET NUMBER: UMD 1.0-004
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (609) 466-3407
CC TELEFAX: (609) 466-2760
CC INFORMATION FOR SEQ ID NO: 10:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 145 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
SQ SEQUENCE 145 AA; 15448 MW; 114931 CN;

Query Match   42.5%;   Score 995;   DB 6;   Length 145;
Best Local Similarity 96.4%; Pred. No. 3.13e-79;
Matches 134;   Conservative   1;   Mismatches   4;   Indels   0;   Gaps   0;

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Db    7  PRCRPINATLAVEKEGCPVCITVNTICAGYCPTMRVLQGVLPALPQVVCNYRDVRFES  66
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  169  PRCRPINATLAVEKEGCPVCITVNTICAGYCPTMRVLQGVLPALPQVVCNYRDVRFES  228
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Db   67 IRLPGPCPRGYVNPVVSYAVALSCQOCALCDSDSTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 126
        |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Qy 229 IRLPGPCPRGYVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 288

Db 127 SLPSPSRLPGPSDTPILPQ 145
        |||||||||||||||||||
Qy 289 SLPSPSRLPGPSDTPILPQ 307

RESULT 8
ID   US-08-050-319B-57   STANDARD;   PRT;   167 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 57, Application US/08050319B.
XX
CC   Sequence 57, Application US/08050319B.
CC   Patent No. 5633145
CC   GENERAL INFORMATION:
CC   APPLICANT: M.Feldmann, P.W. Gray,
CC   APPLICANT: M.J.C. Turner, F.M Brennan
CC   TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC   TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC   NUMBER OF SEQUENCES: 57
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Reed & Robbins
CC   STREET: 635 Bryant Street
CC   CITY: Palo Alto
CC   STATE: California
CC   COUNTRY: USA
CC   ZIP: 94301
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: PatentIn Release #1.0, version #1.25
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/050,319B
CC   FILING DATE: 10-May-1993
CC   CLASSIFICATION: 435
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Robbins, Roberta L.
CC   REGISTRATION NUMBER: 33,208
CC   REFERENCE/DOCKET NUMBER: 5150-0030
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (415) 617-8999
CC   TELEFAX: (415) 327-3231
CC   INFORMATION FOR SEQ ID NO: 57:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 167 amino acids
CC   TYPE: amino acid
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: protein
SQ   SEQUENCE 167 AA; 18626 MW; 139513 CN;

Query Match   42.5%; Score 996; DB 7; Length 167;
Best Local Similarity 100.0%; Pred. No 2.54e-79;
Matches   127; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db   41 DSVCPQGRYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   23 DSVCPQGRYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db 101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db 161 KQNTVCT 167
        |||||||
Qy 143 KQNTVCT 149

RESULT 9
ID   US-08-050-319B-2   STANDARD;   PRT;   167 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 2, Application US/08050319B.
XX
CC   Sequence 2, Application US/08050319B.
CC   Patent No. 5633145
CC   GENERAL INFORMATION:
CC   APPLICANT: M.Feldmann, P.W. Gray,
CC   APPLICANT: M.J.C. Turner, F.M Brennan
CC   TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC   TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC   NUMBER OF SEQUENCES: 57
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Reed & Robbins
CC   STREET: 635 Bryant Street
CC   CITY: Palo Alto
CC   STATE: California
CC   COUNTRY: USA
CC   ZIP: 94301
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: PatentIn Release #1.0, version #1.25
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/050,319B
CC   FILING DATE: 10-May-1993
CC   CLASSIFICATION: 435
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Robbins, Roberta L.
CC   REGISTRATION NUMBER: 33,208
CC   REFERENCE/DOCKET NUMBER: 5150-0030
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (415) 617-8999
CC   TELEFAX: (415) 327-3231
CC   INFORMATION FOR SEQ ID NO: 2:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 167 amino acids
CC   TYPE: amino acid
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: protein
SQ   SEQUENCE 167 AA; 18626 MW; 139513 CN;

Query Match   42.5%; Score 996; DB 7; Length 167;
Best Local Similarity 100.0%; Pred. No 2.54e-79;
Matches   127; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db   41 DSVCPQGRYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   23 DSVCPQGRYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db 101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db 161 KQNTVCT 167
        |||||||
Qy 143 KQNTVCT 149

RESULT 10
ID   US-08-050-319B-4   STANDARD;   PRT;   124 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900

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XX
DE   Sequence 4, Application US/0805031998.
XX
CC   Patent No. 5633145
CC   GENERAL INFORMATION:
CC   APPLICANT: M.Feldmann, P.W. Gray,
CC   APPLICANT: M.J.C. Turner, F.M Brennan
CC   TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC   TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC   NUMBER OF SEQUENCES: 57
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Reed & Robbins
CC   STREET: 635 Bryant Street
CC   CITY: Palo Alto
CC   STATE: California
CC   COUNTRY: USA
CC   ZIP: 94301
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: Patentin Release #1.0, version #1.25
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/050,319B
CC   FILING DATE: 10-May-1993
CC   CLASSIFICATION: 435
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Robbins, Roberta L.
CC   REGISTRATION NUMBER: 33,208
CC   REFERENCE/DOCKET NUMBER: 5150-0030
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (415) 617-8999
CC   TELEFAX: (415) 327-3231
CC   INFORMATION FOR SEQ ID NO: 4:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 124 amino acids
CC   TYPE: amino acid
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: protein
SQ   SEQUENCE 124 AA; 14047 MW; 75840 CN;

Query Match
Best Local Similarity 100.0%;   Score 981;  DB 7;  Length 124;
Matches 124;  Conservative 0;   Pred. No. 6.07e-78;
                                Mismatches 0;  Indels 0;  Gaps 0;

Db    1  VCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSGSFTASENHLRHCLSC   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   25  VCPQGKYIHPQNNSICCTRCHKGTYLYNDCPGPGQDTDCRECESGSGSFTASENHLRHCLSC   84

Db   61  SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHWSENLFQCFNCSLCLNGTVHLSCQEKQ    120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   85  SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHWSENLFQCFNCSLCLNGTVHLSCQEKQ    144

Db  121  NTVC  124
         ||||
Qy  145  NTVC  148

RESULT 11
ID   US-08-050-3198-50       STANDARD;    PRT;    157 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 50, Application US/0805031998.
XX
CC   Patent No. 5633145
CC   GENERAL INFORMATION:
CC   APPLICANT: M.Feldmann, P.W. Gray,
CC   APPLICANT: M.J.C. Turner, F.M Brennan
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CC   TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC   TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC   NUMBER OF SEQUENCES: 57
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Reed & Robbins
CC   STREET: 635 Bryant Street
CC   CITY: Palo Alto
CC   STATE: California
CC   COUNTRY: USA
CC   ZIP: 94301
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: Patentin Release #1.0, version #1.25
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/050,319B
CC   FILING DATE: 10-May-1993
CC   CLASSIFICATION: 435
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Robbins, Roberta L.
CC   REGISTRATION NUMBER: 33,208
CC   REFERENCE/DOCKET NUMBER: 5150-0030
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (415) 617-8999
CC   TELEFAX: (415) 327-3231
CC   INFORMATION FOR SEQ ID NO: 50:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 157 amino acids
CC   TYPE: amino acid
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: protein
SQ   SEQUENCE 157 AA; 17570 MW; 122247 CN;

Query Match
Best Local Similarity 96.2%;   Score 800;  DB 7;  Length 157;
Matches 102;  Conservative 2;  Pred. No. 2.36e-61;
                               Mismatches 2;  Indels 0;  Gaps 0;

Db   36  DREKRECESGSGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWS   95
         |:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   60  DTDCRECESGSGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWS  119

Db   96  ENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCS  141
         |||||||||||||||||||||||||||||||||||||||:|||||:
Qy  120  ENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCA  165

RESULT 12
ID   US-08-425-673-9         STANDARD;    PRT;    114 AA.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 9, Application US/08425673.
XX
CC   Patent No. 5508261
CC   GENERAL INFORMATION:
CC   APPLICANT: Moyle, William R.
CC   APPLICANT: Campbell, Robert K.
CC   TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having
CC   TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and
CC   TITLE OF INVENTION: Methods for Preparing and Using Same
CC   NUMBER OF SEQUENCES: 12
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Richard R. Muccino
CC   STREET: P.O. Box 1267
CC   CITY: Princeton
CC   STATE: New Jersey
CC   COUNTRY: USA
CC   ZIP: 08551
CC   COMPUTER READABLE FORM:
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CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08,425,673
CC FILING DATE:
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/717,151
CC FILING DATE: 18-JUN-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Muccino, Richard R.
CC REGISTRATION NUMBER: 32,538
CC REFERENCE/DOCKET NUMBER: UMD 1.0-004
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (609) 466-2760
CC TELEFAX: (609) 466-3407
CC INFORMATION FOR SEQ ID NO: 9:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 114 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
SQ SEQUENCE 114 AA; 12250 MW; 68564 CN;

Query Match 31.6%; Score 740; DB 6; Length 114;
Best Local Similarity 93.3%; Pred. No. 7.01e-56;
Matches 97; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy   7 PRCRPINATLAVEKEGCPVCITVNTIICAGYCPTMTRVLQGYLPALPQVVCNYRDVRFES 66
         |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db 169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGYLPALPQVVCNYRDVRFES 228

Qy   67 IRLPGCPRGVNPVVSYAVALSCQCALCDSDSTDCGGPKDHPSYC 110
         ||||||||||||||||||||||||||| |||||||||
Db 229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTC 272

RESULT 13
ID US-08-425-673-7 STANDARD; PRT; 114 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 7, Application US/08425673.
XX
CC GENERAL INFORMATION:
CC APPLICANT: Moyle, William R.
CC APPLICANT: Campbell, Robert K.
CC TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having
CC TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and
CC TITLE OF INVENTION: Methods For Preparing and Using Same
CC NUMBER OF SEQUENCES: 12
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Richard R. Muccino
CC STREET: P.O. Box 1267
CC CITY: Princeton
CC STATE: New Jersey
CC COUNTRY: USA
CC ZIP: 08551
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08,425,673

CC FILING DATE:
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/717,151
CC FILING DATE: 18-JUN-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Muccino, Richard R.
CC REGISTRATION NUMBER: 32,538
CC REFERENCE/DOCKET NUMBER: UMD 1.0-004
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (609) 466-2760
CC TELEFAX: (609) 466-3407
CC INFORMATION FOR SEQ ID NO: 7:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 114 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
SQ SEQUENCE 114 AA; 12401 MW; 67071 CN;

Query Match 31.4%; Score 734; DB 6; Length 114;
Best Local Similarity 91.7%; Pred. No. 2.47e-55;
Matches 99; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy   7 PRCRPINATLAVEKEGCPVCITVNTIICAGYCPTMTRVLQGYLPALPQVVCNYRDVRFES 66
         |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db 169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGYLPALPQVVCNYRDVRFES 228

Qy   67 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCTVRGLGPSYCDDPR 114
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Db 229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPR 276

RESULT 14
ID US-08-425-673-11 STANDARD; PRT; 117 AA.
XX
DE Sequence 11, Application US/08425673.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
CC GENERAL INFORMATION:
CC APPLICANT: Moyle, William R.
CC APPLICANT: Campbell, Robert K.
CC TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having
CC TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and
CC TITLE OF INVENTION: Methods For Preparing and Using Same
CC NUMBER OF SEQUENCES: 12
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Richard R. Muccino
CC STREET: P.O. Box 1267
CC CITY: Princeton
CC STATE: New Jersey
CC COUNTRY: USA
CC ZIP: 08551
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08,425,673
CC PRIOR APPLICATION DATA:
CC CLASSIFICATION: 514
CC FILING DATE:
CC APPLICATION NUMBER: US 07/717,151
CC FILING DATE: 18-JUN-1991
CC ATTORNEY/AGENT INFORMATION:

CC NAME: Muccino, Richard R.
CC REGISTRATION NUMBER: 32,538
CC REFERENCE/DOCKET NUMBER: UMD 1.0-004
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (609) 466-3407
CC TELEFAX: (609) 466-2760
CC INFORMATION FOR SEQ ID NO: 11:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 117 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
SQ SEQUENCE 117 AA; 12890 MW; 72412 CN;

Query Match 30.5%; Score 714; DB 6; Length 117;
Best Local Similarity 98.9%; Pred. No. 1.63e-53;
Matches 93; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 7 PRCRPINATLAVEKEGCPVCITVNITICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 66
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Qy 169 PRCRPINATLAVEKEGCPVCITVNITICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

Db 67 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDC 100
|||||||||||||||||||||||||||||||||
Qy 229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDC 262

RESULT 15
ID US-08-425-673-8   STANDARD;   PRT;   114 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 8, Application US/08425673.
XX

CC Sequence 8, Application US/08425673.
CC Patent No. 5508261
CC GENERAL INFORMATION:
CC APPLICANT: Moyle, William R.
CC APPLICANT: Campbell, Robert K.
CC TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having
CC TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and
CC TITLE OF INVENTION: Methods For Preparing and Using Same
CC NUMBER OF SEQUENCES: 12
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Richard R. Muccino
CC STREET: P.O. Box 1267
CC CITY: Princeton
CC STATE: New Jersey
CC COUNTRY: USA
CC ZIP: 08551
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC Compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/425,673
CC FILING DATE:
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/717,151
CC FILING DATE: 18-JUN-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Muccino, Richard R.
CC REGISTRATION NUMBER: 32,538
CC REFERENCE/DOCKET NUMBER: UMD 1.0-004
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (609) 466-3407
CC TELEFAX: (609) 466-2760

CC INFORMATION FOR SEQ ID NO: 8:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 114 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
SQ SEQUENCE 114 AA; 12242 MW; 69571 CN;

Query Match 29.2%; Score 684; DB 6; Length 114;
Best Local Similarity 94.7%; Pred. No. 8.72e-51;
Matches 89; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Db 7 PRCRPINATLAVEKEGCPVCITVNITICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 66
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Qy 169 PRCRPINATLAVEKEGCPVCITVNITICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

Db 67 IRLPGCPRGVNPVVSYAVALSCQCALCDSDSTDC 100
||||||||||||||||||||||||||| : |||
Qy 229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDC 262

Search completed: Wed May 6 08:21:12 1998
Job time : 13 secs.

MPSRCH (TM)

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****************************************************************
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         Distribution rights by Oxford Molecular Ltd
****************************************************************
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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed May   6 10:28:56 1998; MasPar time 67.26 Seconds
                                              941.976 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-3
Description: (1-1202) from US08804166.seq
Perfect Score: 1202
N.A. Sequence: Comp:
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   1 CTCGAGATGGCTACAGGTAA................CCCGATCCTCCACAATAA 1202
     GAGCTCTACCGATGTCCATT.............GGGGCTAGGAGGGTGTTATT
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Scoring table: TABLE default
                  Gap 6

Nmatch STD :   Dbase 0: Query 0

Searched: 10136 seqs, 26354296 bases x 2

Post-processing: Minimum Match 0%
                  Listing first 45 summaries

Database: n-issued
                  1:back1 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:PCT90
                  10:PCT91 11:PCT92 12:PCT93 13:PCT94 14:PCT95 15:PCT96

Statistics: Mean 8.771; Variance 4.649; scale 1.887

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description	Pred. No.
1	424	35.3	2062	7	US-08-050-	Sequence 24, Applicati	1.20e+00
2	424	35.3	2175	7	US-08-321-	Sequence 1, Applicatio	0.00e+00
3	424	35.3	6889	5	US-08-286-	Sequence 2, Applicatio	0.00e+00
4	424	35.3	6889	14	PCT-US95-0	Sequence 2, Applicatio	0.00e+00
5	420	34.9	600	7	US-08-050-	Sequence 47, Applicati	0.00e+00
6	381	31.7	504	7	US-08-050-	Sequence 1, Applicatio	6.06e-276
7	379	31.5	501	7	US-08-050-	Sequence 56, Applicati	2.43e-274
8	370	30.8	372	7	US-08-050-	Sequence 3, Applicatio	3.96e-267
9	302	25.1	2771	7	US-08-273-	Sequence 5, Applicatio	8.84e-213
10	300	25.0	474	7	US-08-050-	Sequence 49, Applicati	3.47e-211
11	301	25.0	4283	7	US-08-343-	Sequence 3, Applicatio	5.54e-212
12	301	25.0	4283	7	US-08-445-	Sequence 1, Applicatio	5.54e-212
13	255	21.2	477	7	US-08-050-	Sequence 53, Applicati	2.07e-175
14	169	14.1	462	7	US-08-050-	Sequence 51, Applicati	1.03e-107
15	103	8.6	138	5	US-08-086-	Sequence 2, Applicatio	5.77e-57
16	99	8.2	138	5	US-08-086-	Sequence 1, Applicatio	5.92e-54
17	88	7.3	7218	7	US-08-232-	Sequence 14, Applicati	9.89e-46
18	69	5.7	534	7	US-08-187-	Sequence 3, Applicatio	8.57e-32
19	69	5.7	654	6	US-08-187-	Sequence 1, Applicatio	8.57e-32
20	59	4.9	321	4	US-07-920-	Sequence 23, Applicati	1.20e-24
21	59	4.9	321	4	US-08-314-	Sequence 23, Applicati	1.20e-24
22	59	4.9	597	6	US-08-187-	Sequence 1, Applicatio	1.20e-24
23	59	4.9	2248	7	US-08-636-	Sequence 1, Applicatio	9.36e-20
24	52	4.3	2248	7	US-08-780-	Sequence 1, Applicatio	9.36e-20
25	52	4.3	2248	6	US-08-369-	Sequence 1, Applicatio	9.36e-20
26	52	4.3	2248	7	US-08-475-	Sequence 1, Applicatio	9.36e-20
27	52	4.3	7218	7	US-08-232-	Sequence 14, Applicati	5.54e-15
28	40	3.3	215	6	US-08-238-	Sequence 1, Applicatio	1.14e-11
29	38	3.2	633	7	US-08-388-	Sequence 1, Applicatio	2.26e-10
30	36	3.0	4810	7	US-08-453-	Sequence 7, Applicatio	4.31e-09
31	36	3.0	4810	13	PCT-US94-0	Sequence 7, Applicatio	4.31e-09
32	36	3.0	4810	12	PCT-US93-0	Sequence 3, Applicatio	4.31e-09
33	36	3.0	4810	14	PCT-US95-0	Sequence 3, Applicatio	4.31e-09
34	36	3.0	4810	7	US-08-188-	Sequence 3, Applicatio	4.31e-09
35	36	3.0	5125	12	PCT-US93-0	Sequence 11, Applicati	4.31e-09
36	36	3.0	5125	7	US-08-453-	Sequence 11, Applicati	4.31e-09
37	36	3.0	5323	12	PCT-US93-0	Sequence 9, Applicatio	4.31e-09
38	36	3.0	5323	7	US-08-453-	Sequence 9, Applicatio	4.31e-09
39	36	3.0	196	6	US-08-239-	Sequence 5, Applicatio	4.31e-09
40	32	2.7	215	6	US-08-238-	Sequence 14, Applicati	1.36e-06
41	32	2.7	1006	7	US-08-050-	Sequence 14, Applicati	1.36e-06
42	30	2.5	33	7	US-08-050-	Sequence 2, Applicatio	2.21e-05
43	26	2.2	74	14	PCT-US95-1	Sequence 94, Applicati	4.79e-03
44	27	2.2	81	14	PCT-US95-1	Sequence 92, Applicati	1.29e-03
45	26	2.2	82	14	PCT-US95-1	Sequence 97, Applicati	4.79e-03

ALIGNMENTS

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RESULT 1
ID    US-08-050-319B-24 STANDARD; DNA; UNC; 2062 BP.
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AC
XX
DT    01-JAN-1900
XX
DE    xxxxxx
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CC    Sequence 24, Application US/08050319B.
CC    Patent No. 5633145
CC    GENERAL INFORMATION:
CC     APPLICANT: M.Feldmann, P.W. Gray,
CC     APPLICANT: M.J.C. Turner, F.M Brennan
CC     TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC     TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC     NUMBER OF SEQUENCES: 57
CC     CORRESPONDENCE ADDRESS:
CC      ADDRESSEE: Reed & Robbins
CC      STREET: 635 Bryant Street
CC      CITY: Palo Alto
CC      STATE: California
CC      COUNTRY: USA
CC      ZIP: 94301
CC     COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Floppy disk
CC      COMPUTER: IBM PC compatible
CC      OPERATING SYSTEM: PC-DOS/MS-DOS
CC      SOFTWARE: Patentin Release #1.0, version #1.25
CC     CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: US/08/050,319B
CC      FILING DATE: 10-May-1993
CC      CLASSIFICATION: 435
CC     ATTORNEY/AGENT INFORMATION:
CC      NAME: Robbins, Roberta L.
CC      REGISTRATION NUMBER: 33,208
CC      REFERENCE/DOCKET NUMBER: 5150-0030
CC     TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: (415) 617-8999
CC      TELEFAX: (415) 327-3231
CC     INFORMATION FOR SEQ ID NO: 24:
CC      SEQUENCE CHARACTERISTICS:
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CC LENGTH: 2062 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: double
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA to mRNA
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 155..1519
SQ Sequence 2062 BP; 429 A; 617 C; 573 G; 443 T; 0 other;

Query Match   35.3%;   Score 424;   DB 7;   Length 2062;
Best Local Similarity 99.8%;   Pred. No. 0.00e+00;
Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db  275  GATAGTGTGTGTCCCCAAGGAAAAATATATCCACCCTCAAAATAATTCGAATTGCTTGTACC  334
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Qy  345  GATAGTGTGTGTCCCCAAGGAAAAATATATCCACCCTCAAAATAATTCGAATTGCTTGTACC  404

Db  335  AAGTGCCACAAAAGGAAACCTACTTGTACAATGACTGTGTCCAGGCCCGGGGCAGGATACGGAC  394
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Qy  405  AAGTGCCACAAAAGGAAACCTACTTGTACAATGACTGTGTCCAGGCCCGGGGCAGGATACGGAC  464

Db  395  TGCAGGGAGTGTGAGAGCGGCGCTCCTTCACCGCTTCAGAAAAACCACCTCAGACACTGCCTC  454
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Qy  465  TGCAGGGAGTGTGAGAGCGGCGCTCCTTCACCGCTTCAGAAAAACCACCTCAGACACTGCCTC  524

Db  455  AGCTGCTCCAAATGCCGAAAAGGAAAATGGGTCAGGTGGAGATCTCTTCTTCTTGCACAGTGGAC  514
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Qy  525  AGCTGCTCCAAATGCCGAAAAGGAAAATGGGTCAGGTGGAGATCTCTTCTTCTTGCACAGTGGAC  584

Db  515  CGGGACACCGTGTGTGGCGTGCAGGAAGAACCAGTACCGGCCATTATTGGGAGTGAAAAACCTT  574
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Qy  585  CGGGACACCGTGTGTGGCGTGCAGGAAGAACCAGTACCGGCCATTATTGGGAGTGAAAAACCTT  644

Db  575  TTCCAGTGCTTCAATTGCACCCTCTGCCCTCAAATGGGACCGTGCACCTCTCCTGCCAGGAG  634
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Qy  645  TTCCAGTGCTTCAATTGCACCCTCTGCCCTCAAATGGGACCGTGCACCTCTCCTGCCAGGAG  704

Db  635  AAACAGAACACCGTTGTGCACCTGCCATGCGAGGTTTCTTTCTAAGAGAAAAACGAGTGTGTC  694
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Qy  705  AAACAGAACACCGTTGTGCACCTGCCATGCGAGGTTTCTTTCTAAGAGAAAAACGAGTGTGTC  764

Db  695  TCCTGT  700
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Qy  765  TCCTGT  770
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RESULT 2
ID US-08-321-668-1 STANDARD; DNA; UNC; 2175 BP.

XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 1, Application US/08321668.
XX
CC Sequence 1, Application US/08321668.
CC Patent No. 5665859
CC GENERAL INFORMATION:
CC APPLICANT: WALLACH, David
CC APPLICANT: BRAKEBUSCH, Cord
CC APPLICANT: VARFOLOMEEV, Eugene
CC APPLICANT: BATNIN, Michael
CC TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
CC TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
CC NUMBER OF SEQUENCES: 42
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: BROWDY AND NEIMARK
CC STREET: 419 Seventh Street, N.W., Suite 300
CC CITY: Washington
CC STATE: D.C.
CC COUNTRY: USA

CC ZIP: 20004
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/321,668
CC FILING DATE: 12-OCT-1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 435
CC FILING DATE: 12-OCT-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: BROWDY, Roger L.
CC REGISTRATION NUMBER: 25,618
CC REFERENCE/DOCKET NUMBER: WALLACH-13
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-628-5197
CC TELEFAX: 202-737-3528
CC TELEX: 248633
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 2175 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 256..1620
SQ Sequence 2175 BP; 474 A; 604 C; 641 G; 456 T; 0 other;

Query Match   35.3%;   Score 424;   DB 7;   Length 2175;
Best Local Similarity 99.8%;   Pred. No. 0.00e+00;
Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db  436  AAGTGCCACAAAAGGAAACCTACTTGTACAATGACTGTGTCCAGGCCCGGGGCAGGATACGGAC  495
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Qy  405  AAGTGCCACAAAAGGAAACCTACTTGTACAATGACTGTGTCCAGGCCCGGGGCAGGATACGGAC  464

Db  496  TGCAGGGAGTGTGAGAGCGGCGGCTCCTTCACCGCTTCAGAAAAACCACCTCAGACACTGCCTC  555
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  465  TGCAGGGAGTGTGAGAGCGGCGGCTCCTTCACCGCTTCAGAAAAACCACCTCAGACACTGCCTC  524

Db  556  AGCTGCTCCAAATGCCGAAAAGGAAAATGGGTCAGGTGGAGATCTCTTCTTCTTGCACAGTGGAC  615
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Qy  525  AGCTGCTCCAAATGCCGAAAAGGAAAATGGGTCAGGTGGAGATCTCTTCTTCTTGCACAGTGGAC  584

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Qy  585  CGGGACACCGTGTGTGGCGTGCAGGAAGAACCAGTACCGGCCATTATTGGGAGTGAAAAACCTT  644

Db  676  TTCCAGTGCTTCAATTGCACCCTCTGCCCTCAAATGGGACCGTGCACCTCTCCTGCCAGGAG  735
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Qy  645  TTCCAGTGCTTCAATTGCACCCTCTGCCCTCAAATGGGACCGTGCACCTCTCCTGCCAGGAG  704

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Qy  705  AAACAGAACACCGTTGTGCACCTGCCATGCGAGGTTTCTTTCTAAGAGAAAAACGAGTGTGTC  764

Db  796  TCCTGT  801
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Qy  765  TCCTGT  770
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RESULT 3
ID US-08-286-740-2 STANDARD; DNA; UNC; 6889 BP.

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AC   xxxxxx
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DT   01-JAN-1900
XX
DE   Sequence 2, Application US/08285740.
XX
     Patent No. 5561053
XX
     Sequence 2, Application US/08285740
CC   GENERAL INFORMATION:
CC   APPLICANT: Crowley, Craig W.
CC   TITLE OF INVENTION: METHOD FOR SELECTING HIGH-EXPRESSING
CC   HOST CELLS
CC   NUMBER OF SEQUENCES: 4
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Genentech, Inc.
CC   STREET: 460 Point San Bruno Blvd
CC   CITY: South San Francisco
CC   STATE: California
CC   COUNTRY: USA
CC   ZIP: 94080
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
CC   COMPUTER: IBM PC compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: patin (Genentech)
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/286,740
CC   FILING DATE: 05-AUG-1994
CC   CLASSIFICATION: 435
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER:
CC   FILING DATE:
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Lee, Wendy M.
CC   REGISTRATION NUMBER:
CC   REFERENCE/DOCKET NUMBER: 798
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: 415/225-1994
CC   TELEFAX: 415/952-9881
CC   TELEX: 910/371-7168
CC   INFORMATION FOR SEQ ID NO: 2:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 6889 bases
CC   TYPE: nucleic acid
CC   STRANDEDNESS: double
CC   TOPOLOGY: linear
SQ   Sequence 6889 BP; 1729 A; 1826 C; 1681 G; 1653 T; 0 other;

Query Match   35.3%;   Score 424;   DB 6;   Length 6889;
Best Local Similarity   99.8%;   Pred. No. 0.00e+00;
Matches   425; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

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Db   1725 GATAGTGTGTGTCCCAAGGAAAATAATATCCACCTCAAAAATAATAATTCGATTTGCTGTACC 1784
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Qy    345 GATAGTGTGTGTCCCAAGGAAAATAATATCCACCTCAAAAATAATAATTCGATTTGCTGTACC  404
Db   1785 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGACCCGGGGCCAGGATACGGAC 1844
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGACCCGGGGCCAGGATACGGAC  464
Db   1845 TGCAGGGAGTGTGAGACGGGGTCCTTCACCGGTTCAGAAAACCACCTCAGACACTGCCTC 1904
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGTGTGAGGAGCGGGCTCTTCACCGGTTCAGAAAACCACCTCAGACACTGCCTC  524
Db   1905 AGCTGCTCCCAAAATGCCCAAGGAAAATGGGTCAGGTGGAGATCTCTTCTTCTTGCACAGTGGAC 1964
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    525 AGCTGCTCCCAAAATGCCCAAGGAAAATGGGTCAGGTGGAGATCTCTTCTTCTTGCACAGTGGAC  584
Db   1965 CGGGACACCGTGTGTGGCTGCAGGAGGAACCAGTACCGGCATTATTGGAGTGAAAAACCTT 2024
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    585 CGGGACACCGTGTGTGGCTGCAGGAGGAACCAGTACCGGCATTATTGGAGTGAAAAACCTT  644
Db   2025 TTCCAGTGCTTCAATTGCAGCCTCTGCCTTCAATTGGACCGTGGCACCTCTTCCTCCCAGGAG 2084
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTTCAATTGGACCGTGGCACCTCTTCCTCCCAGGAG  704
Db   2085 AAACAGAACACCGTGTGCCACCTGCCAGGTTTCTTTCTAAGAGAAGAAAACGAGTGTGTC 2144
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Qy    705 AAACAGAACACCGTGTGCCACCTGCCATGCAGGTTTCTTTCTAAGAGAAGAAAACGAGTGTGTC  764
Db   2145 TCCTGT 2150
          ||||||
Qy    765 TCCTGT  770
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RESULT   4
ID   PCT-US95-09576-2 STANDARD; DNA; UNC; 6889 BP.
XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 2, Application PC/TUS9509576.
XX
     Sequence 2, Application PC/TUS9509576
CC   GENERAL INFORMATION:
CC   APPLICANT: GENENTECH, INC.
CC   TITLE OF INVENTION: METHOD FOR SELECTING HIGH-EXPRESSING
CC   HOST CELLS
CC   NUMBER OF SEQUENCES: 4
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Genentech, Inc.
CC   STREET: 460 Point San Bruno Blvd
CC   CITY: South San Francisco
CC   STATE: California
CC   COUNTRY: USA
CC   ZIP: 94080
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
CC   COMPUTER: IBM PC compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: patin (Genentech)
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: PCT/US95/09576
CC   FILING DATE:
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 08/286740
CC   FILING DATE: 05-AUG-1994
CC   CLASSIFICATION:
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Lee, Wendy M.
CC   REGISTRATION NUMBER: 00,000
CC   REFERENCE/DOCKET NUMBER: 798PCT
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: 415/225-1994
CC   TELEFAX: 415/952-9881
CC   TELEX: 910/371-7168
CC   INFORMATION FOR SEQ ID NO: 2:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 6889 bases
CC   TYPE: nucleic acid
CC   STRANDEDNESS: double
CC   TOPOLOGY: linear
SQ   Sequence 6889 BP; 1729 A; 1826 C; 1681 G; 1653 T; 0 other;

Query Match   35.3%;   Score 424;   DB 14;   Length 6889;
Best Local Similarity   99.8%;   Pred. No. 0.00e+00;
Matches   425; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

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Qy   1725 GATAGTGTGTGTCCCAAGGAAAATAATATCCACCTCAAAAATAATAATTCGATTTGCTGTACC 1784
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    345 GATAGTGTGTGTCCCAAGGAAAATAATATCCACCTCAAAAATAATAATTCGATTTGCTGTACC  404
Qy   1785 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGACCCGGGGCCAGGATACGGAC 1844
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1785 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGACCCGGGGCCAGGATACGGAC 1844
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Qy   405 AGTGCCTCCAAATGCCGAAAAGGAAATGGGTCAGGTGGGAGATCTCTTCTTGCACAGTGGAC 464
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1845 TGCAGGGAGTGTGAGAGGGCCTCCTTCACCGCTTCAGAAAAACCAGTCCAGACACACTGCCTC 1904

Qy   465 TGCAGGGAGTGTGAGAGGGCTCTTTCACCGCTTCAGAAAAACCACCTCAGACACACTGCCTC 524
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1905 AGCTGCTCCAAATGCCGAAAAGGAAATGGGTCAGGTGGGAGATCTCTTCTTGCACAGTGGAC 1964

Qy   525 AGCTGCTCCAAATGCCGAAAAGGAAATGGGTCAGGTGGGAGATCTCTTCTTGCACAGTGGAC 584
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1965 CGGGACACCCGTGTGTGGCTGCGCAGGAAGAGAACCAGTACCGGCCATTATTGGAGTGAAAAACCTT 2024

Qy   585 CGGGACACCCGTGTGTGGCTGCGCAGGAAGAGAACCAGTACCGGCCATTATTGGAGTGAAAAACCTT 644
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2025 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCTCCTGCCGGAG 2084

Qy   645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCTCCTGCCGGAG 704
           |||||||||||||||||||||||||||||||||||||||||
Db   2085 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 2144

Qy   705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2145 TCCTGT 2150

Qy   765 TCCTGT 770
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Db   765 TCCTGT 770

RESULT   5
ID   US-08-050-319B-47 STANDARD; DNA; UNC; 600 BP.
XX
AC   XXXXXX
XX
DT   01-JAN-1900
XX
DE   Sequence 47, Application US/08050319B.
CC   Patent No. 5633145
CC   GENERAL INFORMATION:
CC   APPLICANT: M.Feldmann, P.W.Gray,
CC   APPLICANT: M.J.C. Turner, F.M Brennan
CC   TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC   TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC   NUMBER OF SEQUENCES: 57
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Reed & Robbins
CC   STREET: 635 Bryant Street
CC   CITY: Palo Alto
CC   STATE: California
CC   COUNTRY: USA
CC   ZIP: 94301
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: Patentin Release #1.0, version #1.25
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/050,319B
CC   FILING DATE: 10-May-1993
CC   CLASSIFICATION: 435
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Robbins, Roberta L.
CC   REGISTRATION NUMBER: 33,208
CC   REFERENCE/DOCKET NUMBER: 5150-0030
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (415) 617-8999
CC   TELEFAX: (415) 327-3231
CC   INFORMATION FOR SEQ ID NO: 47:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 600 base pairs
CC   TYPE: nucleic acid

CC   STRANDEDNESS: double
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: cDNA to mRNA
CC   FEATURE:
CC   NAME/KEY: CDS
CC   LOCATION: 1..597
SQ   Sequence 600 BP; 148 A; 157 C; 162 G; 133 T; 0 other;

Query Match   34.9%;   Score 420;   DB 7;   Length 600;
Best Local Similarity 99.3%;   Pred. No. 0.00e+00;
Matches 423;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

Qy   121 GATAGTGTGTGTCCCACAGGAAAATATATCCACCCTCAAATAATATCGATTTGCTGTACC 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   345 GATAGTGTGTGTCCCACAGGAAAATATATCCACCCTCAAATAATATCGATTTGCTGTACC 404

Qy   181 AAGTGCCACAAAAGGAACCTACTTGTACAATGACTGTGTCCAGGCCCGGGCAGGATACGGAC 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   405 AAGTGCCACAAAAGGAACCTACTTGTACAATGACTGTGTCCAGGCCCGGGCAGGATACGGAC 464

Qy   241 TGCAGGGAGTGTGAGAGCGGGCTCCTTCACCGGCTTCAGAAAACCCACCTCAGAGACACTGCC 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   465 TGCAGGGAGTGTGAGAGCGGGCTCCTTCACCGGCTTCAGAAAACCCACCTCAGAGACACTGCC 524

Qy   301 AGCTGCTCCAAATGCCGAAAAGGAAATGGGTCAGGTGGGAGATCTCTTCTTGCACAGTGGAC 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   525 AGCTGCTCCAAATGCCGAAAAGGAAATGGGTCAGGTGGGAGATCTCTTCTTGCACAGTGGAC 584

Qy   361 CGGGACACCCGTGTGTGGCTGCGCAGGAAGAGAACCAGTACCGGCCATTATTGGAGTGAAAAACCTT 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   585 CGGGACACCCGTGTGTGGCTGCGCAGGAAGAGAACCAGTACCGGCCATTATTGGAGTGAAAAACCTT 644

Qy   421 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCTCCTGCCGGAG 480
           |||||||||||||||||||||||||||||||||||||||||
Db   645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCTCCTGCCGGAG 704

Qy   481 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Qy   541 TCCTGT 546
           ||||||
Db   765 TCCTGT 770

RESULT   6
ID   US-08-050-319B-56 STANDARD; DNA; UNC; 504 BP.
XX
AC   XXXXXX
XX
DT   01-JAN-1900
XX
DE   Sequence 56, Application US/08050319B.
CC   Patent No. 5633145
CC   GENERAL INFORMATION:
CC   APPLICANT: M.Feldmann, P.W.Gray,
CC   APPLICANT: M.J.C. Turner, F.M Brennan
CC   TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC   TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC   NUMBER OF SEQUENCES: 57
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Reed & Robbins
CC   STREET: 635 Bryant Street
CC   CITY: Palo Alto
CC   STATE: California
CC   COUNTRY: USA
CC   ZIP: 94301
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC compatible

Left column

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CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: PatentIn Release #1.0, version #1.25
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/050,319B
CC   FILING DATE: 10-May-1993
CC   CLASSIFICATION: 435
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Robbins, Roberta L.
CC   REGISTRATION NUMBER: 33,208
CC   REFERENCE/DOCKET NUMBER: 5150-0030
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (415) 617-8999
CC   TELEFAX: (415) 327-3231
CC   INFORMATION FOR SEQ ID NO: 56:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 504 base pairs
CC   TYPE: nucleic acid
CC   STRANDEDNESS: double
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: cDNA to mRNA
CC   FEATURE:
CC   NAME/KEY: CDS
CC   LOCATION: 1..501
SQ   Sequence 504 BP; 122 A; 137 C; 138 G; 107 T; 0 other;

Query Match          31.7%;    Score 381;  DB 7;  Length 504;
Best Local Similarity 99.7%;   Pred. No. 6.06e-276;
Matches  382;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;
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Db   121 GATAGTGTGTCCCCAGGAAAAATATATCCACCCTCAAAATAAATTAATTCGATTTGCTGTACC 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   345 GATAGTGTGTCCCCAGGAAAAATATATCCACCCTCAAAATAAATTAATTCGATTTGCTGTACC 404

Db   181 AAGTGCCACAAAGGAAACCTACTTGTACAATGACTGTCCAGGCCCGGCGGGGGAGGATACGGAC 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   405 AAGTGCCACAAAGGAAACCTACTTGTACAATGACTGTCCAGGCCCGGCGGGGGAGGATACGGAC 464

Db   241 TGCAGGGAGTGTGAGAGCGGCGCTCCTTCACGGCTTCAGAAAAACCACCTCAGACACTGCCTC 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   465 TGCAGGGAGTGTGAGAGCGGCGCTCTTCACGGCTTCAGAAAAACCACCTCAGACACTGCCTC 524

Db   301 AGCTGCTCCAAATGCCGAAAGGAAAATGGGTCAGGTGGAGATCTCTTCTTTGCACAGTGGAC 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   525 AGCTGCTCCAAATGCCGAAAGGAAAATGGGTCAGGTGGAGATCTCTTCTTTGCACAGTGGAC 584

Db   361 CGGGACACCGTGTGGCTGCAGGAGAGAACCAGTACCGGCATTATTGGAGTGAAAAACCTT 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   585 CGGGACACCGTGTGGCTGCAGGAGAGAACCAGTACCGGCATTATTGGAGTGAAAAACCTT 644

Db   421 TTCCAGTGTGCTTCAATTGCAGCCTCTTGCCCTCAAATGGGACCGTGCACCTCTCCGCCAGGAG 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   645 TTCCAGTGTGCTTCAATTGCAGCCTCTTGCCCTCAAATGGGACCGTGCACCTCTCCGCCAGGAG 704

Db   481 AAACAGAACACCGTGTGCACCTG 503
         |||||||||||||||||||||||
Qy   705 AAACAGAACACCGTGTGCACCTG 727
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RESULT  7
ID   US-08-050-319B-1 STANDARD; DNA; UNC; 501 BP.

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AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 1, Application US/08050319B.
XX
CC   Sequence 1, Application US/08050319B.
CC   Patent No. 5633145
CC   GENERAL INFORMATION:
CC   APPLICANT: M.Feldmann, P.W. Gray,
CC   APPLICANT: M.J.C. Turner, F.M Brennan
```

Right column

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CC   TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC   TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC   NUMBER OF SEQUENCES: 57
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Reed & Robbins
CC   STREET: 635 Bryant Street
CC   CITY: Palo Alto
CC   STATE: California
CC   COUNTRY: USA
CC   ZIP: 94301
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: PatentIn Release #1.0, version #1.25
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/050,319B
CC   FILING DATE: 10-May-1993
CC   CLASSIFICATION: 435
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Robbins, Roberta L.
CC   REGISTRATION NUMBER: 33,208
CC   REFERENCE/DOCKET NUMBER: 5150-0030
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (415) 617-8999
CC   TELEFAX: (415) 327-3231
CC   INFORMATION FOR SEQ ID NO: 1:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 501 base pairs
CC   TYPE: nucleic acid
CC   STRANDEDNESS: double
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: DNA (genomic)
CC   FEATURE:
CC   NAME/KEY: CDS
CC   LOCATION: 1..501
SQ   Sequence 501 BP; 121 A; 137 C; 137 G; 106 T; 0 other;

Query Match          31.5%;    Score 379;  DB 7;  Length 501;
Best Local Similarity 99.7%;   Pred. No. 2.43e-274;
Matches  380;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;
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Db   121 GATAGTGTGTCCCCAGGAAAAATATATCCACCCTCAAAATAAATTAATTCGATTTGCTGTACC 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   345 GATAGTGTGTCCCCAGGAAAAATATATCCACCCTCAAAATAAATTAATTCGATTTGCTGTACC 404

Db   181 AAGTGCCACAAAGGAAACCTACTTGTACAATGACTGTCCAGGCCCGGCGGGGGAGGATACGGAC 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   405 AAGTGCCACAAAGGAAACCTACTTGTACAATGACTGTCCAGGCCCGGCGGGGGAGGATACGGAC 464

Db   241 TGCAGGGAGTGTGAGAGCGGCGCTCCTTCACGGCTTCAGAAAAACCACCTCAGACACTGCCTC 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   465 TGCAGGGAGTGTGAGAGCGGCGCTCTTCACGGCTTCAGAAAAACCACCTCAGACACTGCCTC 524

Db   301 AGCTGCTCCAAATGCCGAAAGGAAAATGGGTCAGGTGGAGATCTCTTCTTTGCACAGTGGAC 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   525 AGCTGCTCCAAATGCCGAAAGGAAAATGGGTCAGGTGGAGATCTCTTCTTTGCACAGTGGAC 584

Db   361 CGGGACACCGTGTGGCTGCAGGAGAGAACCAGTACCGGCATTATTGGAGTGAAAAACCTT 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   585 CGGGACACCGTGTGGCTGCAGGAGAGAACCAGTACCGGCATTATTGGAGTGAAAAACCTT 644

Db   421 TTCCAGTGTGCTTCAATTGCAGCCTCTTGCCCTCAAATGGGACCGTGCACCTCTCCGCCAGGAG 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   645 TTCCAGTGTGCTTCAATTGCAGCCTCTTGCCCTCAAATGGGACCGTGCACCTCTCCGCCAGGAG 704

Db   481 AAACAGAACACCGTGTGCACC 501
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Qy   705 AAACAGAACACCGTGTGCACC 725
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RESULT  8
ID   US-08-050-319B-3 STANDARD; DNA; UNC; 372 BP.
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XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 3, Application US/08050319B.
XX
CC   Patent No. 5633145
XX
CC   GENERAL INFORMATION:
CC   APPLICANT: M.Feldmann, P.W. Gray,
CC   APPLICANT: M.J.C. Turner, F.M Brennan
CC   TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC   TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC   NUMBER OF SEQUENCES: 57
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Reed & Robbins
CC   STREET: 635 Bryant Street
CC   CITY: Palo Alto
CC   STATE: California
CC   COUNTRY: USA
CC   ZIP: 94301
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: Patentin Release #1.0, version #1.25
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/050,319B
CC   FILING DATE: 10-May-1993
CC   CLASSIFICATION: 435
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Robbins, Roberta L.
CC   REGISTRATION NUMBER: 33,208
CC   REFERENCE/DOCKET NUMBER: 5150-0030
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (415) 617-8999
CC   TELEFAX: (415) 327-3231
CC   INFORMATION FOR SEQ ID NO: 3:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 372 base pairs
CC   TYPE: nucleic acid
CC   STRANDEDNESS: double
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: DNA (genomic)
CC   FEATURE:
CC   NAME/KEY: CDS
CC   LOCATION: 1..372
SQ   Sequence 372 BP; 98 A; 102 C; 95 G; 77 T; 0 other;

Query Match    30.8%;   Score 370;  DB 7;  Length 372;
Best Local Similarity   99.7%;   Pred. No. 3.96e-267;
Matches  371;  Conservative   0;  Mismatches   1;  Indels  0;  Gaps  0;

Qy      1 GTGTGTCCCAAGGAAAATANTATNCCACCCTCAAAATAATTCANTTGCTTGTACCAAGTGC 60
          ||||||||||||||||||| |||||||||||||||||| ||||||||||||||||||||||
Db    351 GTGTGTCCCAAGGAAAATANTATNCCACCCTCAAAATAATNATTCGATTTGCTTGTACCAAGTGC 410

Qy     61 CACAAAGGAACCTACTTGTACAAATGACTGTCCAGGCCCCGGGGCCAGGATACGGACTGCAGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    411 CACAAAGGAACCTACTTGTACAAATGACTGTCCAGGCCCCGGGGCCAGGATACGGACTGCAGG 470

Qy    121 GAGTGTGAGAGCGGCTCCTTCACCGGTTCAGAAAAACCAGCACTGCCTCAGCTGC 180
          ||||||||||||||||| ||||||||||||||||||||||    ||||||||||
Db    471 GAGTGTGAGAGCGGCTCTTTCACCGGTTCAGAAAAACCACCTCAGACACTGCCTCAGCTGC 530

Qy    181 TCCAAATGCCAAGGAGAAATGGGTCAGGTGGAGATCTCTTCCTTGCACAGTGGACCGGGAC 240
          |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db    531 TCCAAATGCCAAGGAGAAATGGGTCAGGTGGAGATCTCTTCTTCTTGCACAGTGGACCGGGAC 590

Qy    241 ACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCCANTTATTGGAGTGAAAAACCTTTTCCAG 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    300
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Qy    591 ACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCCGCATTATTGGAGTGAAAAACCTTTTCCAG 650
          |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db    301 TGCTTCAATTGCAGCCICTGCCCTCAAATGGGACACGGTGCAACCTCTCCTGCCAGGAGAAACAG 360

Qy    651 TGCTTCAATTGCAGCCTCTGCCCTCAAATGGGACACGGTGCAACCTCTCCTGCCAGGAGAAACAG 710
          |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db    711 AACACCGTGTGC 722

Qy    361 AACACCGTGTGC 372
          ||||||||||||
Db    711 AACACCGTGTGC 722

RESULT   9
ID    US-08-273-411-5 STANDARD; DNA; UNC; 2771 BP.
XX
AC    xxxxxx
XX
DT    01-JAN-1900
XX
DE    Sequence 5, Application US/08273411.
XX
CC    Patent No. 5625124
CC    GENERAL INFORMATION:
CC    APPLICANT: Falk, Per
CC    APPLICANT: Gordon, Jeffrey I.
CC    TITLE OF INVENTION: Animal Model for Gastro-Intestinal
CC    TITLE OF INVENTION: Disease
CC    NUMBER OF SEQUENCES: 10
CC    CORRESPONDENCE ADDRESS:
CC    ADDRESSEE: Patrea L. Pabst
CC    STREET: 1100 Peachtree Street, Suite 2800
CC    CITY: Atlanta
CC    STATE: Georgia
CC    COUNTRY: USA
CC    ZIP: 30309-4530
CC    COMPUTER READABLE FORM:
CC    MEDIUM TYPE: Floppy disk
CC    COMPUTER: IBM PC compatible
CC    OPERATING SYSTEM: PC-DOS/MS-DOS
CC    SOFTWARE: Patentin Release #1.0, Version #1.25
CC    CURRENT APPLICATION DATA:
CC    APPLICATION NUMBER: US/08/273,411
CC    FILING DATE:
CC    CLASSIFICATION: 435
CC    ATTORNEY/AGENT INFORMATION:
CC    NAME: Pabst, Patrea L.
CC    REGISTRATION NUMBER: 31,284
CC    REFERENCE/DOCKET NUMBER: WU106
CC    TELECOMMUNICATION INFORMATION:
CC    TELEPHONE: (404) 815-6508
CC    TELEFAX: (404) 815-6555
CC    INFORMATION FOR SEQ ID NO: 5:
CC    SEQUENCE CHARACTERISTICS:
CC    LENGTH: 2771 base pairs
CC    TYPE: nucleic acid
CC    STRANDEDNESS: double
CC    TOPOLOGY: linear
CC    MOLECULE TYPE: DNA (genomic)
CC    HYPOTHETICAL: NO
CC    ANTI-SENSE: NO
CC    PUBLICATION INFORMATION:
CC    AUTHORS: Sweetser, et al.
CC    JOURNAL: Genes & Dev.
CC    VOLUME: 2
CC    PAGES: 1318-1332
CC    DATE: 1988
CC    RELEVANT RESIDUES IN SEQ ID NO: 5: FROM 561 TO 629
CC    PUBLICATION INFORMATION:
CC    AUTHORS: Seeburg, et al.
CC    JOURNAL: DNA
CC    VOLUME: 1
CC    PAGES: 239-249
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Left column

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CC  DATE: 1982
CC  RELEVANT RESIDUES IN SEQ ID NO: 5: FROM 620 TO 2771
CC  PUBLICATION INFORMATION:
CC  AUTHORS: Sweetser, et al.
CC  JOURNAL: J. Biol. Chem.
CC  VOLUME: 261
CC  PAGES: 5553-5561
CC  DATE: 1986
CC  RELEVANT RESIDUES IN SEQ ID NO: 5: FROM 1 TO 617
SQ  Sequence 2771 BP; 666 A; 718 C; 704 G; 683 T; 0 other;
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Query Match     25.1%; Score 302; DB 7; Length 2771;
Best Local Similarity 97.6%; Pred. No. 8.84e-213;
Matches   330; Conservative   0; Mismatches   4; Indels   4; Gaps   2;
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Db  680  ATGGCTACAGGTAAGGCGCCCCTAAAAATCCCTTTGGGCACAAATGTGTCCTGAGGGGAGGAGAGG  739
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Qy    7  ATGGCTACAGGTAAGGCGCCCCTAAAAATCCCTTTGGGCACAAATGTGTCCTGAGGGGAGGAGAGG   66

Db  740  CAGCGACCTGTAGAGATGGGGACGGGGGGGCCGGACTAACCCTCAGGTTGTTGGGGCTTCTGAATG--AG  797
         ||||||||||||||||||||||||| || ||||||||| ||||| || || ||||||| |||| | || |
Qy   67  TAGCGACCTGTAGAGATGGGGACGGGGGCCGACTAACCCTGAGGTTGGGGGCTTCTTGAAATGTGAG  126

Db  798  TATCGGCCATGTAAGCCCAGTAT--GGCCAATCTCAGAAAGCTCCCTGGTCCCTGGGAGGGAT  855
         ||||||||||||||||||||||    |||||| ||||||||||||||||||||||||||||||
Qy  127  TATCGGCCATGTAAGCCCAGTATTTGGCCCAATGTCAGAAAGCTCCCTGGTCCCTGGGAGGGAT  186

Db  856  GGAGAGAGAAAAACAAAACAGCTCCTCGGAGCAGGGAGAGTGCTGGCCTCTTGCTCTCCGGC  915
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Qy  187  GGAGAGAGAAAAACAAAACAGCTCCTCGGAGCAGGGAGAGTGCTGGCCTCTTGCTCTCCGGC  246

Db  916  TCCCTCTGTTGCCCTCTGGTTTCTCCCCAGCCTCCCGGACGTCCCCTGGCTTTTG  975
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Qy  247  TCCCTCTGTTGCCCTCTGGTTTCTCCCCCAGCCTCCCGGACGTCCCCTGGCTTTTG  306

Db  976  GCCTGCTCTGCCTGCCCTGGCGTTCAAGGAGGGCAGTGCC  1013
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Qy  307  GCCTGCTCTGCCTGCCCTGGCGTTCAAGGAGGGCAGTGCC  344
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RESULT 10
ID  US-08-050-319B-49 STANDARD; DNA; UNC; 474 BP.

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AC  xxxxxx
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DT  01-JAN-1900
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DE  Sequence 49, Application US/08050319B.
XX
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Sequence 49, Application US/08050319B
Patent No. 5631145
GENERAL INFORMATION:
   APPLICANT: M.Feldmann, P.W. Gray,
   APPLICANT: M.J.C. Turner, F.M Brennan
   TITLE OF INVENTION: Modified human TNFalpha (Tumor
      Necrosis Factor alpha) Receptor
   NUMBER OF SEQUENCES: 57
   CORRESPONDENCE ADDRESS:
      ADDRESSEE: Reed & Robbins
      STREET: 635 Bryant Street
      CITY: Palo Alto
      STATE: California
      COUNTRY: USA
      ZIP: 94301
   COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: PatentIn Release #1.0, version #1.25
   CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/050,319B
      FILING DATE: 10-May-1993
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Right column

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CC  CLASSIFICATION: 435
CC  ATTORNEY/AGENT INFORMATION:
CC  NAME: Robbins, Roberta L.
CC  REGISTRATION NUMBER: 33,208
CC  REFERENCE/DOCKET NUMBER: 5150-0030
CC  TELECOMMUNICATION INFORMATION:
CC  TELEPHONE: (415) 617-8999
CC  TELEFAX: (415) 327-3231
CC  INFORMATION FOR SEQ ID NO: 49:
CC  SEQUENCE CHARACTERISTICS:
CC  LENGTH: 474 base pairs
CC  TYPE: nucleic acid
CC  STRANDEDNESS: double
CC  TOPOLOGY: linear
CC  MOLECULE TYPE: cDNA to mRNA
CC  FEATURE:
CC  NAME/KEY: CDS
CC  LOCATION: 1..471
SQ  Sequence 474 BP; 110 A; 126 C; 132 G; 106 T; 0 other;
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Query Match     25.0%; Score 300; DB 7; Length 474;
Best Local Similarity 97.5%; Pred. No. 3.47e-211;
Matches   308; Conservative   0; Mismatches   8; Indels   0; Gaps   0;
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Db  105  GGACAGGGAGGAGGAGAGAGAGTGTGCAGAGAGCGCTCCTTCACGGCTTCAGAAAACCACCTCAG  164
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Qy  455  GGATACGGACTGCAGGGAGAGTGTGAGAGCGGGGCTCTTTCACGGCTTCAGAAAACCACCTCAG  514

Db  165  ACACTGCCTCAGCTGCTCCCAAATGCCGAAAGGAAAAGGGTCAGGTGGAGAATCTCTTCTTG  224
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Qy  515  ACACTGCCTCAGCTGCTCCAAATGCCGAAAGGAAAAGGGTCAGGTGGAGATCTCTTCTTG  574

Db  225  CACAGTGACCGGGACCACCGTGTTGTCGGCGTCAGGAGAGAACCACTACCGGCCATTATTGGAG  284
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Qy  515  CACAGTGACCGGGACACCGTGTTGGCGTCAGGAGAGAACCAGTACCGGCCATTATTGGAG  634

Db  285  TGAAAAACCTTTTCCAGGTGCTTCAAATTGCCAGCCTTCTGCCTCAATGGGACCGTGCACCTC  344
         ||||||||||||||  ||||| ||||||||| ||||| |||||||||||||||||||||||||
Qy  575  TGAAAAACCTTTTCCAGGTCCTTCAAATTGCAGCCTCCTTGCTCCATGGGACCGTGCACCTC  694

Db  345  CTGCCAGGAGAAACAGAACACCGTGCACCTGCCACCTGCCAGGGTTTCTTTCTAAGAGAAAA  404
         |||||||||||||| ||||||||||||||||||||||||| |||||||||||||||||||||
Qy  695  CTGCCAGGAGAAACAGAACACCGTGCACCTGCCACCTGCCATGGTTTCTTTCTAAGAGAAAA  754

Db  405  CGAGTGTGTCTCCTGT  420
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Qy  755  CGAGTGTGTCTCCTGT  770
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RESULT 11
ID  US-08-343-401A-3 STANDARD; DNA; UNC; 4283 BP.

XX
AC  xxxxxx
XX
DT  01-JAN-1900
XX
DE  Sequence 3, Application US/08343401A.
XX
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Sequence 3, Application US/08343401A
Patent No. 5561132
GENERAL INFORMATION:
   APPLICANT: Swain, William F
   APPLICANT: Macklin, Michael D
   APPLICANT: Eriksson, Elof
   APPLICANT: Andree, Christophe
   TITLE OF INVENTION: Improved Wound Healing
   NUMBER OF SEQUENCES: 4
   CORRESPONDENCE ADDRESS:
      ADDRESSEE: Quarles & Brady
      STREET: PO Box 2113
      CITY: Madison
      STATE: WI
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Left column:

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RESULT  12
ID   US-08-445-265A-1 STANDARD; DNA; UNC; 4283 BP.
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CC   COUNTRY: USA
CC   ZIP: 53701-2113
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: PatentIn Release #1.0, Version #1.30
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/343,401A
CC   FILING DATE: 22-NOV-1994
CC   CLASSIFICATION: 514
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Seay, Nicholas J
CC   REGISTRATION NUMBER: 27,386
CC   REFERENCE/DOCKET NUMBER: 11-229-9103-9
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: 608-251-5000
CC   TELEFAX: 608-251-9166
CC   INFORMATION FOR SEQ ID NO: 3:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 4283 base pairs
CC   TYPE: nucleic acid
CC   STRANDEDNESS: double
CC   TOPOLOGY: circular
CC   MOLECULE TYPE: DNA (genomic)
CC   IMMEDIATE SOURCE:
CC   CLONE: pWRG1630
CC   FEATURE:
CC   NAME/KEY: exon
CC   LOCATION: 713..721
CC   FEATURE:
CC   NAME/KEY: exon
CC   LOCATION: 981..1253
CC   FEATURE:
CC   NAME/KEY: CDS
CC   LOCATION: join(713..721, 981..1253)
CC   FEATURE:
CC   NAME/KEY: sig_peptide
CC   LOCATION: 713..1049
SQ   Sequence 4283 BP; 1023 A; 1095 C; 1114 G; 1051 T; 0 other;

Query Match             25.0%;  Score 301;  DB 7;  Length 4283;
Best Local Similarity   95.3%;  Pred. No. 5.54e-212;
Matches   322;  Conservative    0;  Mismatches   15;  Indels    1;  Gaps    1;

Db    713 ATGGCTACAGGTAAGCGCGCCCCTAAAAATCCCTTTGG-CACAATGTGTCCTGAGGGGAGAGG 771
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Qy      7 ATGGCTACAGGTAAGCGCGCCCCTAAAAATCCCTTTGGGCACAATGTGTCCTGAGGGGAGAGG 66

Db    772 CAGCGACCTGTAGGATGGGGACGGGGGCACTAAACCCTCCAGGGTGTTTGGGGTTTGAATGTGAG 831
          ||||||||||||||||||||||||||||||  |||| |||||||||||| || |||||||||||
Qy     67 TAGCGACCTGTAGGATGGGGACGGGGGCACTAACCCTGAGGTTTGGGGCTTCGAATGTGAG 126

Db    832 TATCGCCATCTAAGCCCCAGTATTTGGCCAATCTCAGAAAGCTCCTGGGCTCCCCTGGAGGAT 891
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Qy    127 TATCGCCATCTAAGCCCCAGTATTTGGCCAATCTCAGAAAGCTCCTGGGCTCCCCTGGAGGAT 186

Db    892 GGAGAGAGAAAAACAAACAGCTCCTGGAGCAGGAGAGTGTTGGCCTCTTGCTCTCCGGC 951
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Qy    187 GGAGAGAGAAAAACAAACAGCTCCTGGAGCAGGAGAGTGTTGGCCTCTTGCTCTCCGGC 246

Db    952 TCCCTCTGTTGCCCCTCTGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTG 1011
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    247 TCCCTCTGTTGCCCCTCTGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTG 306

Db   1012 GCCTGCTCTGCCCTGCCCTGGCTTCAAGAGAGGGCAGTGCC 1049
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Qy    307 GCCTGCTCTGCCCTGCCCTGGCTTCAAGAGAGGGCAGTGCC 344
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Right column:

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XX
AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 1, Application US/08445265A.
XX
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CC   Patent No. 5697901
SQ   Sequence 1, Application US/08445265A.
CC   GENERAL INFORMATION:
CC   APPLICANT: Eriksson, Elof
CC   TITLE OF INVENTION: GENE DELIVERY BY MICRONEEDLE INJECTION
CC   NUMBER OF SEQUENCES: 4
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Quarles & Brady
CC   STREET: 1 South Pinckney Street
CC   CITY: Madison
CC   STATE: WI
CC   COUNTRY: US
CC   ZIP: 53703
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: PatentIn Release #1.0, Version #1.30
CC   REFERENCE/DOCKET NUMBER: 27386
CC   REGISTRATION NUMBER: 27386
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: 608-251-5000
CC   TELEFAX: 608-251-9166
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/445,265A
CC   FILING DATE:
CC   CLASSIFICATION: 604
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Seay, Nicholas J
CC   REGISTRATION NUMBER: 27386
CC   REFERENCE/DOCKET NUMBER: 110229.91080
CC   INFORMATION FOR SEQ ID NO: 1:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 4283 base pairs
CC   TYPE: nucleic acid
CC   STRANDEDNESS: double
CC   TOPOLOGY: circular
CC   MOLECULE TYPE: other nucleic acid
CC   DESCRIPTION: /desc = "Plasmid DNA"
CC   FEATURE:
CC   NAME/KEY: CDS
CC   LOCATION: join(713..721, 981..1250)
SQ   Sequence 4283 BP; 1023 A; 1095 C; 1114 G; 1051 T; 0 other;

Query Match             25.0%;  Score 301;  DB 7;  Length 4283;
Best Local Similarity   95.3%;  Pred. No. 5.54e-212;
Matches   322;  Conservative    0;  Mismatches   15;  Indels    1;  Gaps    1;

Qy    713 ATGGCTACAGGTAAGCGCGCCCCTAAAAATCCCTTTGG-CACAATGTGTCCTGAGGGGAGAGG 771
          |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db      7 ATGGCTACAGGTAAGCGCGCCCCTAAAAATCCCTTTGGGCACAATGTGTCCTGAGGGGAGAGG 66

Qy    772 CAGCGACCTGTAGGATGGGGACGGGGGCACTAAACCCTCCAGGGTGTTTGGGGTTTGAATGTGAG 831
          ||||||||||||||||||||||||||||||  |||| |||||||||||| || |||||||||||
Db     67 TAGCGACCTGTAGGATGGGGACGGGGGCACTAACCCTGAGGTTTGGGGCTTCGAATGTGAG 126

Qy    832 TATCGCCATCTAAGCCCCAGTATTTGGCCAATCTCAGAAAGCTCCTGGGCTCCCCTGGAGGAT 891
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    127 TATCGCCATCTAAGCCCCAGTATTTGGCCAATCTCAGAAAGCTCCTGGGCTCCCCTGGAGGAT 186

Qy    892 GGAGAGAGAAAAACAAACAGCTCCTGGAGCAGGAGAGTGTTGGCCTCTTGCTCTCCGGC 951
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    187 GGAGAGAGAAAAACAAACAGCTCCTGGAGCAGGAGAGTGTTGGCCTCTTGCTCTCCGGC 246

Qy    952 TCCCTCTGTTGCCCCTCTGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTG 1011
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    247 TCCCTCTGTTGCCCCTCTGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTG 306
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Db   1012 GCCTGCTGCTCTGCCTGCCTGGCTTCAAGAGGCCAGTGCC 1049
          ||||||||||||||||||||||||||||||||||||||||
Qy    307 GCCTGCTCTGCCTGCCTGGCTTCAAGAGGCCAGTGCC     344

RESULT  13
ID   US-08-050-319B-53 STANDARD; DNA; UNC; 477 BP.

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AC   xxxxxx
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DT   01-JAN-1900
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DE   Sequence 53, Application US/08050319B.
XX
CC   Patent No. 5633145
CC   GENERAL INFORMATION:
CC   APPLICANT: M.Feldmann, P.W. Gray,
CC   APPLICANT: M.J.C. Turner, F.M Brennan
CC   TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC   TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC   NUMBER OF SEQUENCES: 57
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Reed & Robbins
CC   STREET: 635 Bryant Street
CC   CITY: Palo Alto
CC   STATE: California
CC   COUNTRY: USA
CC   ZIP: 94301
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: PatentIn Release #1.0, version #1.25
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/050,319B
CC   FILING DATE: 10-May-1993
CC   CLASSIFICATION: 435
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Robbins, Roberta L.
CC   REGISTRATION NUMBER: 33,208
CC   REFERENCE/DOCKET NUMBER: 5150-0030
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (415) 617-8999
CC   TELEFAX: (415) 327-3231
CC   INFORMATION FOR SEQ ID NO: 53:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 477 base pairs
CC   TYPE: nucleic acid
CC   STRANDEDNESS: double
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: cDNA to mRNA
CC   FEATURE:
CC   NAME/KEY: CDS
CC   LOCATION: 1..474
SQ   Sequence 477 BP; 117 A; 122 C; 131 G; 107 T; 0 other;

Query Match      21.2%;  Score 255; DB 7; Length 477;
Best Local Similarity  98.9%;
Matches   258;  Conservative   0;  Mismatches   3;  Indels   0;  Gaps   0;

Db   121 GATATGTGTGTCCCAAGGAAAATAATATCCCTCAAAATAATTCGATTTGCTGTACC 180
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Qy   345 GATATGTGTGTCCCAAGGAAAATAATATCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db   181 AAGTGCCACAAAGGAACCTACTTGTACAAATGACTGTCCAGGCCGCCGGGGCCAGGAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   405 AAGTGCCACAAAGGAACCTACTTGTACAAATGACTGTCCAGGCCGCCGGGATACGGAC 464

Db   241 TGCAGGGAGTGTGAGAGCGGGCTCCTTCACCGCTTCAGACAAACCACTTGCCTC 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   465 TGCAGGGAGTGTGAGAGCGGGCTCTTCACCGCTTCAGACAAACCACTCAGACACTGCCTC 524
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Db   301 AGCTGCTCCAAATGCCGAAAGGAAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 360
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Qy   525 AGCTGCTCCAAATGCCGAAAGGAAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db   361 CGGGACACCGTGTGTGTACCTGC 381
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Qy   585 CGGGACACCGTGTGTGGCTGC   605

RESULT  14
ID   US-08-050-319B-51 STANDARD; DNA; UNC; 462 BP.

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AC   xxxxxx
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DT   01-JAN-1900
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DE   Sequence 51, Application US/08050319B.
XX
CC   Patent No. 5633145
CC   GENERAL INFORMATION:
CC   APPLICANT: M.Feldmann, P.W. Gray,
CC   APPLICANT: M.J.C. Turner, F.M Brennan
CC   TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC   TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC   NUMBER OF SEQUENCES: 57
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Reed & Robbins
CC   STREET: 635 Bryant Street
CC   CITY: Palo Alto
CC   STATE: California
CC   COUNTRY: USA
CC   ZIP: 94301
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: PatentIn Release #1.0, version #1.25
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/050,319B
CC   FILING DATE: 10-May-1993
CC   CLASSIFICATION: 435
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Robbins, Roberta L.
CC   REGISTRATION NUMBER: 33,208
CC   REFERENCE/DOCKET NUMBER: 5150-0030
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (415) 617-8999
CC   TELEFAX: (415) 327-3231
CC   INFORMATION FOR SEQ ID NO: 51:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 462 base pairs
CC   TYPE: nucleic acid
CC   STRANDEDNESS: double
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: cDNA to mRNA
CC   FEATURE:
CC   NAME/KEY: CDS
CC   LOCATION: 1..459
SQ   Sequence 462 BP; 116 A; 119 C; 121 G; 106 T; 0 other;

Query Match      14.1%;  Score 169; DB 7; Length 462;
Best Local Similarity  100.0%;
Matches   169;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Db   240 CTGCAGGAAAGAACCAGTACCGCCGCCATTATTGGGTAGTGAAAACCTTTTCCAGTGCTTCAATTG 299
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Qy   602 CTGCAGGAAAGAACCAGTACCGCCGCCATTATTGGGTAGTGAAAACCTTTTCCAGTGCTTCAATTG 661

Db   300 CAGCCTCTGCCTCAAATGGGACGGTGCACCTCTCCTGCCAGGAGGAGAAACAGAACACCGTGTG 359
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Qy     662 CAGGCTTCTGCCTCAATTGGGACCGGTGCCACCTCTCCTGCCAGGAGAAACAGAACACCGTGTG 721
Db     360 CACCTGCCAATGCACGGTTTCTTCTTCTTCTTAAGAGAAAACGAGGTGTGTCTCCTGT 408
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Qy     722 CACCTGCCAATGCACGGTTTCTTCTTCTTCTTAAGAGAGAAAAACGAGTGTGTCTCCTGT 770
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RESULT 15
ID   US-08-086-915-2 STANDARD; DNA; UNC; 138 BP.

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AC   xxxxxx
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DT   01-JAN-1900
XX
DE   Sequence 2, Application US/08086915.
XX
CC   Patent No. 5444167
CC   GENERAL INFORMATION:
CC   APPLICANT: Petersson, Kim SI
CC   TITLE OF INVENTION: Variant Luteinizing Hormone Encoding DNA
CC   NUMBER OF SEQUENCES: 17
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Adduci, Mastriani, Schaumberg & Schill
CC   STREET: 1140 Connecticut Avenue, N.W., Suite 250
CC   CITY: Washington
CC   STATE: D.C.
CC   COUNTRY: U.S.A.
CC   ZIP: 20036
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC Compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: Patentin Release #1.0, Version #1.25
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/086,915
CC   FILING DATE: 07-JUL-1993
CC   CLASSIFICATION: 536
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Kubovcik, Ronald J.
CC   REGISTRATION NUMBER: 25,401
CC   REFERENCE/DOCKET NUMBER: 15873005
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: 202-466-6300
CC   TELEFAX: 202-466-2006
CC   INFORMATION FOR SEQ ID NO: 2:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 138 base pairs
CC   TYPE: nucleic acid
CC   STRANDEDNESS: double
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: DNA (genomic)
CC   HYPOTHETICAL: NO
CC   ANTI-SENSE: NO
CC   ORIGINAL SOURCE:
CC   ORGANISM: Homo sapiens
CC   DEVELOPMENTAL STAGE: Adult
SQ   Sequence 138 BP; 24 A; 51 C; 42 G; 21 T; 0 other;

Query Match   99.0%; Score 103; DB 5; Length 138;
Best Local Similarity   8.6%;
Matches 104; Conservative   0; Mismatches   1; Indels   0; Gaps   0;
           Pred. No. 5.77e-57;

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Db      34 CCACGGTGCCACCCCATCAATGCCACCCCTGGCCTGTGGAGAAGGAGGGGCTTGCCCGTGTGC 93
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Qy     783 CCACGGTGCGCGCCCCCATCAATGCCACCCCTGGCCTGTGGAGAAGGAGGGGCTGCCCGTGTGC 842

Db      94 ATCACCGTCAAACACCACCATCTGTGCGCGGCTACTGCCCCACCATG 138
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Qy     843 ATCACCGTCAACACCACCATCTGTGCCGGCGCTACTGCCCCACCATG 887
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MPSRCH (TM)

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MPsrch_nn   n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed May 6 12:20:06 1998; MasPar time 1075.89 Seconds
                   1491.095 Million cell updates/sec

Title: >US-08-804-166-1 from US08804166.seq
Description: (1-1049) from US08804166.seq
Perfect Score: 1049
N.A. Sequence: 1 TCCACATGGCTACAAGGTAAG.........TTATTATTCACAAATCTTAAG 1049
Comp: AGGTGTACCGGATGTCCATTC.........AATAATAGTGTTTAGAAATTC

Scoring table: TABLE default
                   Gap 6

Nmatch STD :   Dbase 0: Query 0

Searched: 436399 seqs, 76466465 bases x 2

Post-processing: Minimum Match 08
                   Listing first 45 summaries

Database: embl53
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Statistics: Mean 11.026; Variance 4.973; scale 2.217

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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## SUMMARIES

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| 1 | 424 | 40.4 | 483 | 25 | A29099 | Synthetic DNA for TNF- | 0.00e+00 |
| 2 | 424 | 40.4 | 510 | 25 | A21525 | Oligonucleotide probe. | 0.00e+00 |
| 3 | 424 | 40.4 | 600 | 25 | A20257 | Synthetic nucleotide s | 0.00e+00 |
| 4 | 424 | 40.4 | 1331 | 25 | A29103 | H.sapiens mRNA for TNF | 0.00e+00 |
| 5 | 424 | 40.4 | 1368 | 25 | A29098 | Synthetic DNA for TNF- | 0.00e+00 |
| 6 | 424 | 40.4 | 2050 | 27 | HUMTNFRP | Human tumor necrosis f | 0.00e+00 |
| 7 | 424 | 40.4 | 2050 | 27 | HUMTNFR | Sequence 24 from paten | 0.00e+00 |
| 8 | 424 | 40.4 | 2062 | 25 | I43805 | TNF alpha gene. | 0.00e+00 |
| 9 | 424 | 40.4 | 2062 | 25 | A21522 | Human tumor necrosis f | 0.00e+00 |
| 10 | 424 | 40.4 | 2087 | 27 | HUMTNFR | Homo sapiens tumor nec | 0.00e+00 |
| 11 | 424 | 40.4 | 2111 | 25 | A26412 | cDNA for (55kD TNF-BP) | 0.00e+00 |
| 12 | 424 | 40.4 | 2111 | 27 | HUMTNFRC | Human tumor necrosis f | 0.00e+00 |
| 13 | 424 | 40.4 | 2161 | 27 | HSNFR1A | H.sapiens TNF-R mRNA f | 0.00e+00 |
| 14 | 424 | 40.4 | 2175 | 25 | A43873 | Sequence 1 from Patent | 0.00e+00 |
| 15 | 424 | 40.4 | 2175 | 25 | I64751 | Sequence 1 from patent | 0.00e+00 |
| 16 | 424 | 40.4 | 2176 | 25 | A19907 | Synthetic nucleotide s | 0.00e+00 |
| 17 | 424 | 40.4 | 6889 | 25 | I26928 | Sequence 2 from patent | 0.00e+00 |
| 18 | 424 | 40.0 | 600 | 25 | I43808 | Sequence 47 from paten | 0.00e+00 |
| 19 | 417 | 39.8 | 2061 | 25 | A20255 | 55kD receptor gene for | 0.00e+00 |
| 20 | 381 | 36.3 | 504 | 25 | A20713 | Synthetic nucleotide s | 1.71e-240 |
| 21 | 381 | 36.3 | 504 | 25 | I43786 | Sequence 56 from paten | 1.71e-240 |
| 22 | 379 | 36.1 | 501 | 25 | A20254 | Sequence 1 from patent | 1.71e-240 |
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| 25 | 370 | 35.3 | 372 | 25 | HUMGHCSA | Synthetic nucleotide 5 | 0.00e+00 |
| 26 | 326 | 31.1 | 66495 | 27 | HUMGHCSA | Human growth hormone ( | 1.10e-264 |
| 27 | 304 | 29.0 | 581 | 15 | FCU72344 | Felis catus tumour nec | 3.28e-244 |
| 28 | 302 | 28.8 | 474 | 25 | A22259 | Synthetic nucleotide s | 2.37e-242 |
| 29 | 302 | 28.8 | 474 | 25 | I43809 | Sequence 49 from paten | 2.37e-242 |
| 30 | 300 | 28.6 | 1826 | 25 | I02855 | Human messenger RNA fo | 1.05e-237 |
| 31 | 300 | 28.6 | 1964 | 27 | HSGROW2 | Human germ line gene f | 1.71e-240 |
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| 33 | 300 | 28.6 | 2771 | 25 | I41411 | Sequence 5 from patent | 1.71e-240 |
| 34 | 298 | 28.4 | 2657 | 27 | HUMGHN | Human growth hormone g | 1.23e-238 |
| 35 | 298 | 28.4 | 4283 | 25 | I63120 | Sequence 3 from patent | 1.23e-238 |
| 36 | 297 | 28.3 | 2004 | 15 | SSU19994 | Sus scrofa p55 TNF rec | 1.05e-237 |
| 37 | 258 | 24.6 | 621 | 27 | HSGONA | Human messenger RNA fo | 1.39e-201 |
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| 40 | 250 | 23.8 | 2740 | 27 | HUMCS3 | Human chorionic somato | 3.37e-194 |
| 41 | 248 | 23.6 | 2301 | 27 | HUMCS1 | Human chorionic somato | 2.35e-192 |
| 42 | 245 | 23.4 | 2457 | 25 | IO2856 | Sequence 2 from Patent | 1.37e-189 |
| 43 | 245 | 23.4 | 2967 | 27 | HUMPLA | Human placental lactog | 1.37e-189 |
| 44 | 240 | 22.9 | 2440 | 15 | BTU90937 | Bos taurus tumor necro | 5.52e-185 |
| 45 | 239 | 22.8 | 2734 | 27 | HUMCS5 | Human chorionic somato | 4.60e-184 |

## ALIGNMENTS

### RESULT 1

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DEFINITION  Synthetic DNA for TNF-binding polypeptide from patent EP0393438.
ACCESSION   A29099
NID         g1248893
KEYWORDS    unidentified.
SOURCE      unidentified.
  ORGANISM  unclassified.
REFERENCE   1  (bases 1 to 483)
  AUTHORS   Hauptmann,R., Himmler,A., Maurer-Fogy,I. and Stratowa,C.
  TITLE     TNF-receptor, TNF-binding protein and DNA coding therefor
  JOURNAL   Patent: EP 0393438-A 49 24-OCT-1990;
            BOEHRINGER INGELHEIM INTERNATIONAL G.M.B.H
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Best Local Similarity 99.8%;
Matches 425;    Conservative 0;    Mismatches 1;    Indels 0;    Gaps 0;

Pred. No. 0.00e+00;

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Qy   404 AAGTGCCACAAAGGAACCTACTTGTTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 463
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RESULT  2

LOCUS          A21525         510 bp    DNA             PAT       26-JUL-1994
DEFINITION     oligonucleotide probe.
ACCESSION      A21525
NID            g583574
KEYWORDS       .
SOURCE         unidentified.
  ORGANISM     unidentified
               unclassified.
REFERENCE      1  (bases 1 to 510)
  AUTHORS
  JOURNAL      Patent: GB 2246569-A 4 05-FEB-1992;
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BASE COUNT       136 a    132 c    133 g    109 t
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Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
Matches  425;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

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Qy    524 AGCTGCTCCAAATGCCGAAAGGAAAATGGGTCAGGTGGAGAGATCTCTTCTTGCACAGTGGAC 583
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Qy    104 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCGCCCGGGGGCCAGGATACGGAC 463
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LOCUS          A20257         600 bp    DNA             PAT       20-SEP-1995
DEFINITION     Synthetic nucleotide sequence of plasmid p-TNFRecd.
ACCESSION      A20257
NID            g1247896
KEYWORDS       .
SOURCE         unidentified.
  ORGANISM     unidentified
               unclassified.
REFERENCE      1  (bases 1 to 600)
  AUTHORS
  TITLE        MODIFIED HUMAN TNFALPHA (TUMOR NECROSIS FACTOR ALPHA) RECEPTOR
  JOURNAL      Patent: WO 9207076-A 25 30-APR-1992;
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Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
Matches  425;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Db    121 GATAGTGTGTGTCCCCAAGGAGAAAAATATATCCACCCTCAAAAATAATTCGATTTGCTGTACC 180

Db    181 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCGCCCGGGGGCCAGGATACGGAC 240

RESULT  4

LOCUS          A29103         1331 bp   DNA             PAT       03-JUL-1995
DEFINITION     H.saplens mRNA for TNF-binding polypeptide from patent EP0393438.
ACCESSION      A29103
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Left record

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NID             g1247517
SOURCE          human.
KEYWORDS        .
ORGANISM        Homo sapiens
                Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
                Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE       1  (bases 1 to 1331)
  AUTHORS       Hauptmann,R., Himmler,A., Maurer-Fogy,I. and Stratowa,C.
  TITLE         TNF-receptor, TNF-binding protein and DNA coding therefor
  JOURNAL       Patent: EP 0393438-A 53 24-OCT-1990;
                BOEHRINGER INGELHEIM INTERNATIONAL G.M.B.H
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Best Local Similarity 99.8%;  Pred. No. 0.00e+00;
Matches   425;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy  344 GATAGTGTGTGTCCCCAGGAAAATATATCCACCCTCAAAATAATAATTCGATTTGCTGTACC 403
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Qy  404 AAGTGCCACAAAAGGAACCTACTTGTACAAATGACTGTCCAGGCCCCGGGGCAGGATACGGAC 463
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Db  393 AAGTGCCACAAAAGGAACCTACTTGTACAAATGACTGTCCAGGCCCCGGGGCAGGATACGGAC 452

Qy  464 TGCAGGGAGTGTGAGAGCGGCGGCTCCTTCACCCGCTTCAGAAAAACCACCACTGCCCTC 523
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DEFINITION      Synthetic DNA for TNF-receptor from patent EP0393438.
ACCESSION       A29098
NID             g1248892
KEYWORDS        .
SOURCE          unidentified.
ORGANISM        unidentified
                unclassified.
REFERENCE       1  (bases 1 to 1368)
  AUTHORS       Hauptmann,R., Himmler,A., Maurer-Fogy,I. and Stratowa,C.
  TITLE         TNF-receptor, TNF-binding protein and DNA coding therefor
  JOURNAL       Patent: EP 0393438-A 48 24-OCT-1990;
                BOEHRINGER INGELHEIM INTERNATIONAL G.M.B.H
FEATURES
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Right record

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Best Local Similarity 99.8%;  Pred. No. 0.00e+00;
Matches   425;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

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Qy  764 TCCTGT 769
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LOCUS           HUMTNFRP      2050 bp       mRNA          PRI     11-OCT-1991
DEFINITION      Human tumor necrosis factor receptor(TNF) mRNA, complete cds.
ACCESSION       M60275 M37764
NID             g339759
KEYWORDS        .
MEDLINE         91017509
JOURNAL
COMMENT         Draft entry and computer-readable sequence for [Proc. Natl. Acad.
                Sci. U.S.A. (1990) In press] kindly submitted
                by P.W.Gray, 13-AUG-1990.
REFERENCE       1  (bases 1 to 2050)
  AUTHORS       Gray,P.W., Barrett,K.J., Chantry,D., Turner,M. and Feldman,M.
  TITLE         Cloning of human tumor necrosis factor (TNF) receptor cDNA and
                expression of recombinant soluble TNF-binding protein
  JOURNAL       Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384 (1990)
SOURCE          Human placenta, cDNA to mRNA.
ORGANISM        Homo sapiens
                Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
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DEFINITION  Sequence 24 from patent US 5633145.
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NID         g2468903
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 2062)
AUTHORS     Feldmann,M., Gray,P.W., Turner,M.J.C. and Brennan,F.M.
TITLE       TNF.alpha. receptor-derived binding protein
JOURNAL     Patent: US 5631145-A 24 27-MAY-1997;
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ORIGIN

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Best Local Similarity 99.8%;   Pred. No. 0.00e+00;
Matches  425;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

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Best Local Similarity 99.8%;   Pred. No. 0.00e+00;
Matches  425;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

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Db  335 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCACCGGGGGAGGGGGATAGGAC  394
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Qy  404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCACCGGGGGAGGGGGATAGGAC  463

Db  395 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAAAACCACTGCCCTC  454
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Qy  464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAAAACCACTGCCCTC  523

Db  455 AGCTGCTCCAAAATGCCGAAAGGAAAATGGGTCAGGTGGAGATCTCTTCTTCTTGCACAGTGGAC  514
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Qy  524 AGCTGCTCCAAAATGCCGAAAGGAAAATGGGTCAGGTGGAGATCTCTTCTTCTTGCACAGTGGAC  583

Db  515 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCCATTATTGGAGTGAAAACCTT  574
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Qy  584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCCATTATTGGAGTGAAAACCTT  643

Db  575 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAAATGGGACCGTGCACCTCTCCTGCCAGGAG  634
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Qy  644 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAAATGGGACCGTGCACCTCTCCTGCCAGGAG  703

Db  635 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTTAAGAGAAATCGAGTGTGTC  694
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Qy  704 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTTAAGAGAAATCGAGTGTGTC  763

Db  695 TCCTGT  700
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Qy  764 TCCTGT  769

RESULT
LOCUS      8   A21522      2062 bp    RNA         PAT      26-JUL-1994
DEFINITION  TNF alpha gene.
ACCESSION   A21522
NID         g579599
KEYWORDS
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 2062)
AUTHORS
JOURNAL     Patent: GB 2246569-A 1 05-FEB-1992;
FEATURES    Location/Qualifiers
source      1..2062
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            /db_xref="taxon:9606"
gene        155..1522
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CDS         155..1522
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            KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPVI
            FGLCLLSLLFIGLMYRYQRWKSKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPT
            PGFTPTLGFSPVPSSTFTSSSTYTPGDCPNFAAPREVAPPYQGADPILATALASDPI
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RESULT 9

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LOCUS       HUMTNFR      2087 bp    mRNA             PRI       10-NOV-1993
DEFINITION  Human tumor necrosis factor receptor mRNA, complete cds.
ACCESSION   M33294
NID         g339744
KEYWORDS    cell surface receptor; tumor necrosis factor receptor.
SOURCE      Human placenta, cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2087)
  AUTHORS   Schall,T.J., Lewis,M., Koller,K.J., Lee,A.L., Rice,G.C., Wong,G.H.,
            Gatanaga,T., Granger,G.A., Lentz,R., Raab,H., Kohr,W.J. and
            Goedel,D.V.
  TITLE     Molecular cloning and expression of a receptor for human tumor
            necrosis factor
  JOURNAL   Cell 61, 361-370 (1990)
  MEDLINE   9035285
COMMENT     Draft entry and computer-readable sequence for [1] kindly submitted
            by T.Schall, 26-MAR-1990.
FEATURES             Location/Qualifiers
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     CDS             182..1549
                     /codon_start=1
                     /note="tumor necrosis factor receptor"
                     /db_xref="PID:g339745"
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                     SKCRKEMGQVEISSCTVRDRTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE
                     KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVI
                     FFGLCLLSLLFIGLMYRYQRWKSKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPT
                     PGFTPTLGFSPVPSSTFTSSSTYTPGDCDPNFAAPRREVAPPYQGADPILATALASDPI
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Query Match     40.4%;  Score 424;  DB 25;  Length 2062;
Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
Matches  425;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

BASE COUNT      429 a    617 c    573 g    443 t
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Db  275 GATAGTGTGTGTCCCAAGGAAAATATATCCACCCTCAAATAATAATTCGATTTGCTGTACC 334
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Qy  344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATATTCCATTTGCTGTACC 403

Db  335 AAGTGCCACAAAAGGAAACCTACTTGTACAATGACTGTCCAGGCCCCGGGCCAGGATACGGAC 394
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Qy  404 AAGTGCCACAAAAGGAAACCTACTTGTACAATGACTGTCCAGGCCCCGGGCCAGGATACGGAC 463

Db  395 TGCAGGGAGTGTGAGAGCGGGGTCCTTCACCGGTTCAGAAAAACACCTCAGACACTGCCTC 454
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Qy  464 TGCAGGGAGTGTGAGAGCGGGGTCCTTCACCGGTTCAGAAAAACACCTCAGACACTGCCTC 523

Db  455 AGCTGCTCCAAATGCCGAAAGGAAAATGGGTCAGGTGGAGGATCTCTTCTTCTGCACAGTGGAC 514
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Qy  524 AGCTGCTCCAAATGCCGAAAGGAAAATGGGTCAGGTGGAGGATCTCTTCTTCTGCACAGTGGAC 583

Db  515 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 574
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Qy  584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Db  575 TTCCAGTGCTTCAATTGCAGTCTGTGCCTCTGCCGACCGTGCCACCCTCTGCCAGGAG 634
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Qy  644 TTCCAGTGCTTCAATTGCAGTCTGTGCCTCTGCCGACCGTGCCACCCTCTGCCAGGAG 703

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Qy  704 AAACAGAACACCGTGTGCACCTCCCATGCAGGTTTCTTTCTTAAGAGAAAACGAGTGTGTC 763

Db  695 TCCTGT 700
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Qy  764 TCCTGT 769
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PSLLR"

RESULT 10

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LOCUS       HUMTNFRB     2111 bp    mRNA             PRI       14-NOV-1990
DEFINITION  Homo sapiens tumor necrosis factor receptor mRNA, complete cds.
ACCESSION   M58286 M33480
NID         g339753
KEYWORDS    tumor necrosis factor receptor.
SOURCE      Human cell line HL60, cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2111)
  AUTHORS   Loetscher,H., Pan,Y.-C.E., Lahm,H.-W., Gentz,R., Brockhaus,M.,
            Tabuchi,H. and Lesslauer,W.
  TITLE     Molecular cloning and expression of the human 55 kd tumor necrosis
            factor receptor
  JOURNAL   Cell 61, 351-359 (1990)
  MEDLINE   9035284
FEATURES             Location/Qualifiers
     source          1..2111
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                     /gene="TNF receptor"
     CDS             187..1554
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                     /product="tumor necrosis factor receptor"
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Query Match     40.4%;  Score 424;  DB 27;  Length 2087;
Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
Matches  425;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

BASE COUNT      433 a    624 c    581 g    449 t
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PSLLR"

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PGFTPTLGFSPVPSSTFTSSSTYTPGDCDPNFAAPRREVAPPYQGADPILATALASDPI
PNPLQKWEDSAHKPQSLDTDDPANLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQN
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Qy  344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATATTCCATTTGCTGTACC 403

Db  362 AAGTGCCACAAAAGGAAACCTACTTGTACAATGACTGTCCAGGCCCCGGGCCAGGATACGGAC 421
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Qy  404 AAGTGCCACAAAAGGAAACCTACTTGTACAATGACTGTCCAGGCCCCGGGCCAGGATACGGAC 463

Db  422 TGCAGGGAGTGTGAGAGCGGGGTCCTTCACCGGTTCAGAAAACACCTCAGACACTGCCTC 481
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Qy  464 TGCAGGGAGTGTGAGAGCGGGGTCCTTCACCGGTTCAGAAAACACCTCAGACACTGCCTC 523

Db  482 AGCTGCTCCAAATGCCGAAAGGAAAATGGGTCAGGTGGAGGATCTCTTCTTCTGCACAGTGGAC 541
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Qy  524 AGCTGCTCCAAATGCCGAAAGGAAAATGGGTCAGGTGGAGGATCTCTTCTTCTGCACAGTGGAC 583

Db  542 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 601
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Qy  584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

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Qy  644 TTCCAGTGCTTCAATTGCAGTCTGTGCCTCTGCCGACCGTGCCACCCTCTGCCAGGAG 703

Db  662 AAACAGAACACCGTGTGCACCTCCCATGCAGGTTTCTTTCTTAAGAGAAAACGAGTGTGTC 721
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Qy  704 AAACAGAACACCGTGTGCACCTCCCATGCAGGTTTCTTTCTTAAGAGAAAACGAGTGTGTC 763

Db  722 TCCTGT 727
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Qy  764 TCCTGT 769
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RESULT 11

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LOCUS       A26412    2111 bp    DNA          PAT       26-APR-1995
DEFINITION  cDNA for (55kD TNF-BP) tumor necrosis factor binding protein from
ACCESSION   A26412
NID         g904968
KEYWORDS
SOURCE      unidentified.
ORGANISM    unidentified
            unclassified.
REFERENCE   1  (bases 1 to 2111)
AUTHORS     Brockhaus,M., Dembic,Z., Gentz,R., Lesslauer,W., Loetscher,H. and
            Schlaeger,E.J.
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            FFGLCLLSLLFIGLMYRYQRWKSKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPT
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            /product="tumor necrosis factor receptor"
BASE COUNT   445 a    629 c    587 g    450 t
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Query Match        40.4%;  Score 424;  DB 27;  Length 2111;
Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
Matches  425;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Db   307  GATAGTGTGTGTCCCCAAGGAAGAAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC  366
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Qy   344  GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC      403

Db   367  AAGTGCCACAAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCCGGGGCAGGATACGGAC  426
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Qy   404  AAGTGCCACAAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCCGGGGCAGGATACGGAC  463

Db   427  TGCAGGGAGTGTGAGAGCGGCGGCGGCTCCTTCAGAAAACCACCTCAGACACTGCCTC         486
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Qy   464  TGCAGGGAGTGTGAGAGCGGCGGCTCCTTCACCGCTTCAGAAAAACCACCTCAGACACTGCCTC   523

Db   487  AGCTGCTCCAAATGCCGAAAAGGAAAATGGGTCAGGTGGGAGATCTCTTCTTGCACAGTGGAC     546
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Qy   524  AGCTGCTCCAAATGCCGAAAAGGAAAATGGGTCAGGTGGGAGATCTCTTCTTGCACAGTGGAC     583

Db   547  CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGGCATTATTGGAGTGAAAACCTT       606
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Qy   584  CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGGCATTATTGGAGTGAAAACCTT       643

Db   607  TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG       666
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Qy   644  TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG       703

Db   667  AAACAGAACACCGTGTGCCACCTGCCACTGCAGGTTTCTTTTCTAAGAGAAAACGAGAGTGTGTC   726
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Qy   704  AAACAGAACACCGTGTGCCACCTGCCACTGCAGGTTTCTTTTCTAAGAGAAAAACGAGAGTGTGTC  763

Db   727  TCCTGGT  732
          |||||||
Qy   764  TCCTGGT  769
```

RESULT 12

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LOCUS       HUMTNFRC   2112 bp    mRNA         PRI       30-SEP-1991
DEFINITION  Human tumor necrosis factor receptor (TNF receptor) mRNA, complete
            cds.
ACCESSION   M63121 M75861
NID         g339755
KEYWORDS
SOURCE      tumor necrosis factor receptor.
            Human cDNA to mRNA.
ORGANISM    Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2112)
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TITLE      TNF-binding proteins
JOURNAL    Patent: EP 0417563-A 24 20-MAR-1991;
           F. HOFFMANN-LA ROCHE AG
FEATURES             Location/Qualifiers
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BASE COUNT   445 a    629 c    587 g    450 t
ORIGIN
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Query Match        40.4%;  Score 424;  DB 25;  Length 2111;
Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
Matches  425;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Db   307  GATAGTGTGTGTCCCCAAGGAAGAAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC  366
          ||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Qy   344  GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC      403

Db   367  AAGTGCCACAAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCCGGGGCAGGATACGGAC  426
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   404  AAGTGCCACAAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCCGGGGCAGGATACGGAC  463

Db   427  TGCAGGGAGTGTGAGAGCGGCGGCGGCTCCTTCAGAAAACCACCTCAGACACTGCCTC         486
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Qy   464  TGCAGGGAGTGTGAGAGCGGCGGCTCCTTCACCGCTTCAGAAAAACCACCTCAGACACTGCCTC   523

Db   487  AGCTGCTCCAAATGCCGAAAAGGAAAATGGGTCAGGTGGGAGATCTCTTCTTGCACAGTGGAC     546
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Qy   524  AGCTGCTCCAAATGCCGAAAAGGAAAATGGGTCAGGTGGGAGATCTCTTCTTGCACAGTGGAC     583

Db   547  CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGGCATTATTGGAGTGAAAACCTT       606
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Qy   584  CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGGCATTATTGGAGTGAAAACCTT       643

Db   607  TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG       666
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Qy   644  TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG       703

Db   667  AAACAGAACACCGTGTGCCACCTGCCACTGCAGGTTTCTTTTCTAAGAGAAAACGAGAGTGTGTC   726
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Qy   704  AAACAGAACACCGTGTGCCACCTGCCACTGCAGGTTTCTTTTCTAAGAGAAAAACGAGAGTGTGTC  763

Db   727  TCCTGGT  732
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Qy   764  TCCTGGT  769
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REFERENCE   1 (bases 1 to 2112)

AUTHORS   Himmler,A., Maurer-Fogy,I., Kroenke,M., Scheurich,P.,
          Pfizenmaier,K., Lantz,M., Olsson,I., Hauptmann,R., Stratowa,C. and
          Adolf,G.R.
TITLE   Molecular cloning and expression of human and rat tumor necrosis
          factor receptor chain (p60) and its soluble derivative, tumor
          necrosis factor-binding protein
JOURNAL   DNA Cell Biol. 9, 705-715 (1990)
MEDLINE   91090841
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     mat_peptide   294..1571
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BASE COUNT   435 a   632 c   589 g   456 t
ORIGIN

Query Match 40.4%;   Score 424;   DB 27;   Length 2112;
Best Local Similarity 99.8%;   Pred. No. 0.00e+00;
Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db   327 GATAGTGTGTGTCCCAAGGAAAATAATATCCACCCTCAAAATAATATTCGATTTGCTGTACC 386
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Qy   344 GATAGTGTGTGTCCCAAGGAAAATAATATCCACCCTCAAAATAATATTCGATTTGCTGTACC 403

Db   387 AAGTGCCACAAAGGAAACCTACTTGTACAATGACGTGTCCAGGCCCGGGGGCAGGATACGGAC 446
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Qy   404 AAGTGCCACAAAGGAAACCTACTTGTACAATGACGTGTCCAGGCCCGGGGGCAGGATACGGAC 463

Db   447 TGCAGGGAGTGTGAGAGCGGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 506
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Qy   464 TGCAGGGAGTGTGAGAGCGGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

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Db   567 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCCATTATTGGAGTGAAAACCTT 626
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Qy   704 AAACAGAACACCGTGTGCACCTGCCATGCAGGGTTCTTTCTTAAGAGAGAAAACGAGTGTGTC 763

Db   747 TCCTGT 752
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Qy   764 TCCTGT 769

RESULT   13
LOCUS   HSTNFRIA   2161 bp   RNA   PRI   18-JAN-1993
DEFINITION H.sapiens TNF-R mRNA for tumor necrosis factor receptor type 1.
ACCESSION   X55313
NID   g37223
KEYWORDS   TNF-R gene; tumor necrosis factor receptor 1.
SOURCE   human.
  ORGANISM Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 2161)
  AUTHORS   Nophar,Y., Kemper,O., Brakebusch,C., Englemann,H., Zwang,R.,
            Aderka,D., Holtmann,H. and Wallach,D.
  TITLE   Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA
            for the type I TNF-R, cloned using amino acid sequence data of its
            soluble form, encodes both the cell surface and a soluble form of
            the receptor
  JOURNAL   EMBO J. 9 (10), 3269-3278 (1990)
  MEDLINE   91006021
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Best Local Similarity 99.8%;   Pred. No. 0.00e+00;
Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db   376 GATAGTGTGTGTCCCAAGGAAAAATATATCCACCCTCAAAATAATATTCGATTTGCTGTACC 435
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Qy   464 TGCAGGGAGTGTGAGAGCGGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

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DEFINITION   Sequence 1 from Patent EP0657536.
ACCESSION    A43873
NID          g2299022
KEYWORDS     .
SOURCE       unidentified.
  ORGANISM   unidentified
             unclassified.
REFERENCE    1 (bases 1 to 2175)
  AUTHORS    Wallach,D., Brackebusch,C., Varfolomeev,E. and Batkin,M.
  TITLE      Proteases capable of shedding the soluble TNF-receptor and TNF-R
             derived peptides and antibodies against the proteases inhibiting
             the shedding
  JOURNAL    Patent: EP 0657536-A 1 14-JUN-1995;
             YEDA RES & DEV (IL);
             Other publication ZA 9407962 951121
             Other publication JP 7194376 950801
             Other publication AU 7574294 950504
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BASE COUNT    474 a    641 c    604 g    456 t
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Best Local Similarity   99.8%;  Pred. No. 0.00e+00;
Matches  425;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    344 GATAGTGTGTGTCCCCAAGGAAAAATAATATCCACCCTCAAAAATAATTCGATTTGCTGTACC 403
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Db    556 AGCTGCTCCAAATGCCGAAAAGGAAAATGGGTCAGGTGGAGATCTCTTTCTTCTTGCACAGTGGAC 615

Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCAATTATTGGAGTGAAAACCTT 643
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Qy    704 AAACAGAACACCGTGTGTGGCCACCTGCCATGCAGGTTTCTTTCTTCTTAAGAGAAAACGAGTGTC 763
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ACCESSION    I64751
NID          g2481645
KEYWORDS     .
SOURCE       Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE    1 (bases 1 to 2175)
  AUTHORS    Wallach,D., Brakebusch,C., Varfolomeev,E. and Batkin,M.
  TITLE      Molecules influencing the shedding of the TNF receptor, their
             preparation and their use
  JOURNAL    Patent: US 5665859-A 1 09-SEP-1997;
FEATURES             Location/Qualifiers
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BASE COUNT    474 a    641 c    604 g    456 t
ORIGIN
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Query Match     40.4%;  Score 424;  DB 25;  Length 2175;
Best Local Similarity   99.8%;  Pred. No. 0.00e+00;
Matches  425;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    344 GATAGTGTGTGTCCCCAAGGAAAAATAATATCCACCCTCAAAAATAATTCGATTTGCTGTACC 403
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Qy    404 AAGTGCCCACAAAGGAACCTACTTGTACAAATGACTGTCCAGGCCGCCGGGGGGCCAGGGATACGGAC 463
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Db    436 AAGTGCCCACAAAGGAACCTACTTGTACAAATGACTGTCCAGGCCGCCGGGGGGCCAGGGATACGGAC 495

Qy    464 TGCAGGGGAGTGTGAGAGACGGCGCTCCTTCACCCGCTTCAGAAAAACCACCTCAGAACACTGCCTC 523
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Db    496 TGCAGGGGAGTGTGAGAGACGGCGCTCCTTCACCCGCTTCAGAAAAACCACCTCAGAACACTGCCTC 555

Qy    524 AGCTGCTCCAAATGCCGAAAAGGAAAATGGGTCAGGTGGAGATCTCTTTCTTCTTGCACAGTGGAC 583
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Db    556 AGCTGCTCCAAATGCCGAAAAGGAAAATGGGTCAGGTGGAGATCTCTTTCTTCTTGCACAGTGGAC 615

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Qy    704 AAACAGAACACCGTGTGGCCACCTGCCATGCAGGTTTCTTTCTTCTTAAGAGAAAACGAGTGTC 763
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Db    736 AAACAGAACACCGTGTGGCCACCTGCCATGCAGGTTTCTTTCTTCTTAAGAGAAAACGAGTGTC 795

Qy    764 TCCTGT 769
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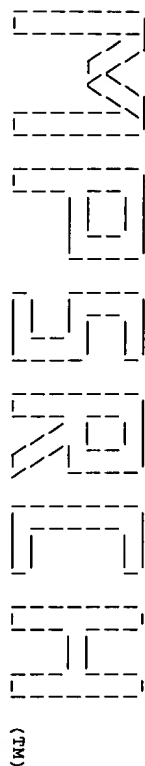          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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MPSRCH (TM)

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             Copyright (c) 1993-1997  University of Edinburgh, U.K.
                    Distribution rights by Oxford Molecular Ltd
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MPsrch.nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed May 6 12:55:12 1998; MasPar time 137.48 Seconds
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Description: (1-1049) from US0804166.seq
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N.A. Sequence: 1 TCCACATGGCTACAGGTAAG................TTATTATCACAAATCTTAAG 1049
Comp: AGGTGTACCGAGTCCATTC.................AATAATAGTGTTTAGAATTC

Scoring table: TABLE default
               Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 159651 seqs, 57698962 bases x 2

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database: n-geneseq30
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               8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
               14:part14 15:part15 16:part16 17:part17 18:part18
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Statistics: Mean 9.090; Variance 5.026; scale 1.809

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match Length	DB	ID	Description	Pred. No.
1	424	40.4	4	Q24441	Encodes truncated TNF	2.42e-296
2	424	40.4	6	Q06282	Plasmid Tumour Necros	2.42e-296
3	424	40.4	8	Q49932	Lambda-derived TNF-R	2.42e-296
4	424	40.4	3	Q20973	Encodes TNF-alpha 55k	2.42e-296
5	424	40.4	2	Q10883	TNF-alpha binding pro	2.42e-296
6	424	40.4	2	Q10955	30kD TNF inhibitor pr	2.42e-296
7	424	40.4	1	Q06285	Encodes human 55kD TN	2.42e-296
8	424	40.4	1	Q90511	Human Tumour Necrosis	2.42e-296
9	424	40.4	15	T15931	p55 TNF-R gene.	2.42e-296
10	424	40.4	18	T15931	DHFR/intron (WTrasSD)	2.42e-296
11	422	40.2	9	Q50870	p55 Tumour necrosis f	8.37e-295
12	422	40.2	2	Q12215	Type I TNF receptor.	8.37e-295
13	381	36.3	4	Q24445	Encodes truncated TNF	2.76e-263
14	302	28.8	4	Q24442	Encodes truncated TNF	8.62e-203
15	300	28.5	31	T76770	Rat Fabp1 gut-specif1	2.90e-201

ALIGNMENTS

16	298	28.4	33	T62826	Human growth hormone	9.73e-200
17	291	27.7	6	Q41459	Human growth hormone	2.12e-194
18	259	24.7	17	T03236	Single chain gonadotr	4.80e-170
19	259	24.7	17	T03235	Single chain gonadotr	4.80e-170
20	259	24.7	17	T03224	Single chain gonadotr	4.80e-170
21	259	24.7	17	T03219	Single chain gonadotr	4.80e-170
22	259	24.7	17	T03233	Single chain gonadotr	4.80e-170
23	259	24.7	17	T03231	Single chain gonadotr	4.80e-170
24	259	24.7	17	T03221	Single chain gonadotr	4.80e-170
25	259	24.7	17	T03227	Single chain gonadotr	4.80e-170
26	259	24.7	17	T03229	Single chain gonadotr	4.80e-170
27	259	24.7	17	T03212	Single chain gonadotr	4.80e-170
28	258	24.6	24	Q10075	Engineered human alph	2.76e-169
29	258	24.6	24	T41695	Dimeric glycoprotein	2.76e-169
30	255	24.3	4	Q24444	Encodes truncated TNF	5.24e-167
31	251	23.9	17	T03238	Gonadotropin alpha su	5.69e-164
32	251	23.9	17	T03243	Gonadotropin alpha su	5.69e-164
33	230	21.9	4	Q06284	Rat Tumour Necrosis F	4.62e-148
34	206	19.6	4	N30032	Sequence of gene for	6.00e-130
35	176	16.8	4	Q03846	Porcine alpha subunit	1.95e-107
36	169	16.1	4	Q24443	Encodes truncated TNF	3.28e-102
37	166	15.8	2	Q10059	Ovine FSH alpha subun	5.66e-100
38	164	15.6	2	Q03843	Single chain gonadotr	1.75e-98
39	150	14.3	1	Q03849	Bovine alpha subunit	4.39e-88
40	146	13.9	2	Q03820	Equine alpha subunit	4.02e-85
41	132	12.6	1	Q10878	Gene encoding equine	4.45e-75
42	103	9.8	11	Q65374	Partial sequence of c	1.12e-53
43	101	9.6	2	N91174	Equine alpha subunit	1.39e-52
44	80	7.6	11	Q65373	Fish gonadotropic hor	2.70e-37
45	79	7.5	3	N50521	Sequence encoding sal	1.36e-36

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RESULT   1
AC   Q24441
DT   05-NOV-1992  (first entry).
DE   Encodes truncated TNF-alpha, 55kD receptor (197 amino acids).
KW   tumour necrosis factor alpha; extracellular binding domain;
KW   treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
KW   malaria; viral meningitis; graft versus host disease;
KW   autoimmune disease; rheumatoid arthritis.
OS   Homo sapiens.
PN   WO9207076-A.
PD   30-APR-1992.
PF   18-OCT-1991; WO9207076-A.
PR   18-OCT-1990; GB-022648.
PA   (CHAR-) CHARING CROSS SUNLEY RES CENT.
PI   Brennan FM, Feldmann M, Gray PW, Turner MJC;
DR   WPI; 92-167156/20.
DR   P-PSDB; R24080.
PT   New polypeptide capable of binding human TNF alpha - comprises
PT   first three cysteine-rich subdomains of TNF alpha receptor for
PT   treating autoimmune disease, septic shock, HIV etc.
PS   Example; Fig 7; 43pp; English.
CC   This sequence encodes the designed TNF-alpha 55kD receptor
CC   derivative, as present in pTNFRecd. This was produced as described in
CC   Q24441. This derivative lacks the 81 carboxyl terminal residues of
CC   the cytoplasmic domain. The derivative could be used in the
CC   regulation of TNF-alpha mediated responses by binding and
CC   sequestering human TNF-alpha e.g. in the treatment of pulmonary
CC   diseases; septic shock, HIV infection, malaria, viral meningitis,
CC   graft versus host disease and autoimmune diseases, esp. rheumatoid
CC   arthritis.
CC   See also Q24440-51, R24000, R24080-84, R27585, Q29236-8
SQ   Sequence     608 BP;      148 A;      159 C;      165 G;      136 T;

Query Match       40.4%;  Score 424;  DB 4;  Length 608;
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Matches  425;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Db          129 gatagtgtgtgtcccaaggaaaatatccaccctcaaaataattcgatttgctgtacc 188
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RESULT 2

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AC   Q06282;
DT   29-JAN-1991 (first entry)
DE   Plasmid Tumour Necrosis Factor-Binding Protein 15 cDNA insert.
KW   Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
OS   Homo sapiens.
FH   Key                 Location/Qualifiers
FT   CDS                 213..1325
FT   /tag=  a
FT   /product=TNF-BP
PN   EP-393438-A.
PD   24-OCT-1990.
PF   06-APR-1990; 106624.
PR   21-APR-1989; DE-913101.
PR   21-JUN-1989; DE-920282.
PA   (BOEH ) BOEHRINGER INGELHEIM INT.
PI   Hauptmann R, Himmler A, Maurer-Fogy I, Stratowa C;
PI   WPI; 90-321987/43.
DR   P-PSDB; R07449.
PT   DNA encoding TNF binding protein and TNF- receptor - used in
PT   tumour treatment and to understand mechanismsm to TNF action
PS   Disclosure; Fig 1(1-3); 51pp; German.
CC   pTNF-BP15 is one of 30 positives clones in a screened cDNA library
CC   from induced TNF-induced fibrosarcoma cells. A TNF-BP had been
CC   isolated from the urine of patients with uraemia and probes/primers
CC   were constructed from the determined amino acid sequence.
CC   To produce a vector expressing a soluble form of TNF-binding
CC   protein, this plasmid was cut with XmnI, amplified by PCR and the
CC   amplified DNA cut with BamHI and EcoRI.
CC   The resulting 0.75 kb DNA fragment was inserted into pT7/T3 alpha-19
CC   (BRL) cut with the same enzymes to recover pTNF-BP. This was cut
CC   with BamHI and EcoRI, and the recovered fragment inserted into
CC   pAD-CMVl (Q06283) to give the required plasmid pADTNF-BP.
CC   See also Q06283 (Q06283)
SQ   Sequence 1334 BP; 299 A; 409 C; 342 G; 284 T;
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Qy  404 AAGTGCCACAAAGGAAGCTACTTGTACAATGACTGTCCAGGCCCCGGGGCAGGGGATACGGAC 463
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Qy  464 TGCAGGGGAGTGTGAGAGCGGCCTCTTCACCCGCTTCAGAAAACCACCTCAGACACTGCCTC 523
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Qy  524 AGCTGCTCCAAATGCCGAAAGGAAAATGGGTCAGGTGGAGATCTCCTCTTTTGTCACAGTGGAC 583
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Qy  764 TCCTGT 769
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Db  764 TCCTGT 769
```

RESULT 3

```
ID   Q49932 standard; cDNA to mRNA; 1368 BP.
AC   Q49932;
DT   29-APR-1994 (first entry)
DE   Lambda-derived TNF-R cDNA.
KW   Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;
KW   IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;
KW   rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;
KW   pulmonary fibrosis; silicosis; allograft; xenograft; rejection;
KW   graft verses host disease; sepsis; inflammation; allergy;
KW   autoimmune dysfunction; ss.
OS   Homo sapiens.
OS   Lambda-gt10-7-ctnfbp.
FH   Key                 Location/Qualifiers
FT   CDS                 1..1366
FT   /tag=  a
FT   /product= hINF-R
FT   sig_peptide         1..120
FT   /tag=  b
FT   mat_peptide         121..1363
FT   /tag=  c
PN   WO9319777-A.
PD   14-OCT-1993.
PF   26-MAR-1993; U02938.
PR   30-MAR-1992; US-860710.
PA   (IMMV ) IMMUNEX CORP.
PI   Smith CA;
PI   WPI; 93-336592/42.
DR   P-PSDB; R42059.
PT   New fusion protein tumour necrosis factor and human interleukin-1
PT   receptor - useful in therapy, diagnosis and assays of e.g.
PT   rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.
PS   Disclosure; Page 57-59; 85pp; English.
CC   The sequences given in Q49931-32 encode human tumour necrosis factor
CC   receptor (TNF-R) and the sequences in Q49933-34 encode human
CC   interleukin-1 receptor (IL-1R). These sequences were used in the
CC   production of a fusion protein which conformed to one of the
CC   formulae:
CC   TNF-R-linker-TNF-R-linker-IL-1R
```

```
Db  333 gatagtgtgtgtccccaaggagaaaatatatccacccctcaaaaataattcgatttgctgtgtacc 392
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  344 GATAGTGTGTGTCCCCAAGGAAAATAATATACCCACCCTCAAAAATAATTCGATTTGCTGTGTACC 403

Db  393 aagtgccacaaaggaacctactgtgtcagtgccgggggcaggggatacggac 452
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  404 AAGTGCCACAAAGGAAGCTACTTGTACAATGACTGTCCAGGCCCCGGGGCAGGGGATACGGAC 463

Db  453 tgcaggggagtgtgagagcggcctcttcacccgcttcagaaaaccacctcagacactgcctc 512
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  464 TGCAGGGGAGTGTGAGAGCGGCCTCTTCACCCGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db  513 agctgctccaaatgccgaaaggaaaatgggtcaggtggagatctcctctttgtcacagtggac 572
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  524 AGCTGCTCCAAATGCCGAAAGGAAAATGGGTCAGGTGGAGATCTCCTCTTTTGTCACAGTGGAC 583

Db  573 cgggacaccgtgtggtgctgcaggaagaaaccagtaccggcattattgggagtgaaaacctt 632
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  584 CGGGACACCGTGTGGTGCTGCAGGAAGAAACCAGTACCGGCATTATTGGGAGTGAAAACCTT 643

Db  633 ttccagtgcttcaattgcagccctctgcctcaatgggaccgtgaccctcttcctgccaggag 692
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  644 TTCCAGTGCTTCAATTGCAGCCCTCTGCCTCAATGGGACCGTGACCCTCTTCCTGCCAGGAG 703

Db  693 aaacagaaccgtgtgcacctgccatgcaggtttctttcttcctaagagaaaacgagagtgtgtc 752
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  704 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTTCCTAAGAGAAAACGAGAGTGTGTC 763

Db  753 tcctgt 758
        ||||||
Qy  764 TCCTGT 769
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Left column

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CC   IL-1R-linker-TNF-R-linker-TNF-R or
CC   TNF-R-linker-TNF-R
CC   The linker may comprise 5-100 amino acids selected from Gly, Asp,
CC   Ser, Thr and Ala. These linkers separate the individual moieties
CC   by such a distance that each component of the fusion protien is
CC   capable of folding into the secondary or tertiary structure required
CC   for its biological activity. These fusion proteins may be used in
CC   therapy, diagnosis and assays for conditions mediated by TNF or IL-1,
CC   particularly in conditions in which both TNF and IL-1 play a causitive
CC   role. They may be used to treat cachexia, rheumatoid arthritis,
CC   diabetes, multiple sclerosis, pulmonary fibrosis and silicosis,
CC   cerebral malaria, allograft and xenograft rejection in graft verses
CC   host disease, sepsis, septic shock, inflammation, allergies and
CC   autoimmune dysfunctions.
SQ   Sequence 1368 BP;  292 A;  424 C;  376 G;  276 T;

Query Match            40.4%;
Best Local Similarity  99.8%;             Score 424;  DB 8;  Length 1368;
Matches  425;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Db   121 gatagtgtgtccccaaggaaaatatatccacccctccaaaataattcgcattgctgtacc 180
             |||||||| ||||||||||||||||||||||||||||||||||||| |||| |||||||||
Qy   344 GATAGTGTGTCTCCCCAAGGAAAATATATCCACCCTCCAAAATAATTCCATTTGCTGTACC 403

Db   181 aagtgccacaaaggaacctacttgtacaatgactgtccaggccccgggggcaggatacggac 240
             |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Qy   404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGGCAGGATACGGAC 463

Db   241 tgcaggaggtgagagcggctccctccaccgcctccagaaaaccacctcagaacactgcctc 300
             |||||||||| |||||||  |||| |||||| ||||||||||||||||||||||||||||
Qy   464 TGCAGGAGGTGTGAGAGCGGCGGCTCCCTTCACCGCCTTCAGAAAACCACCTCAGAACACTGCCTC 523

Db   301 agctgctccaaatgccgaaagggaaatgggtcaggtggagatctctcttcttcttgcacagtggac 360
             ||||||||||||||||||||| ||||||||||||||||||||||| |||||||||||||||
Qy   524 AGCTGCTCCAAATGCCGAAAAGGGAAATGGGTCAGGTGGAGATCTCTTCTTCTTGCACAGTGGAC 583

Db   361 cgggacaaccgtgtgtggctgcaggaagaacagtaccggccattattggagtgaaaacctt 420
             ||||||| |||||||||||||||||||||||||||||||||||||||||||||| |||||
Qy   584 CGGGACACCGTGTGTGGCTGCAGGAAGAACAGTACCGGCCATTATTGGAGTGAAAAACCTT 643

Db   421 ttcccagtgcttcaattgcagcctccatggac...                          480
             |||| |||||||||||||||||||||||||||
Qy   644 TTCCAGTGCTTCAATTGCAGCCTCCATGGAC...                           703

Db   481 aaacagaacaccgtgtgcacctgccatgcacaggt...                       540
             |||||||||||||||||||||||||||||||
Qy   704 AAACAGAACACCGTGTGCACCTGCCATGCAGGT...                         763

Db   541 tcctgt                                                       546
             ||||||
Qy   764 TCCTGT                                                       769
```

```
RESULT 4

ID   Q24440 standard; DNA; 2062 BP.
AC   Q24440;
DT   05-Nov-1992 (first entry)
DE   Encodes TNF-alpha 55kD receptor.
KW   tumour necrosis factor alpha; extracellular binding domain;
KW   treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
KW   malaria; viral meningitis; graft versus host disease;
OS   Homo sapiens.
KW   autoimmune disease; rheumatoid arthritis.
FH   Key             Location/Qualifiers
FT   CDS             156..1517
FT   /product= human TNF-alpha
FT   mat_peptide     1265..1267
FT   /tag= a
FT   mat_peptide     1265..1267
FT   /tag= b
FT   /note= "3"
FT   mat_peptide     1265..1267
FT   /tag= c
FT   /codon= seq:"TGG", aa:Thr
```

Right column

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FT   mat_peptide     1258..1260
FT   /tag= d
FT   /codon= Seq:"AAG", aa:Leu
FT   mat_peptide     1433..1435
FT   /tag= e
FT   /codon= Seq:"GAC", aa:Asn
FT   mat_peptide     156..274
FT   /tag= f
FT   /codon= Seq:"GAC", aa:Asn

PT   New polypeptide capable of binding human TNF alpha - comprises
PT   first three cysteine-rich subdomains of TNF alpha receptor for
PT   treating autoimmune disease, septic shock, HIV etc.
PS   Claim 4; Fig 1; 43pp; English.

CC   This sequence encodes human TNF-alpha 55kD receptor . A placenta cDNA
CC   library in gt10 was screened with probe Q29236. Ten hybridising clones
CC   were plaque purified and cDNA size determined by PAGE against an
CC   Eco RI digested phage DNA. The inserts of two cDNA clones were then
CC   sequenced. The coding region of the majority of the human TNF-alpha
CC   55kD receptor was isolated as an EcoRI fragment encoding 374 amino
CC   acids, and cloned into a mammalian cell expression vector, resulting
CC   in prTNFR. A derivative of the TNF-alpha receptor was produced by
CC   engineering a termination codon just prior to the transmembrane
CC   domain. PCR with primers Q29237,8 generated a 300bp
CC   restriction fragment which was cloned into prTNFR, giving pTNFRcd.
CC   DNA sequencing confirmed this contained the designed DNA sequence.
CC   The TNF-alpha receptor expression plasmids were then transfected
CC   into monkey COS-7 cells.
CC   See also Q24440-51, R24000, R24080-84, R27585, Q29236-8
SQ   Sequence 2062 BP;  429 A;  618 C;  572 G;  443 T;

Query Match            40.4%;
Best Local Similarity  99.8%;             Score 424;  DB 4;  Length 2062;
Matches  425;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Db   275 gatagtgtgtccccaaggaaaatatatccacccctccaaaataattcgcattgctgtacc 334
             |||||||| |||||||||||||||||||||||||||||||||||||| |||| |||||||
Qy   344 GATAGTGTGTCTCCCCAAGGAAAATATATCCACCCTCCAAAATAATTCCATTTGCTGTACC 403

Db   335 aagtgccacaaaggaacctacttgtacaatgactgtccaggccccggggcaggatacggac 394
             ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Qy   404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGGCAGGATACGGAC 463

Db   395 tgcaggaggtgagagcggcggctcccttcaccgccttcagaaaaccacctcagaacactgcctc 454
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   464 TGCAGGAGGTGTGAGAGCGGCGGCTCCCTTCACCGCCTTCAGAAAACCACCTCAGAACACTGCCTC 523

Db   455 agctgctccaaatgccgaaagggaaatgggtcaggtggagatctcttcttcttgcacagtggac 514
             |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Qy   524 AGCTGCTCCAAATGCCGAAAAGGGAAATGGGTCAGGTGGAGATCTCTTCTTCTTGCACAGTGGAC 583

Db   515 cgggacaccgtgtgtggctgcaggaagaaccagtaccggccattattggagtgaaaacctt 574
             ||||||||||||||||||||||||||||| ||||||||||||||||||||||||| |||||
Qy   584 CGGGACACCGTGTGTGGCTGCAGGAAGAACAGTACCGGCCATTATTGGAGTGAAAAACCTT 643

Db   575 ttccagtgcttcaattgcagcctccatggggaccgtgcaagttttcaattgcagcctccatggac 634
             |||||||||||||||||||||||||||||
Qy   644 TTCCAGTGCTTCAATTGCAGCCTCCATGGAC...                             703

Db   635 aaacagaacaccgtgtgcacctgccatgcacaggttttcttctaagagaaaacagagggtgtgtc 694
             ||||||||||||||||||||||||||||
Qy   704 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTTCTTCTAAGAGAAAACGAGAGTGTGTC 763

Db   695 tcctgt                                                        700
             ||||||
Qy   764 TCCTGT                                                        769
```

RESULT 5

ID   Q20973 standard; DNA; 2062 BP.
AC   Q20973;
DT   11-MAY-1992 (first entry)
DE   TNF-alpha binding protein gene.
KW   Tumour necrosis factor alpha; autoimmune diseases; cachectin; ss;
OS   Homo sapiens.
FH   Key   Location/Qualifiers
FT   CDS   155..1522
FT   /*tag=   a
FT   sig_peptide   155..274
FT   /*tag=   b
FT   mat_peptide   275..1522
FT   /*tag=   c
FT   misc_feature   473..532
FT   /*tag=   d
FT   misc_feature   242..751
FT   /*tag=   e
FT   /note=   "encodes the extracellular domain of human
CC   TNF alpha receptor"
PN   05-FEB-1992
PR   GB224569-A.
PR   15-JUN-1990; 013410.
PR   15-JUN-1990; GB-013410.
PA   (CHAR-) CHARING CROSS SUNLE.
PI   Feldman M, Gray P, Turner M, Brennan F;
DR   WPI; 92-043613/06.
DR   P-PSDB; R20787.
PT   New tumour necrosis factor alpha binding protein and polypeptide
PT   - useful in treating cachexia, sepsis and auto immune diseases
PT   e.g. rheumatoid arthritis
PS   Disclosure; Fig 1; 25pp; English.
CC   The sequence is that of DNA encoding a human placental cDNA library
CC   binding protein which was obtd. from a human placental cDNA library
CC   in lambda gt11 using a probe (Q20974). The DNA also encodes the
CC   extracellular domain of human TNF alpha receptor and as such it is
CC   useful for treating diseases where TNF alpha is involved as a
CC   causative agent, e.g. cachexia, sepsis and autoimmune diseases,
CC   specifically rheumatoid arthritis. See also Q20974.
SQ   Sequence 2062 BP;

Query Match   40.4%; Score 424; DB 3; Length 2062;
Best Local Similarity 99.8%; Pred. No. 2.42e-296;
Matches   425; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

```
Qy    275 gatagtgtgtgtcccaaggaaaatataccacccctcaaaataattcgattttgctgtacc 334
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    616 gatagtgtgtgtcccaaggaaaatataccacccctcaaaataattcgattttgctgtacc 573

Qy    335 aagtgcccacaaggaaacctacttgtacaatgactgtccaggacccgggggcaggataccggac 394
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    573 aagtgcccacaaggaaacctacttgtacaatgactgtccaggacccgggggcaggataccggac 514

Qy    395 tgcaggggagtgtgagagcggcgctcctcacgctccagaaaaccacctcagacactgcctc 454
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    463 tgcaggggagtgtgagagcggcgctcctcacgctccagaaaaccacctcagacactgcctc 404

Qy    455 agctgctccaaatgccgaaaggaaatgggtcagtgtggagatctctcttcttgcacagtggac 514
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    404 AGTGCTCCAAATGCCGAAAGGAAATGGGTCAGTGTGGAGATCTCTCTTCTTGCACAGTGGAC 463

Qy    515 cgggacaccgtgtgtggctcgaggaagaacaccagtacgcggccgcatttattgggagtgaaaacctt 574
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    335 CGGGACACCGTGTGTGGCTCGAGGAAGAACACCAGTACGCGGCCGCATTTATTGGGAGTGAAAACCTT 394

Qy    575 ttccagtgtcttcaattgcagcctctgcctctgcctcctgccaggag 634
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    584 ttccagtgtcttcaattgcagcctctgcctctgcctcctgccaggag 644

Qy    635 aaacagaaccacgtgtgcacctgcatgcaggttcttctaagagaaaacgagtgtgtc 694
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    575 TTCCAGTGTCTTCAATTGCAGCCTCTGCCTCTGCCTCCTGCCACCTCCTCCTGCCAGGAG 515
```

RESULT 6

ID   Q10883 standard; cDNA; 2088 BP.
AC   Q10883;
DT   13-MAY-1991 (first entry)
DE   30kD TNF inhibitor precursor gene in lambda-gt10-7ctnfbp.
KW   Tumour necrosis factor; inhibitor; ss;
OS   Homo sapiens.
FH   Key   Location/Qualifiers
FT   CDS   171..1536
FT   /*tag=   a
PN
PR   AU9058976-A.
PR   24-JAN-1991.
PR   16-JUL-1990; 058976.
PR   18-JUL-1989; US-381080.
PR   11-DEC-1989; US-450329.
PR   07-FEB-1990; US-479661.
PA   (SYNE-) SYNERGEN INC.
DR   WPI; 91-073847/11.
DR   P-PSDB; R10986.
PT   Tumour necrosis factor inhibitor - for suppression of TNF-alpha
PT   and -beta, useful as therapeutic agent.
PS   Disclosure; Fig 21; 142pp; English.
CC   The sequence encodes the entire 30 kD TNF inhibitor. The clone from
CC   which the sequence was obtd. was isolated from a cDNA library
CC   prepd. from RNA form U937 cells treated with PMA/PHA. The whole
CC   gene can be inserted into expression vectors for prepn. of TNF
CC   inhibitor for use in the treatment of inflammatory and degenerative
CC   diseases. See also Q10878, Q10884 and Q10907.
SQ   Sequence 2088 BP;

Query Match   40.4%; Score 424; DB 2; Length 2088;
Best Local Similarity 99.8%; Pred. No. 2.42e-296;
Matches   425; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

```
Qy    289 gatagtgtgtgtcccaaggaaaatataccacccctcaaaataattcgattttgctgtacc 348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    439 gatagtgtgtgtcccaaggaaaatataccacccctcaaaataattcgattttgctgtacc 444

Qy    349 aagtgcccacaaggaaacctacttgtacaatgactgtccaggacccgggggcaggataccggac 408
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Db    404 AAGTGCCCACAAGGAAACCTACTTGTACAATGACTGTCCAGGCCCGGGGGCAGGATACGGAC 463

Qy    409 tgcaggggagtgtgagagcggcgctcctcacgctccagaaaaccacctcagacactgcctc 468
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    464 TGCAGGGAGTGTGAGAGCGGCGCTCCTCACGCTCCAGAAAACCACCTCAGACACTGCCCTC 523

Qy    469 agctgctccaaatgccgaaaggaaatgggtcagtgtggagatctctcttcttgcacagtggac 528
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGTGTGGAGATCTCTCTTCTTGCACAGTGGAC 583

Qy    529 cgggacaccgtgtgtggctcgaggaagaacaccagtacgcggccgcatttattgggagtgaaaacctt 588
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    584 CGGGACACCGTGTGTGGCTCGAGGAAGAACACCAGTACGCGGCCGCATTTATTGGGAGTGAAAACCTT 643

Qy    589 ttccagtgtcttcaattgcagcctctgcctctgcctcctgccaggag 648
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    644 TTCCAGTGTCTTCAATTGCAGCCTCTGCCTCTGCCTCCTGCCACGGAG 703

Qy    649 aaacagaaccacgtgtgcacctgcatgcaggttcttctaagagaaaacgagtgtgtc 708
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    704 AAACAGAACCACGTGTGCACCTGCATGCAGGTTTCTTCTAAGAGAAAACGAGTGTGTC 763

Qy    709 tcctgt 714
          ||||||
Db    704 AAACAGAACACCGTGTGCACCTGCATGCAGGTTTCTTCTAAGAGAAAACGAGTGTGTC 763

Qy    704 AAACAGAACACCGTGTGCACCTGCATGCAGGTTTCTTCTAAGAGAAAACGAGTGTGTC 763
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    695 tcctgt 700

Qy    764 TCCTGT 769
          ||||||
Db    709 tcctgt 714
```

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Qy    764 TCCTGT 769

RESULT 7
ID    Q10955 standard; cDNA; 2111 BP.
AC    Q10955;
DT    24-MAY-1991 (first entry)
DE    Encodes human 55kD TNF-binding protein.
KW    Tumour Necrosis Factor; binding proteins; septic shock;
KW    autoimmune glomerulonephritis; lymphokine; cytokine.
OS    Homo sapiens.
FH    Key             Location/Qualifiers
FT    sig_peptide     187..273
FT    /*tag=    a
FT    mat_peptide     274..1551
FT    /*tag=    b
FT    /product= 55kD TNF-BP
PN    7
PD    20-MAR-1991.
PF    31-AUG-1990; 116707.
PF    12-SEP-1989; CH-003319.
PF    08-MAR-1990; CH-000746.
PR    20-APR-1990; CH-001347.
PA    (HOFF) HOFFMANN-LA ROCHE AG.
PI    Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;
PI    Schlaeger EJ;
DR    WPI; 91-081851/12.
DR    P-PSDB; R11082.
PT    EP-417563-A.
PS    Claim 4: Fig 1; 26pp; German.
PT    Insoluble tumour necrosis factor binding proteins - and DNA
PT    encoding them, useful in pharmaceutical prods. and for antibody
PT    prodn.
CC    Partial amino acid sequences were determined for the 55 and 75kD
CC    TNF-BPs (see R11072-R11081) and oligonucleotide primers were
CC    synthesised based on these partial sequences. The primers were used
CC    to produce a cDNA fragment for use as aprobe to screen a human
CC    placental cDNA bank constructed in lambda gt11. Positive clones were
CC    identified and sequenced. DNA constructs comprising the TNF-BP coding
CC    sequence may also contain a fragment encoding a human Ig domain.
CC    Recombinant constructs are used to transform cells to confer
CC    Improved TNF-binding properties.
CC    See also Q10956.
SQ    Sequence 2111 BP;   445 A;   628 C;   588 G;   450 T;

Query Match           40.4%;  Score 424;  DB 2;  Length 2111;
Best Local Similarity 99.8%;  Pred. No. 2.42e-296;
Matches  425;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Db    307 gatagtgtgtcccaaggaaaataatatccacacctcaaaataattcgatttgctgtacc 366
          ||||||| ||||||||||||||||| |||||||| |||||||||||||| |||||||||||
Qy    344 GATAGTGTGTGTCCCAAGGAAAATAATATCCACCCTCAAAATAATTCGTTTGCTGTACC 403

Db    367 aagtgcacaaaggaaacctactgtacaaatgactgtgtccaggtcccaggatacggac 426
          |||||| ||||||||||||||| |||||| |||||||||||||||||||||||||||||
Qy    404 AAGTGCCACAAAGGAAACCTACTTGTACAAATGACTGTGTCCAGGTCCCAGGATACGGAC 463

Db    427 tgcaggaagtgtgagagcgggctcctccaccgcgcttcaggaaaaccaccactgcctc 486
          |||||| ||||||||||||||||||||| ||||| ||||||||||| ||||||||| |||
Qy    464 TGCAGGGAGTGTGAGAGCGGGCTCCTTCACCGCTTCAGGAAAAACCACCACTGCCCTC 523

Db    487 agctgctccaaatgccgaaatgggtcagtgtggagatctcttcttcttgcacagtggac 546
          ||||||||||||||||||||| ||||||| |||||||||||||||||||||||||||||
Qy    524 AGCTGCTCCAAATGCCGAAAGGGATCAGTGTGGAGATCTCTTCTTCTTGCACAGTGGAC 583

Db    547 cgggaacaccgtgtgtgctgcaggaagaaccagtaccggccattattgggagtgaaacctt 606
          ||||| |||||||||| ||||||||||||||||||||||||||||||| |||||||||||||
Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCCATTATTGGAGTGAAACCTT 643

Db    607 ttccagtgcttcaattgcagccctctgctcctcctctcctgccaggag 666
          ||||||||||||||||||||||||||||||||||||||||||||||||
Qy    644 TTCCAGTGCTTCAATTGCAGCCCTCTGCTCCTCCTCTCCTGCCAGGAG 703

Db    667 aaacagaacaccgtgcacctgcccatgcaggttctcttctaagagaaaacgagtgtgtc 726
          |||||||||||||| |||||||||||||||||| ||||||| |||||||||||||||||||
Qy    704 AAACAGAACACCGTGTGCACCTGCCCATGCAGGTTCTCTTCTTAAGAGAAAACGAGTGTGTC 763
```

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Qy    704 AAACAGAACACCGTGTGCACCTGCCCATGCAGGTTCTCTTCTTAAGAGAAAACGAGTGTGTC 763

Db    727 tcctgt 732
          ||||||
Qy    764 TCCTGT 769

RESULT 8
ID    Q06285 standard; DNA; 2141 BP.
AC    Q06285;
DT    29-JAN-1991 (first entry)
DE    Human Tumour Necrosis Factor-Receptor cDNA insert.
KW    Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
KW    lambdaTNF-R2; raTNF-R8; ss.
OS    Homo sapiens.
FH    Key             Location/Qualifiers
FT    CDS             213..1577
FT    /*tag=    a
FT    /label=huTNF-R
PN    8
PD    24-OCT-1990.
PF    06-APR-1990; 106924.
PF    21-APR-1989; DE-913101.
PR    21-JUN-1989; DE-920282.
PA    (BOEH ) BOEHRINGER INGELHEIMINT.
PI    Hauptmann R, Himmler A, Maurer-Fogy I, Stratowa C;
DR    WPI; 90-321987/43.
DR    P-PSDB; R07451.
PT    Disclosure: Fig 91(1-2); 51pp; German.
PT    DNA encoding TNF binding protein and TNF- receptor - used in
PT    tumour treatment and to understand mechanism to TNF action
CC    raTNF-R8 (Q06284) was used to screen the HS913T cDNA library.
CC    LambdaTNF-R2 encodes the complete human TNF-R2 and was used to
CC    construct a plasmid (pADTNF-R) expressing the product the same way
CC    as pADTNF-BP (see Q06282).
CC    See also Q06282-Q06285.
SQ    Sequence 2141 BP;   455 A;   633 C;   593 G;   460 T;

Query Match           40.4%;  Score 424;  DB 1;  Length 2141;
Best Local Similarity 99.8%;  Pred. No. 2.42e-296;
Matches  425;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Db    333 gatagtgtgtcccaaggaaaatatatccacacctcaaaataattcgatttgctgtacc 392
          ||||||| ||||||||||||||||||||||||| |||||||||||||| |||||||||||
Qy    344 GATAGTGTGTGTCCCAAGGAAAATATATCCACCCTCAAAATAATTCGTTTGCTGTACC 403

Db    393 aagtgcccacaaaggaaacctacttgtacaatgactgtgtccaggtcccaggatacggac 452
          ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    404 AAGTGCCACAAAGGAAACCTACTTGTACAATGACTGTGTCCAGGTCCCAGGATACGGAC 463

Db    453 tgcaggaggtgtgagagcggcgctcctccacgcgcttcaggaaaaaccaccactgcctc 512
          ||||||| ||||||||||||||||||||| ||| ||||||||||||||||||||||| |||
Qy    464 TGCAGGGAGTGTGAGAGCGGCGCTCCTTCACCGCTTCAGGAAAAAACCACCACTGCCCTC 523

Db    513 agctgctccaaatgccgaaaggatgggtcaggtggagatctctcttcttgcacagtggac 572
          ||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Qy    524 AGCTGCTCCAAATGCCGAAAGGATGGGTCAGGTGGAGATCTCTTCTTCTTGCACAGTGGAC 583

Db    573 cgggacaccgtgtgtgggctgcaggaagaaccagtaccggccattattggagtgaaacctt 632
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    584 CGGGACACCGTGTGTGGGCTGCAGGAAGAACCAGTACCGGCCATTATTGGAGTGAAACCTT 643

Db    633 ttccagtgcttcaattgcagccctctgctcctcctctcctgccaggag 692
          ||||||||||||||||||||||||||||||||||||||||||||||||
Qy    644 TTCCAGTGCTTCAATTGCAGCCCTCTGCTCCTCCTCTCCTGCCAGGAG 703

Db    693 aaacagaacaccgtgcacctgcccatgcaggtttcttcttaagagaaaacgagtgtgtc 752
          |||||||||||||| |||||||||||||||||||| |||||||||||||||||||||||||
Qy    704 AAACAGAACACCGTGTGCACCTGCCCATGCAGGTTTCTTCTTAAGAGAAAACGAGTGTGTC 763

Db    753 tcctgt 758
          ||||||
Qy    764 TCCTGT 769
```

RESULT 9

```
ID   Q90513 standard; DNA; 2175 BP.
AC   Q90513;
DT   19-JAN-1996 (first entry)
DE   p55 TNF-R gene.
KW   p55; tumour necrosis factor receptor; TNF-R; human; murine; chimera;
KW   epidermal growth factor receptor; EGF-R; protease; inhibitor;
KW   phorbol myristate acetate; PMA; ss.
OS   Homo sapiens.
FH   Key            Location/Qualifiers
FT   CDS            256..1623
FT                  /*tag= a
FT                  /product= p55 TNF-R
FT   misc_signal    2143..2149
FT                  /*tag= b
FT                  /note= "possible poly-A signal"
PN   AU9475742-A.
PD   04-MAY-1995.
PF   11-OCT-1994; 075742.
PR   12-OCT-1993; IL-107268.
PA   (YEDA ) YEDA RES & DEV CO LTD.
PI   Batkin M, Brakebusch C, Varfolomeev E, Wallach D;
PT   New protease capable of cleaving soluble tumour necrosis factor
PT   (TNF) receptor - from cell-bound TNF-receptor, useful for
PT   antagonising deleterious effects of TNF.
PS   Disclosure; Fig 1; 40pp; English.
```

CC This sequence represents human p55 tumour necrosis factor (TNF-R) DNA.
CC Expression of this receptor is regulated by shedding of the extracellular
CC receptor fragment. The p55 TNF-R can be shed in response to different
CC inducing agents, e.g. phorbol myristate acetate (PMA), depending on cell
CC type. The only region of the receptor whose structure affects the
CC shedding response is the spacer region (see R75012) in the extracellular
CC domain. This region is located close to a site of cleavage of the
CC molecule, and links the Cys rich module to the transmembrane domain. The
CC spacer region of the encoded protein was used to create the chimera
CC between human p55 TNF-R and murine epidermal growth factor receptor
CC (EGF-R) that are represented by R75007-11. This spacer region was
CC subjected to deletion mutations (R75013-25) and substitutions
CC (R75026-47). Of the spacer region, the most important residues are
CC Asn 172, Lys 174 and Gly 175, with Val 173 being the most
CC important of these. The shedding of the receptor is independent of the
CC side chain identity of these residues, with the exception of a limited
CC dependence on the identity of Val 173. Mutations which alter the
CC conformation of the protein adversely effect the shedding process. The
CC mutations shown in R75013-47 were introduced in order to create an
CC inhibitor of a protease that is capable of cleaving the soluble TNF-R
CC from the cell bound TNF-R. Fragments of these inhibitors can be seen in
CC R75017-9, R75025, R75033-5 and R75042-3. These protease inhibitors can
CC be used for enhancing TNF function.
SQ Sequence 2175 BP;

```
Query Match           40.4%;  Score 424;  DB 15;  Length 2175;
Best Local Similarity 99.8%;  Pred. No. 2.42e-296;
Matches   425;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Sequence 2175 BP; 474 A; 642 C; 603 G; 456 T;

Qy  524 AGCTGCTCCAAATGCCGAAAGGAAAGATGGGTCAGGTGGAGATCTTCTTGCACAGTGGAC 583
        ||||||||||||||||||||| ||| ||||||||||||||||| ||||||||||||||||
Db  616 cgggcaccgtgtgtggctgcaggaggaaccagtacggcattattggagtggaaacctt  675

Qy  584 CGGGACACCGTGTGTGGCTGCAGGAGGAACCAGTACGCCATTATTGGAGTGGAAACCTT 643
Db  676 tccagtgcttcaattgcagcctctgcctccaatgtgaccgtgcaccctcctccggag  735

Qy  644 TTCCAGCGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCGCCAGGAG 703
Db  736 aaacaagaacaccgtgctgcacctgccatgcaggatttcttctaagagaaaacggtgtc 795

Qy  704 AAAACGAACACCGTGCTGCACCTGCACCAGGTTTCTTCTTAAGAGAGAAAAACGGTGTC 763
Db  796 tcctgt 801

Qy  764 TCCTGT 769

Db  376 gatagtgtgtgtcccccaaggaaaaatatatccaccccaaaataattcgattgctgtacc 435
        |||||||||||| |||||||||||||||||||||||| ||||||||||| ||||||||||
Qy  344 GATAGTGTGTGTCCCCAAGGAAAAATATATCCACCCTCAAAATAATTCCATTTGCTGTACC 403

Db  436 aagtgccacaaaggaacctacttgtaccaatgactgtgccagggatacggac 495
Qy  404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTGCCAGCCCGGGATACGGAC 463

Db  496 tgcaggagtgtgagagcgggctcctcaccgcttcagaaaacaccacctgcctc 555
Qy  464 TGCAGGGAGTGTGAGAGCGGGCTCCTTCACCGCTTCAGAAAACCACCTGCCTC 523

Db  556 agctgctccaaatgccgaaagtgggtcaggtggagatctcttcttgcacagtggac 615
```

RESULT 10

```
ID   T15931 standard; DNA; 6889 BP.
AC   T15931;
DT   20-JUN-1996 (first entry)
DE   DHFR/intron (WTrasSD)-TnFr-IgG dicistronic vector.
KW   DHFR; ras splice donor; dicistronic vector; selectable marker;
KW   immunoadhesin; TnFr-IgG; tumour necrosis factor; ds.
OS   Synthetic.
OS   WO9604391-A1.
PN   WO9604391-A1.
PD   15-FEB-1996.
PF   28-JUL-1995; U09576.
PR   05-AUG-1994; US-286740.
PA   (GETH ) GENENTECH INC.
PI   Crowley CW;
PT   Improved process for the selection of recombinant host cells
PT   expressing high level of a desired product - uses eukaryotic host
PT   cells contg. a DNA construct comprising a selectable gene
PS   Example 2; Page 36-42; 137pp; English.
```

CC A dicistronic vector (T15930) comprises a regulatory region
CC derived from the cytomegalovirus immediate-early gene, a
CC selectable dihydrofolate reductase gene positioned within an
CC intron having a 5' wild-type ras splice donor site, a downstream
CC sequence coding for an immunoadhesin, TnFr-IgG, capable of binding
CC tumour necrosis factor, and a poly-A sequence. Transfection of
CC DHFR- cells and subsequent methotrexate amplification and growth of
CC the cells in nutrient-rich medium gave TnFr-IgG in yields of 9.5
CC ug/ml (15-fold higher compared to conventional vector amplified
CC pools).
SQ Sequence 6889 BP;

```
Query Match           40.4%;  Score 424;  DB 18;  Length 6889;
Best Local Similarity 99.8%;  Pred. No. 2.42e-296;
Matches   425;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Sequence 6889 BP; 1729 A; 1826 C; 1681 G; 1653 T;

Qy   344 GATAGTGTGTGTCCCCAAGGAAAAATATATCCACCCTCAAAATAATTCCATTTGCTGTACC 403
         |||||||||||| |||||||||||||||||||||||| ||||||||||| ||||||||||
Db  1725 gatagtgtgtgtcccccaaggaaaaatatatccaccccaaaataattcgattgctgtacc 1784

Qy   404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTGCCAGCCCGGGATACGGAC 463
Db  1785 aagtgccacaaaggaacctacttgtaccaatgactgtgccagggatacggac 1844

Qy   464 TGCAGGGAGTGTGAGAGCGGGCTCCTTCACCGCTTCAGAAAACCACCTGCCTC 523
Db  1845 tgcaggagtgtgagagcgggctcctcaccgcttcagaaaacaccacctgcctc 1904

Qy   524 AGCTGCTCCAAATGCCGAAAGGAAAGATGGGTCAGGTGGAGATCTTCTTGCACAGTGGAC 583
Db  1905 agctgctccaaatgccgaaagtgggtcaggtggagatctcttcttgcacagtggac 1964

Qy   584 CGGGACACCGTGTGTGGCTGCAGGAGGAACCAGTACGCCATTATTGGAGTGGAAACCTT 643
Db  1965 cgggaccacgtgtgtggctgcaggaggaccagtacgcattattggagtggaaacctt 2024
```

```
Qy    584  CGGGACACCGTGTGTGGCTGCAGGAAGACCAGTACCGGCATTATTGGAGTGAAAACCTT 643
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2025  ttccagtgtcttcaattgcagccctctgcttcaatgggaccgtgcacctctcctgccaggag 2084
Qy    644  TTCCAGTGTCTTCAATTGCAGCCCTCTGCTTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 703
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2085  aaacagaacaccgtgtgcacctgcagaggtgtctc 2144
Qy    704  AAACAGAACACCGTGTGCACCTGCAGGTTTCTTTCTCAGGAAGAAAACGAGTGTGTC 763
           |||||||||||||||||||||||||||||
Db   2145  tcctgt 2150
           ||||||
Qy    764  TCCTGT 769
```

RESULT 11

```
ID    Q50870  standard; DNA; 2170 BP.
AC    Q50870;
DT    13-MAY-1994  (first entry)
DE    p55 Tumour necrosis factor receptor coding sequence.
KW    TNF; tumour necrosis factor; receptor; disease; autoimmunity;
KW    rheumatoid arthritis; graft rejection; graft vs. host; septic shock;
OS    Homo sapiens.
KW    effector protein; ss.
FH    Key                  Location/Qualifiers
FT    CDS                  256..1623
FT    /tag= a
FT    /product= p55 Tumour necrosis factor receptor.
PN    EP-568925-A.
PD    10-NOV-1993.
PF    29-APR-1993; IL-101769.
PF    03-MAY-1992; IL-101769.
PI    (YEDA ) YEDA RES & DEV CO LTD.
PA    Brakebusch C, Wallach D;
WPI   93-353057/45.
DR    P-PSDB; R42197.
PT    Modulating activity of tumour necrosis factor receptor - using
PT    peptides(s), antibodies, etc. which interact with critical regions
PT    of receptor or effector protein, for controlling auto-immune
PT    disease, septic shock, etc.
PS    Claim 2; Figure 1; 17pp; English.
CC    Modification of the tumour necrosis factor receptor by mutation or
CC    deletion modulates signal transduction and/or cleavage effected by
CC    the receptor. This modulation of activity can also be achieved
CC    using effector proteins which interact with the TNF receptor.
CC    Molecules which interact with the TNF receptor or the effector
CC    proteins can be used to treat or prevent diseases associated with
CC    TNF activity e.g. autoimmune disease; rheumatoid arthritis; graft
CC    rejection; graft vs. host disease or septic shock. They can also
CC    be used to treat overdoses of exogenous TNF.
SQ    Sequence 2170 BP;    474 A;    657 C;    584 G;    455 T;
```

Query Match 40.2%; Score 422; DB 9; Length 2170;
Best Local Similarity 99.5%; Pred. No. 8.37e-295;
Matches 424; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Db    376  gatagtgtgtccccaaggaaaatatatccacccctcaaaataattcgatttgttgttgtacc 435
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    344  GATAGTGTGTGTCCCCAAGGAAAATAATATCCACCCTCAAAATAATTCCATTTGCTGTTACC 403
Db    436  aagtgccacaaaggaacctactctgtacaatgactgtccaggcccgggggcaggatacggac 495
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    404  AACTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGACCGGAC 463
Db    496  tgcaggggagtgtgagaggcggctcctcaccgctccagaaaaaccaacctcagaacactgcctc 555
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    464  TGCAGGGGAGTGTGAGAGGCGGCTCCTCACCGCTCCAGAAAAACCAACACTGCCTC 523
Db    556  agctgctccaaatgccgaaatgggatctcttcttgcacagtggac 615
           |||||||||||||||||||||||||||||||||||||||
Qy    524  AGCTGCTCCAAATGCCGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583
Db    616  cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaacctt 675
```

```
Qy    584  CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    676  ttccagtgtcttcaattgcagccctctgcttcaatgggaccgtgcacctctcctgccaggag 735
Qy    644  TTCCAGTGTCTTCAATTGCAGCCCTCTGCTTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 703
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    736  aaacagaacaccgtgtgcacctgccaggtttcttttctcaggaagaaaacgagtgtgtc 795
Qy    704  AAACAGAACACCGTGTGCACCTGCAGGTTTCTTTCTCAGGAAGAAAACGAGTGTGTC 763
           ||||||||||||||||||||||||||||||
Db    796  tcctgt 801
           ||||||
Qy    764  TCCTGT 769
```

RESULT 12

```
ID    Q12215  standard; DNA; 2176 BP.
AC    Q12215;
DT    12-SEP-1991  (first entry)
DE    Type I TNF receptor.
KW    Tumour Necrosis Factor; TNF; binding protein; TBP-I; ss.
OS    Homo sapiens.
FH    Key                  Location/Qualifiers
FT    terminator           244..246
FT    /tag= a
FT    /note= "in-frame termination codon"
FT    CDS                  256..1620
FT    /tag= a
FT    /product= type I TNF receptor
FT    sig_peptide          256..318
FT    /tag= b
FT    mat_peptide          319..1620
FT    /tag= c
FT    misc_RNA             319..864
FT    /tag= d
FT    /label= soluble_domain
FT    /note= "may be 2 codons shorter or a few codons
FT    longer"
FT    misc_feature         376..414
FT    /tag= e
FT    /note= "TBP-I derived sequence"
FT    misc_feature         583..627
FT    /tag= f
FT    /note= "TBP-I derived sequence"
FT    misc_feature         850..858
FT    /tag= g
FT    /note= "TBP-I derived sequence"
FT    misc_RNA             889..957
FT    /tag= h
FT    /label= transmembrane_domain
FT    repeat_unit          385..504
FT    /tag= 1
FT    /number= 1
FT    repeat_unit          505..633
FT    /tag= j
FT    /number= 2
FT    repeat_unit          634..756
FT    /tag= k
FT    /number= 3
FT    repeat_unit          757..858
FT    /tag= l
FT    /number= 4
FT    polyA_signal         2145..2150
FT    /tag= m
PN    EP-433900-A.
PD    26-JUN-1991.
PF    13-DEC-1990; 124133.
PF    13-DEC-1990; IL-092697.
PR    12-JUL-1990; IL-095064.
PA    (YEDA ) YEDA RES & DEV CO LTD.
PI    Wallach D, Nophar Y, Kemper O, Engelmann H, Brakebusch C;
PI    Aderka D;
```

RESULT 13

DR   WPI; 91-186774/26.
DR   P-PSDB; R12550.
PT   Recombinant tumour necrosis factor binding protein I - prepd. by
PT   transfecting eukaryotic cells with vector contg. deoxyribonucleic
PT   acid encoding human type I TNF receptor or soluble domain
PS   Disclosure; Fig 1(D); 30pp; English;
CC   The Tumour Necrosis Factor Binding Protein I is the soluble form of
CC   type I TNF-receptor and constitutes a fragment of the cell surface
CC   form of this receptor, corresp. to its extracellular domain.
CC   There is no characteristic poly(A) addition signal near the 3' end
CC   of the cDNA. The sequence ACTAAA (tag m) may serve as an
CC   alternate to its signal, but with low efficiency.
CC   See also O12212-15.
SQ   Sequence 2176 BP;

         475 A;   644 C;   602 G;   455 T;

Query Match   40.2%; Score 422; DB 2; Length 2176;
Best Local Similarity   99.5%; Pred. No. 8.37e-295;
Matches 424; Conservative   0; Mismatches 2; Indels   0; Gaps   0;

Qy   376 gatagtgtgtgtcccccaaggaaaatatataccacccctccaaaatataatccgatttgcagtacc 435
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCCTCCAAAATAATTCCATTTGCTGTACC 403

Qy   436 aagtgccacaaaggaaacctacttgtacaaatactgtccaggccccgggggcaggatacggac 495
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   404 AAGTGCCACAAAGGAAACCTACTTGTACAAATGACTGTCCAGGCCCGGGGGCAGGATACGGAC 463

Qy   496 tgcaggggagtgtgacgacggcgtcttcctccagaaaaccacctcagacactgcctc 555
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   464 TGCAGGGGAGTGTGACGACGGCGTCTTCCTCCAGAAAAACCACCTCAGACACTGCCTC 523

Qy   556 agctgctccaaatgccgaaaggaaatggtcaggtggagatctcttcttcttgcacagttggac 615
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTCTTGCACAGTGGGAC 583

Qy   616 cgggacaccgtgttgggctgcaggaagaacaccagtaccggcattattggagtgaaaacctt 675
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   584 CGGGACACCGTGTTGTGGCCTGCAGGAAGAACACCAGTACCGGCATTATTGGAGTGAAAAACCTT 643

Qy   676 ttccagtgtgcttcaattgcagccctctgcctcaatggaccgtgcacctctcctgccaggag 735
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   644 TTCCAGTGTGCTTCAATTGCAGCCCTCTGCCTCAATGGACCGTGCACCTCTCCTGCCAGGAG 703

Qy   736 aaacagaacaccgtgtgcacctgccaatgcaggtttcttctttctttctttaagagaagaaaagagagtgtgtc 795
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   704 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTCTTTCTTTAAGAGAAGAAAAGAGAGTGTGTC 763

Qy   796 tcctgt 801
          ||||||
Db   764 TCCTGT 769

───

RESULT 14

ID   Q24445 standard; DNA; 504 BP.
AC   Q24445;
DT   05-NOV-1992 (first entry)
DE   Encodes truncated TNF-alpha 55kD receptor (165 amino acids).
KW   tumour necrosis factor alpha; extracellular binding domain;
KW   treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
KW   malaria; viral meningitis; graft versus host disease;
KW   autoimmune disease; rheumatoid arthritis.
OS   Homo sapiens.
PN   WO9207076-A.
PD   30-APR-1992.
PF   18-OCT-1991; G01826.
PR   18-OCT-1990; GB-022648.
PA   (CHAR-) CHARING CROSS SUNLEY RES CENT.
PI   Brennan FM, Feldmann M, Gray PW, Turner MJC;
DR   WPI; 92-167156/20.
DR   P-PSDB; R24084.
PT   New polypeptide capable of binding human TNF alpha - comprises
PT   first three cysteine-rich subdomains of TNF alpha receptor for
PT   treating autoimmune disease, septic shock, HIV etc.

Query Match   42.4%; Score 424;
Best Local Similarity   99.5%; Conservative   0; Mismatches 2; Indels   0; Gaps   0;
Matches 424;

───

(Second page column)

PS   Example; Fig 11; 43pp; English.
CC   This sequence encodes the designed TNF-alpha 55kD receptor
CC   derivative, as present in pdelta IV. This construct was generated by
CC   cloning of the BglII/HindIII digested product of a PCR using
CC   primers 5A and 4D into BglII/HindIII 5'-delta1a. This introduced
CC   a termination codon after amino acid 167, to yield pdeltaIV.
CC   This derivative lacks the membrane proximal 4th subdomain, yet
CC   retains the ability to bind TNF-alpha with high affinity
CC   (110power8 - 10power9 Mpower-1) The deriv. can be used in the
CC   regulation of human TNF-alpha mediated responses by binding and
CC   sequestering human TNF-alpha e.g. in the treatment of pulmonary
CC   diseases, septic shock, HIV infection, malaria, viral meningitis,
CC   graft versus host disease and autoimmune diseases, esp. rheumatoid
CC   arthritis. The deriv. is given at 10-100ug/dose.
CC   See also Q24440-51, R24000, R24080-84, R27585, Q29236-8
SQ   Sequence 504 BP;   122 A;   137 C;   138 G;   107 T;

Query Match   36.3%; Score 381; DB 4; Length 504;
Best Local Similarity   99.7%; Pred. No. 2.76e-263;
Matches 382; Conservative   0; Mismatches 1; Indels   0; Gaps   0;

Db   121 gatagtgtgtgtcccccaaggaaaatatataccacccctccaaaatataatccgatttgctgtacc 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCCTCCAAAATAATTCCATTTGCTGTACC 403

Db   181 aagtgccacaaaggaaacctacttgtacaaatgactgtccaggccccgggggcaggatacggac 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   404 AAGTGCCACAAAGGAAACCTACTTGTACAAATGACTGTCCAGGCCCGGGGGCAGGATACGGAC 463

Db   241 tgcaggggagtgtgacgacggcgtcttcctccagaaaaccacctcagacactgcctc 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   464 TGCAGGGGAGTGTGACGACGGCGTCTTCCTCCAGAAAAACCACCTCAGACACTGCCTC 523

Db   301 agctgctccaaatgccgaaaggaaatggtcaggtggagatctcttcttcttgcacagttggac 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTCTTGCACAGTGGGAC 583

Db   361 cgggacaccgtgtggctgcaggaagaacaccagtaccggcattattggagtgaaaacctt 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   584 CGGGACACCGTGTTGTGGCCTGCAGGAAGAACACCAGTACCGGCATTATTGGAGTGAAAAACCTT 643

Db   421 ttccagtgtgcttcaattgcagccctctgcctcaatggaccgtgcacctctcctgccaggag 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   644 TTCCAGTGTGCTTCAATTGCAGCCCTCTGCCTCAATGGACCGTGCACCTCTCCTGCCAGGAG 703

Db   481 aaacagaacaccgtgtgcacctg 503
          |||||||||||||||||||||||
Qy   704 AAACAGAACACCGTGTGCACCTG 726

───

(Third page column)

RESULT 14

ID   Q24442 standard; DNA; 474 BP.
AC   Q24442;
DT   05-NOV-1992 (first entry)
DE   Encodes truncated TNF-alpha 55kD receptor (155 amino acids).
KW   tumour necrosis factor alpha; extracellular binding domain;
KW   treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
KW   malaria; viral meningitis; graft versus host disease;
KW   autoimmune disease; rheumatoid arthritis.
OS   Homo sapiens.
PN   WO9207076-A.
PD   30-APR-1992.
PF   18-OCT-1991; G01826.
PR   18-OCT-1990; GB-022648.
PA   (CHAR-) CHARING CROSS SUNLEY RES CENT.
PI   Brennan FM, Feldmann M, Gray PW, Turner MJC;
DR   WPI; 92-167156/20.
DR   P-PSDB; R24081.
PT   New polypeptide capable of binding human TNF alpha - comprises
PT   first three cysteine-rich subdomains of TNF alpha receptor for
PT   treating autoimmune disease, septic shock, HIV etc.
PS   Example; Fig 8; 43pp; English.
CC   This sequence encodes the designed TNF-alpha 55kD receptor

CC derivative, as present in pdeltaI. This construct was generated by
CC joining PCR fragments by means of overlaps introduced into the
CC primers used for PCR. Gel purified products of PCR's using
CC 5'Cla, IA, IB, and 5D primers were mixed and subjected to further
CC amplification using 5'Cla and 5D as primers. The resulting fragment
CC was digested with ClaI and BglII and cloned into ClaI/BglII
CC digested pTNFRed, to yield pdeltaI, containing the sequence given.
CC This derivative could be used to regulate TNF-alpha mediated responses
CC by binding and sequestering human TNF-alpha e.g. in the treatment of
CC rheumatoid arthritis.
CC pulmonary diseases, septic shock, HIV infection, malaria, viral
CC meningitis, graft versus host disease and autoimmune diseases, esp.
CC See also Q24440-51, R24000, R24080-84, R27585, Q29236-8
SQ Sequence 474 BP; 110 A; 126 C; 132 G; 106 T;

Query Match
Best Local Similarity 97.8%;
Matches 309; Conservative 0; Pred. No. 8.62e-203; Mismatches 7; Indels 0; Gaps 0;
Score 302; DB 4; Length 474;

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Db 105 ggacagggagagaagagaagtgtgagagacggcgtctccttcaccgcttcagaaaacaactcag 164
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Qy 454 GGATACGGACGTGCAGGGAGTGTGAGAGACGGCGGCTCCTTCACCCGTTCAGAAAACACCTCAG 513

Db 165 acactgcctcagctgctccaaatgccgaaaggaaatgggtcaggtggagatctctcttg 224
        ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 514 ACACTCGCCTCAGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTCTTG 573

Db 225 cacagtggaccgggaacaccgtgtgtgctgcaggaagaacaagtaccggcattattggag 284
        |||||||||||||| |||||||||||| |||||||||||||| |||||||| ||||||||
Qy 574 CACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCAATTATTGGAG 633

Db 285 tgaaaaccttttccagtgctcaattgcagcctctgcctcaatggacggtgcacctc 344
        ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 634 TGAAAAACCTTTTCCAGTGCTCAATTGCAGCCTCTGCCTCAATGGACGGTGCACCTCTC 693

Db 345 ctgccaggagagaacagaacaccgtgtgccacctgccacctgcaggtttctcttattggag 404
        |||||||||| |||||||| ||||| ||||||||||  |||||||||||| |||| |||
Qy 694 CTGCCAGGAGAAACAGAACAGACCGTGCCACCTGCCATGCAGGTTTCTTTCTTAAGAGAGAAA 753

Db 405 cgagtgtgtctcctgt 420
        ||||||||||||||||
Qy 754 CGAGTGTGTCTCCTGT 769
```

RESULT 15
ID T76770 standard; cDNA; 2771 BP.
AC T76770.;
DT 15-SEP-1997 (first entry)
DE Rat Fabp1 gut-specific promoter and human growth hormone exon 1.

PT Animal model for Helicobacter pylori infection - comprising
PT transgenic mouse expressing human enzyme promoting intestinal
PT adhesion
PS Example 2: Columns 25-28; 24pp; English.

CC A claimed transgenic mouse expresses, in its intestinal epithelial
CC cells, the enzyme human GDP-L-fucose:beta-D-galactoside-2-alpha-L-
CC fucosyltransferase (also called alpha 1,2 FT) or human GDP-L-fucose:
CC beta-D-N-acetylglucosamide 3/4-alpha-L-fucosyltransferase (also
CC called alpha 1,3/4 FT). The enzyme is expressed under the
CC control of a gut epithelial cell-specific promoter and Helicobacter
CC pylori adheres to the transgenic cells. The transgenic mouse and
CC intestinal epithelial cells from it are useful as models for screening
CC compounds for the ability to inhibit adhesion of H. pylori to gut
CC epithelial cells. The first 617 nucleotides of the present chimeric
CC sequence encode the promoter from rat liver fatty acid binding protein
CC (Fabpl) which can direct foreign gene expression to the pit cell
CC lineage of the mouse gastric epithelium, to proliferating and non-
CC proliferating cells in intestinal crypts, as well as to the four
CC principal differentiated cell lineages along the crypt-to-villus axis
CC of the small intestine. The remainder of the chimeric sequence
CC corresponds to exon 1 of the human growth hormone (hGH) gene, into
CC which a sequence coding for a human fucosyltransferase (hFT) can be
CC inserted. No hGH will be produced because the initiator Met codon
CC and the first translation stop codon will be from the hFT sequence
CC and there is no ribosome re-entry sequence. The hGH exon 1 ensures
CC efficient splicing of the transgene primary transcript, improves
CC stability of the cytoplasmic hFT mRNA and allows transgene
CC expression to be monitored by in situ hybridisation using a
CC digoxigenin-labelled hGH oligonucleotide.

KW Human GDP-L-fucose:beta-D-galactoside-2-alpha-L-fucosyltransferase;
KW GDP-L-fucose:beta-D-N-acetylglucosamide 3/4-alpha-L-fucosyltransferase;
KW alpha 1,2 FT; alpha 1,3/4 FT; tissue-specific promoter;
KW rat liver fatty acid binding protein; transgene; transgenic mouse;
KW animal model; intestinal adhesion; Helicobacter pylori infection;
KW stomach; small intestine; gut; epithelial cell; surface receptor;
KW carbohydrate antigen; gastritis; peptic ulcer; neoplasia;
KW gastric adenocarcinoma; Lewis antigen; fucosylation; ds.
OS Chimeric - Homo sapiens.
OS Chimeric - Rattus sp.
FH Key Location/Qualifiers
FT promoter
FT 1..617
FT /note= "Corresponds to nucleotides -596 to +21 of
FT the rat liver fatty acid binding protein
FT gene"
FT exon 620..2771
FT /tag= b
FT /number= 1
FT /note= "Corresponds to nucleotides +3 to +2150 of
FT the human growth hormone (hGH) gene; it is
FT desirable for cDNA coding for a human
FT fucosyltransferase to be inserted into
FT exon1 of the hGH gene"

Query Match
Best Local Similarity 97.3%;
Matches 329; Conservative 0; Pred. No. 2.90e-201; Mismatches 5; Indels 4; Gaps 2;
Score 300; DB 31; Length 2771;
Sequence 2771 BP; 666 A; 718 C; 704 G; 683 T;

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Db 680 atggctacaggtaagcgcccctaaaatccctttgggcacaatgtgtcctgaggggagagg 739
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Qy 6  ATGGCTACAGGTAAGCGCCCCTAAAATCCCTTTGGGCACAATGTGTCCTGAGGGGAGAGG 65

Db 740 cacggacctgtagatgggacgggggcactaaccctcaggtttggggcttctgaatg--ag 797
        ||||||||||||||||||||||||||||||||||||||||||||||| ||| |
Qy 66 CACGGACCTGTAGATGGGACGGGGGCACTAACCCTCAGGTTTGGGGCTTCTCAATCTCAC 125

Db 798 tatcgccatgtaagcccagtat--ggccaatctcagaaaagctcctggtccctggagggat 855
        ||||||||||||||||||||||  ||||| ||||||||||||||||| |||||||||||
Qy 126 TATCGCCATGTAAGCCCAGTATTTGGCCAAATCTCAGAAAAGCTCCTCCTCCGGAGGGAT 185

Db 856 gggagaagaaaacaaacaagctcctggaagagagtgctggcctcttgctctccgc 915
        |||| | ||||||||||| ||||||||||||||||||||||||||||||||| ||
Qy 186 GGAGCAGAGAAAAACAAACAGCTCCTGGAAGAGAGTGCTGGCCTCTTGCTCTCCGGC 245

Db 916 tccctctgttgccctctggttttctccccagggctccccgggacgtccctgtcctggcttttg 975
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Qy 246 TCCCTCTGTTGCCCTCTGGTTTTCTCCCCAGGGCTCCCCGGGACGTCCCTGTCCTGGCTTTTG 305

Db 976 gcctgctcctgccctggcttcaagaggggcagtggc 1013
        |||||||||||||||||||||||||||||||||| |
Qy 306 GCCTGCTCCTGCCCTGGCTTCAAGAGGGGCAGTGCC 343
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Search completed: Wed May 6 12:57:36 1998
Job time : 144 secs.

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 MPSRCH (TM)
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*******************************************************************
*                                                                 *
*   Release 3.0.5AA John F. Collins, Biocomputing Research Unit.   *
*   Copyright (c) 1993-1997 University of Edinburgh, U.K.          *
*   Distribution rights by Oxford Molecular Ltd                    *
*                                                                 *
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MPsrch_nn   n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed May 6 12:38:32 1998;   MasPar time 969.27 Seconds
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Tabular output not generated.

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Description: (1-1049) from US08804166.seq
Perfect Score: 1049
N.A. Sequence: 1 TCCACATGGCTACAGGTAAG.........TTATTATCACAAATCTTAAG 1049
Comp: AGGTGTACCGATGTCCATTC.........AATAATAGTGTTTAGAATTC

Scoring table: TABLE default
                 Gap 6

Nmatch STD :   Dbase 0; Query 0

Searched: 1610801 seqs, 60785969 bases x 2

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database: embl-est
                 1:em_est1 2:em_est2 3:em_est3 4:em_est4 5:em_est5
                 6:em_est6 7:em_est8 8:em_gss 9:em_est13

Database: genbank-est
                 10:gb_est1 11:gb_est2 12:gb_est3 13:gb_est4 14:gb_est5
                 15:gb_est6 16:gb_est7 17:gb_est8 18:gb_est9 19:gb_est10
                 20:gb_est11 21:gb_sts 22:gb_gss 23:gb_est12 24:gb_est13
                 25:gb_est14 26:gb_est15 27:gb_est16 28:gb_est17
                 29:gb_est18 30:gb_est19 31:gb_est20

Statistics: Mean 11.127; Variance 1.959; scale 5.680

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query % Match	Length	DB	ID	Description	Pred. No.
1	258	24.6	373	23	HUM505B08B	Human placenta cDNA 5'	0.00e+00
2	258	24.6	379	23	C18240	Human placenta cDNA 5'	0.00e+00
3	258	24.6	392	11	R76249	Human placenta Homo sapien	0.00e+00
4	258	24.5	464	23	C17209	Human placenta cDNA 5'	0.00e+00
5	257	24.5	467	11	R71429	Human placenta Homo sapien	0.00e+00
6	257	24.5	423	12	H00861	Homo sapien	0.00e+00
7	256	24.4	433	11	R23843	Homo sapien	0.00e+00
8	256	24.4	452	12	H00781	Homo sapien	0.00e+00
9	254	24.2	478	23	C17142	Human placenta cDNA 5'	0.00e+00
10	254	23.9	458	11	C18403	Human placenta cDNA 5'	0.00e+00
11	251	23.9	438	11	R77385	Human placenta Homo sapien	0.00e+00
12	248	23.6	482	12	H03289	Homo sapien	0.00e+00
13	245	23.4	336	23	HUM530G10B	Human placenta cDNA 5'	0.00e+00
14	236	22.5	519	23	C18044	Human placenta cDNA 5'	0.00e+00
15	234	22.3	519	31	AA779136	zj46h11.s1 Soares feta	0.00e+00
16	232	22.1	423	23	C17966	Human placenta cDNA 5'	0.00e+00
17	229	21.8	471	12	H47149	Homo sapien	0.00e+00
18	227	21.6	403	11	R65664	Homo sapien	0.00e+00
19	227	21.6	430	12	H00795	Homo sapien	0.00e+00
20	226	21.5	386	17	W86567	Homo sapien	0.00e+00
21	226	21.5	439	12	H01069	Homo sapien	0.00e+00
22	221	21.1	513	23	AA441787	Homo sapien	0.00e+00
23	219	20.9	336	11	R79875	Homo sapien	0.00e+00
24	219	20.9	468	11	R23095	Human placenta cDNA 5'	0.00e+00
25	216	20.6	365	23	HUM505C02B	Human placenta cDNA 5'	0.00e+00
26	216	20.6	526	16	H94810	Homo sapien	0.00e+00
27	216	20.6	527	31	AA777267	yh31g05.r1 Homo sapien	0.00e+00
28	215	20.5	294	10	T48916	Homo sapien	0.00e+00
29	214	20.4	348	11	R33236	Homo sapien	0.00e+00
30	213	20.3	429	13	H77743	Homo sapien	0.00e+00
31	212	20.2	478	31	AA778170	zf45c10.s1 Soares feta	0.00e+00
32	212	20.2	420	10	T49525	Homo sapien	0.00e+00
33	205	19.5	291	23	HUM511F08B	Human placenta cDNA 5'	0.00e+00
34	203	19.4	365	11	R23453	Homo sapien	0.00e+00
35	203	19.4	393	11	R33285	Homo sapien	0.00e+00
36	203	19.4	465	29	AA704477	Homo sapien	0.00e+00
37	202	19.3	261	23	HUM525D05B	Human placenta cDNA 5'	0.00e+00
38	201	19.2	438	14	N57230	Homo sapien	0.00e+00
39	197	18.8	465	14	W01919	Homo sapien	0.00e+00
40	196	18.7	479	11	R68866	Homo sapien	0.00e+00
41	195	18.6	347	11	R34458	Homo sapien	0.00e+00
42	194	18.5	512	12	H04324	Homo sapien	0.00e+00
43	194	18.5	450	29	AA677403	Homo sapien	0.00e+00
44	192	18.3	344	11	R27121	Homo sapien	0.00e+00
45	188	17.9	267	13	N40676	Homo sapien	0.00e+00

ALIGNMENTS

RESULT
LOCUS   HUM505B08B   373 bp   mRNA   EST   21-MAY-1996
DEFINITION Human placenta cDNA 5'-end GEN-505B08.
ACCESSION   D58574
NID   g968208
KEYWORDS   EST; EST(expressed sequence tag); Human placenta; similar to
            known(May 29,1995).
SOURCE   Homo sapiens cDNA to mRNA, clone_1lib:clontech human placenta polyA+
            mRNA (#6518).
ORGANISM   Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
            Homo.
REFERENCE   1 (bases 1 to 373)
AUTHORS   Fujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Nagata,M.,
            Okuno,S., Ozaki,R., Shimizu,F., Shinada,Y., Shinomiya,H.,
            Takaichi,A., Takeda,S., Watanabe,T., Takahashi,E., Hirai,Y.,
            Maekawa,H., Shin,S. and Nakamura,Y.
TITLE   Unpublished (004)
JOURNAL   Unpublished (1995)
REFERENCE   2 (bases 1 to 373)
AUTHORS   Fujiwara,T.
TITLE   Direct Submission
JOURNAL   Submitted (30-MAY-1995) to the DDBJ/EMBL/GenBank databases. Tsutomu
            Fujiwara, Otsuka GEN Research Institute,Otsuka Pharmaceutical
            Co.,Ltd; 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01,
            Japan (Tel:0886-65-2888, Fax:0886-37-1035)
COMMENT   Submitted (30-May-1995) to DDBJ by:
            Tsutomu Fujiwara
            Otsuka GEN Research Institute
            Otsuka Pharmaceutical Co.,Ltd
            463-10 kagasuno Kawauchi-cho
            Tokushima, Tokushima
            771-01
            Japan
            Phone: 0886-65-2888

FEATURES   Fax : 0886-37-1035.
  source   Location/Qualifiers
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BASE COUNT   94 a   88 c   84 g   107 t
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Query Match   24.6%; Score 258; DB 23; Length 373;
Best Local Similarity 99.2%; Pred. No. 0.00e+00;
Matches 260; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

Qy   47 TTGCCCAGAAATGCACGCTACAGAGAAAACCCAATTCTTCTTCCCAGCCGCGGGTGCCCAATACT 106
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Qy   787 TTGCCCAGAAATGCACGCTACAGGAAAAACCCAATTCTTCTTCCCAGCCGCGGGTGCCCAAGAAGAC 846
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Db   787 TCAGTGCCATGGGCCTGCTTCTTCCTCCAGAGCATATCCCACTCAAGGTCCAAGAAGAC 846

Db   107 TCAGTGCCATGGGCCTGCTTCTTCCTCCAGAGCATATCCCACTCAAGGTCCAAGAAGAC 166
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   847 TCAGTGCCATGGGCCTGCTTCTTCCTCCAGAGCATATCCCACTCAAGGTCCAAGAAGAC 906

Db   167 GATGTGTTGGGTCCAAAAAGAAACGTCACCTCAGAGTCTCCACTTGCTGTGTGAGCTAAAATCATATAA 226
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Qy   907 GATGTGTTGGGTCCAAAAAGAAACGTCACCTCAGAGTCTCCACTTGCTGTGTGAGCTAAAATCATATAA 966

Db   227 CAGGGTCACAGTAATGGGGGGTTTCAAAGTGGAGAACCACACGGGCCGTGCCACTGCAGTAC 286
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Qy   967 CAGGGTCACAGTCATGGGGGGTTTCAAAGTGGAGAACCACACGGGGGTGCCACTGCAGTAC 1026

Db   287 TTGTTATTATTCACAAATCTTAA 308
           |||||||||||||||||||||||
Qy   1027 TTGTTATTATCACAAATCTTAA 1048

RESULT 2
LOCUS   C18240   379 bp   mRNA   EST   09-SEP-1996
DEFINITION   Human placenta cDNA 5'-end GEN-559D08.
ACCESSION   C18240
NID   g1579842
KEYWORDS   EST; EST(expressed sequence tag); Human placenta.
SOURCE   Homo sapiens placenta cDNA to mRNA, clone:559D08.
  ORGANISM Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
            Homo.
REFERENCE   1 (sites)
  AUTHORS   Fujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y.,
            Kyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y.,
            Shinomiya,H., Suzuki,M., Takichi,A., Takeda,S., Watanabe,T.,
            Maekawa,H., Nakamura,Y. and Takahashi,E.
  JOURNAL   Otsuka cDNA project
            Unpublished (1996)
REFERENCE   2 (bases 1 to 379)
  AUTHORS   Fujiwara,T.
  TITLE   Direct Submission
  JOURNAL   Submitted (24-JUN-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu
            Fujiwara, Otsuka GEN Research Institute, Otsuka Pharmaceutical
            Co.,Ltd; 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01,
            Japan (Tel:+81-886-65-2888, Fax:+81-886-37-1035)
FEATURES   Location/Qualifiers
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                  /clone="559D08"
                  /tissue_type="placenta"
BASE COUNT   94 a   95 c   85 g   104 t   1 others
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Query Match   24.6%; Score 258; DB 23; Length 379;
Best Local Similarity 98.9%; Pred. No. 0.00e+00;
Matches 259; Conservative   1; Mismatches   2; Indels   0; Gaps   0;

Db   67 TTGCCCAGAAATGCACGCTACAGAGAAAACCCAATTCTTCTTCCCAGCCGCGGGTGCCCAATACT 126
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Qy   787 TTGCCCAGAAATGCACGCTACAGGAAAAACCCAATTCTTCTTCCCAGCCGCGGGTGCCCAAGAAGAC 846

Db   127 TCAGTGCATGGGCCTGCTTCTTCCTCCAGAGCATATCCCACTCAAGGTCCAAGAAGAC 186
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   847 TCAGTGCCATGGGCCTGCTTCTTCCTCCAGAGCATATCCCACTCAAGGTCCAAGAAGAC 906

Db   187 GATGTGTTGGGTCCAAAAAGAAACGTCACCTCAGAGTCTCCACTTGCTGTGTGAGCTAAAATCATATAA 246
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   907 GATGTGTTGGGTCCAAAAAGAAACGTCACCTCAGAGTCTCCACTTGCTGTGTGAGCTAAAATCATATAA 966

Db   247 CAGGGTCACAGTAATGGGGGGTTTCAAAGTGGAGAACCACACGGGCCGTGCCACTGCAGTAC 306
           ||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||
Qy   967 CAGGGTCACAGTCATGGGGGGTTTCAAAGTGGAGAACCACACGGGGGTGCCACTGCAGTAC 1026

Db   307 TTGTTATTATTCACAAATCTTAA 328
           |||||||||||||||||||||||
Qy   1027 TTGTTATTATCACAAATCTTAA 1048

RESULT 3
LOCUS   R76249   392 bp   mRNA   EST   06-JUN-1995
DEFINITION   yl72b05.r1 Homo sapiens cDNA clone 144753 3' similar to gb:V00518
             GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (HUMAN);.
ACCESSION   R76249
NID   g850931
KEYWORDS   EST.
SOURCE   human clone=144753 library=Soares placenta Nb2HP vector=pT73D
             (Pharmacia) with a modified polylinker host=DH10B (ampicillin
             resistant) primer=-21m13 Rsite1-Not I Rsite2-Eco RI Female
             placenta obtained at birth (full term). 1st strand cDNA was primed
             with a Not I - oligo(dT) primer (5'
             AACTGGAAGAATTCGGCGCCGCAGATTTTTTTTTTTTTTTT 3', double-stranded
             cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
             I and cloned into the Not I and Eco RI sites of the modified pT73
             vector. Library went through one round of normalization. Library
             constructed by Bento Soares and M.Fatima Bonaldo.
  ORGANISM Homo sapiens
            Eukaryotae; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 392)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE   The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT   Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 328
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES   Location/Qualifiers
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                  /clone="144753"
BASE COUNT   100 a   90 c   89 g   112 t   1 others
ORIGIN

Query Match   24.6%; Score 258; DB 11; Length 392;
Best Local Similarity 99.2%; Pred. No. 0.00e+00;

Matches   260;   Conservative   0;   Mismatches   2;   Indels   0;   Gaps   0;

Db   35 TTGCCCAGAATGCACGCTACAGGAGAAAACCCATTCTTCTTCCCCAGCCGGGGGTGCCCAATACT 94
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   787 TTGCCCAGAATGCACGCTACAGGAGAAAACCCATTCTTCTTCCCCAGCCGGGGGTGCCCAATACT 846

Db   95 TCAGTGCATGGGCTGCGCTGCTTCTCTCTAGAGCATATCCCACTCCACTCAAGGTCCAAGAAGAC 154
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   847 TCAGTGCATGGGCTGCGCTGCTTCTCTCTAGAGCATATCCCACTCCACTCAAGGTCCAAGAAGAC 906

Db   155 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTGTAGCTAAATCATATAA 214
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   847 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTGTAGCTAAATCATATAA 906

Qy   1027 TTGTTATTATCACAAATCTTAA 1048

Db   275 TTGTTATTATCACAAATCTTAA 296
           ||||||||||||||||||||||

RESULT   4

LOCUS   C17209   464 bp   mRNA   EST   04-SEP-1996
DEFINITION   Human placenta cDNA 5'-end GEN-541F08.
ACCESSION   C17209
NID   g1571916
KEYWORDS   EST; EST(expressed sequence tag); Human placenta.
SOURCE   Homo sapiens placenta cDNA to mRNA, clone:541F08.
ORGANISM   Homo sapiens
              Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
              Vertebrata; Eutheria; Primates; Catarrhini; Hominidae;
              Homo.
REFERENCE   1 (sites)
AUTHORS   Fujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y.,
              Kyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y.,
              Shinomiya,H., Suzuki,M., Takaichi,A., Takeda,S., Watanabe,T.,
              Maekawa,H., Nakamura,Y. and Takahashi,E.
TITLE   Otsuka cDNA project
JOURNAL   Unpublished (1996)
REFERENCE   2 (bases 1 to 464)
AUTHORS   Fujiwara,T.
TITLE   Direct Submission
JOURNAL   Submitted (13-MAY-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu
              Fujiwara, Otsuka GEN Research Institute, Otsuka Pharmaceutical
              Co.,Ltd; 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01,
              Japan (Tel:+81-886-65-2888, Fax:+81-886-37-1035)
FEATURES   Location/Qualifiers
    source   1..464
              /organism="Homo sapiens"
              /db_xref="taxon:9606"
              /clone="541F08"
              /tissue_type="placenta"
BASE COUNT   114 a   117 c   95 g   138 t
ORIGIN

Query Match   24.6%;   Score 258;   DB 23;   Length 464;
Best Local Similarity   99.2%;   Pred. No. 0.00e+00;
Matches 260; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db   39 TTGCCCAGAATGCACGCTACAGGAGAAAACCCATTCTTCTTCCCCAGCCGGGGGTGCCCAATACT 98
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   787 TTGCCCAGAATGCACGCTACAGGAGAAAACCCATTCTTCTTCCCCAGCCGGGGGTGCCCAATACT 846

Db   99 TCAGTGCATGGGCTGCGCTGCTTCTCTCTAGAGCATATCCCACTCCACTCAAGGTCCAAGAAGAC 158
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   847 TCAGTGCATGGGCTGCGCTGCTTCTCTCTAGAGCATATCCCACTCCACTCAAGGTCCAAGAAGAC 906

Db   159 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGTCTGTGTGTAGCTAAATCATATAA 218
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   907 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTGTAGCTAAATCATATAA 966

Db   219 CAGGGTCACAGTCATGGGGGGTTTCAAAGTGGGAGAACCACACGGGGGTGCCACTGCAGTAC 278
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   967 CAGGGTCACAGTCATGGGGGGTTTCAAAGTGGGAGAACCACACGGGGGTGCCACTGCAGTAC 1026

Db   279 TTGTTATTATCACAAATCTTAA 300
           ||||||||||||||||||||||
Qy   1027 TTGTTATTATCACAAATCTTAA 1048

RESULT   5

LOCUS   R71429   467 bp   mRNA   EST   01-JUN-1995
DEFINITION   yl51d03.r1 Homo sapiens cDNA clone 142757 5' similar to gb:V00518
              GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (HUMAN);.
ACCESSION   R71429
NID   g849946
KEYWORDS   EST.
SOURCE   human clone-142757 library-Soares placenta Nb2HP vector-pT73D
              (Pharmacia) with a modified polylinker host-DH10B (ampicillin
              resistant) primer-M13RP1 Rsite1-Not I Rsite2-Eco RI Female placenta
              obtained at birth (full term). 1st strand cDNA was primed with a
              Not I - oligo(dT) primer [5'
              AACTGGAAGAATTCGCGGCCGCAGGAATTTTTTTTTTTTTTTTT 3'], double-stranded
              cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
              I and cloned into the Not I and Eco RI sites of the modified pT73
              vector. Library went through one round of normalization. Library
              constructed by Bento Soares and M.Fatima Bonaldo.
ORGANISM   Homo sapiens
              Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
              Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
              Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
              Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 467)
AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
              Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
              Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
              Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
              Wilson,R.
TITLE   The WashU-Merck EST Project
JOURNAL   Unpublished (1995)
COMMENT   Contact: Wilson RK
              WashU-Merck EST Project
              Washington University School of Medicine
              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
              Tel: 314 286 1800
              Fax: 314 286 1810
              Email: est@watson.wustl.edu
              High quality sequence stops: 386
              Source: IMAGE Consortium, LLNL
              This clone is available royalty-free through LLNL ; contact the
              IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES   Location/Qualifiers
    source   1..467
              /organism="Homo sapiens"
              /clone="142757"
BASE COUNT   113 a   114 c   98 g   139 t   3 others
ORIGIN

Query Match   24.6%;   Score 258;   DB 11;   Length 467;
Best Local Similarity   99.2%;   Pred. No. 0.00e+00;
Matches 260; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db   50 TTGCCCAGAATGCACGCTACAGGAGAAAACCCATTCTTCTTCCCCAGCCGGGGGTGCCCAATACT 109
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   787 TTGCCCAGAATGCACGCTACAGGAGAAAACCCATTCTTCTTCCCCAGCCGGGGGTGCCCAATACT 846

Db   110 TCAGTGCATGGGCTGCGCTGCTTCTCTCTAGAGCATATCCCACTCCACTCAAGGTCCAAGAAGAC 169
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   847 TCAGTGCATGGGCTGCGCTGCTTCTCTCTAGAGCATATCCCACTCCACTCAAGGTCCAAGAAGAC 906

Db   170 GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTGTAGCTAAATCATATAA 229

Qy   907 GATGTTGGTCGTCCAAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTGTAGCTAAATCATATAA
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   230 CAGGGTCACAGTAATGGGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCCAGTAC 289
           ||||||||||| ||||||||| |||||||||| |||||||||||| |||||||||||||||
Qy   967 CAGGGTCACAGTCATGGGGGGGTTTCAAAGTGGGAGAACCACACGGGGTGCCACTGCCAGTAC 1026
Db   290 TTGTTATTTATCACAAAATCTTAA 311
           ||||||||||||||||||||||||
Qy   1027 TTGTTATTTATCACAAAATCTTAA 1048

RESULT 6

LOCUS   H00861   423 bp   mRNA   EST   19-JUN-1995
DEFINITION   yj31h01.r1 Homo sapiens cDNA clone 150385 5' similar to gb:V00518
             GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (HUMAN);.
ACCESSION   H00861
NID   g863794
KEYWORDS   EST.
SOURCE   human clone-150385 library-Soares placenta Nb2HP vector-pT713D
             (Pharmacia) with a modified polylinker host-DH10B (ampicillin
             resistant) primer-M13RP1 Rsite1-Not I Rsite2-Eco RI Female placenta
             obtained at birth (full term). 1st strand cDNA was primed with a
             Not I - oligo(dT) primer [5'
             AACTGGAAGAATTCGGCGGCCGCGAGGAATTTTTTTTTTTTTTTTT 3'], double-stranded
             cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
             I and cloned into the Not I and Eco RI sites of the modified pT713
             vector. Library went through one round of normalization. Library
             constructed by Bento Soares and M.Fatima Bonaldo.
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Bilateria; Coelomata;
             Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
             Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
             Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 423)
AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
             Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
             Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
             Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
             Wilson,R.
TITLE   The WashU-Merck EST Project
JOURNAL   Unpublished (1995)
COMMENT   Contact: Wilson RK
             WashU-Merck EST Project
             Washington University School of Medicine
             4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
             Tel: 314 286 1800
             Fax: 314 286 1810
             Email: estewatson.wustl.edu
             High quality sequence stops: 344
             Source: IMAGE Consortium, LLNL
             This clone is available royalty-free through LLNL; contact the
             IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES   Location/Qualifiers
             source   1..423
                      /organism="Homo sapiens"
                      /clone="150385"
BASE COUNT   109 a   95 c   119 g   95 t   5 others
ORIGIN

Query Match   24.5%;   Score 257;   DB 12;   Length 423;
Best Local Similarity   98.9%;
Matches 259;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

Qy   787 TTGCCCAGAATGCACGCTACAGGANACACCATTCTTCTCCCAGCCCCAATACT 846
           ||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   18 TTGCCCAGAATGCACGCTACAGGANACACCATTCTTCTCCCAGCCCCAATACT 77
Qy   847 TCAGTGCAIGGGCTGCTGCTTCTTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 906
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   78 TCAGTGCAIGGGCTGCTGCTTCTTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 137

Db   138 GATGTTGGTCGTCCAAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTGTAGCTAAATCATATAA 197
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   907 GATGTTGGTCGTCCAAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTGTAGCTAAATCATATAA 966
Db   198 CAGGGTCACAGTAATGGGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCCAGTAC 257
           ||||||||||| ||||||||| |||||||||| ||||||||||||| |||||||||||||
Qy   967 CAGGGTCACAGTCATGGGGGGGTTTCAAAGTGGGAGAACCACACGGGGTGCCACTGCCAGTAC 1026
Db   258 TTGTTATTTATCACAAAATCTTAA 279
           ||||||||||||||||||||||||
Qy   1027 TTGTTATTTATCACAAAATCTTAA 1048

RESULT 7

LOCUS   R23843   433 bp   mRNA   EST   20-APR-1995
DEFINITION   yh48c04.r1 Homo sapiens cDNA clone 132966 5' similar to gb:V00518
             GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (HUMAN);.
ACCESSION   R23843
NID   g778731
KEYWORDS   EST.
SOURCE   human clone-132966 library-Soares placenta Nb2HP vector-pT713D
             (Pharmacia) with a modified polylinker host-DH10B (ampicillin
             resistant) primer-M13RP1 Rsite1-Not I Rsite2-Eco RI Female placenta
             obtained at birth (full term). 1st strand cDNA was primed with a
             Not I - oligo(dT) primer [5'
             AACTGGAAGAATTCGGCGGCCGCGAGGAATTTTTTTTTTTTTTTTT 3'], double-stranded
             cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
             I and cloned into the Not I and Eco RI sites of the modified pT713
             vector. Library went through one round of normalization. Library
             constructed by Bento Soares and M.Fatima Bonaldo.
ORGANISM   Homo sapiens
             Eukaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
             Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 433)
AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
             Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
             Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
             Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
             Wilson,R.
TITLE   The WashU-Merck EST Project
JOURNAL   Unpublished (1995)
COMMENT   Contact: Wilson RK
             WashU-Merck EST Project
             Washington University School of Medicine
             4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
             Tel: 314 286 1800
             Fax: 314 286 1810
             Email: estewatson.wustl.edu
             High quality sequence stops: 334
             Source: IMAGE Consortium, LLNL
             This clone is available royalty-free through LLNL; contact the
             IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES   Location/Qualifiers
             source   1..433
                      /organism="Homo sapiens"
                      /clone="132966"
BASE COUNT   111 a   104 c   90 g   127 t   1 others
ORIGIN

Query Match   24.4%;   Score 256;   DB 11;   Length 433;
Best Local Similarity   98.1%;
Matches 261;   Conservative 0;   Mismatches 5;   Indels 0;   Gaps 0;

Qy   783 CAGGTTGCCCAGAATGCACGCTACAGGAAAAACCATTCTTCTCTCCCAGCCCCAA 842
           ||||| |||| ||||||||||||||||||||||||||||||||||||||||||||
Db   2 CAGGATTGCGAGAATGCACGCTACAGGAAAAACCATTCTTCTCTCCCAGCCCCAA 61
Qy   843 TACTTCAGTGCATGGGGCTGCTGCTTCTTCTAGAGCATATCCCACTCCACTAAGGTCCAAGA 902
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   62 TACTTCAGTGCATGGGGCTGCTGCTTCTTCTAGAGCATATCCCACTCCACTAAGGTCCAAGA 121

RESULT 8

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Db  122  AGACGATGTTGGTCCAAAAAGAAGGACGTCACCTCAGAGTCCACTTGCGTCGTCTGTAGCTAAATCAT  181
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Qy  903  AGACGATGTTGGTCCAAAAAGAAGGACGTCACCTCAGAGTCCACTTGCGTCGTCTGTAGCTAAATCAT  962

Db  182  ATAACAGGGTCACAGTAATGGCGGGGGGTTTCAAAGTGGAGAACCACACGGGGGTGCCACTGCA  241
         ||||||||||||||| ||| |||||||||||||||||||||||||||||||||||||||||||
Qy  963  ATAACAGGGTCACAGTCATGGGGGGGTTTCAAAGTGGAGAACCACACGGGGGTGCCACTGCA  1022

Db  242  GTACTTGTTATTATCACAAATCTTAA  267
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Qy  1023 GTACTTGTTATTATCACAAATCTTAA  1048
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LOCUS   H00781   452 bp   mRNA   EST   19-JUN-1995
DEFINITION yj30d01.r1 Homo sapiens cDNA clone 150241 5' similar to gb:V00518
            GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (HUMAN);.
ACCESSION   H00781
NID   g863714
KEYWORDS   EST.
SOURCE   human clone=150241 library=Soares placenta Nb2HP vector=pT7T3D
            (Pharmacia) with a modified polylinker host=DH10B (ampicillin
            resistant) primer=M13RP1 Rsite1=Not I Rsite2=Eco RI Female placenta
            obtained at birth (full term). 1st strand cDNA was primed with a
            Not I - oligo(dT) primer [5'
            AACTGGAAGAATTCGGCGGCCGCCGGGATAATTTTTTTTTTTTTTTTT 3'], double-stranded
            cDNA was ligated to Eco RI and Not I and Eco RI adaptors
            (Pharmacia), digested with Not I and cloned into the Not I and Eco RI
            sites of the modified pT7T3 vector. Library went through one round of
            normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.
  ORGANISM Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 452)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE   The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT   Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: estewatson.wustl.edu
            High quality sequence stops: 322
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES   Location/Qualifiers
     source   1. .452
                     /organism="Homo sapiens"
                     /clone="150241"
BASE COUNT   107 a   104 c   103 g   133 t   5 others
ORIGIN

Query Match   24.48%;   Score 256;   DB 12;   Length 452;
Best Local Similarity   99.2%;   Pred. No. 0.00e+00;
Matches 258;   Conservative   0;   Mismatches 2;   Indels 0;   Gaps 0;

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Db   44  TTGCCCAGAATGCACGCTACAGGAGAAAACCCATTCTTCTTCCCAGCGCCGGGGTGCCCAATACT  103
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Qy  787  TTGCCCAGAATGCACGCTACAGGAGAAAACCCATTCTTCTTCCCAGCGCCGGGGTGCCCAATACT  846

Db  104  TCAGTGCATGGGCGTCGCTGCTTCTCTGAGACCATATCCCACTCCACTAAGGTCCAAGAGAC  163
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RESULT 9

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Qy  847  TCAGTGCATGGGCGTCGCTGCTTCTCTGAGACCATATCCCACTCCACTAAGGTCCAAGAAGAC  906
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LOCUS   C17142   478 bp   mRNA   EST   04-SEP-1996
DEFINITION Human placenta cDNA 5'-end GEN-539G04.
ACCESSION   C17142
NID   g1571849
KEYWORDS   EST; EST(expressed sequence tag); Human placenta.
SOURCE   Homo sapiens placenta cDNA to mRNA, clone:539G04.
  ORGANISM Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
            Homo.
REFERENCE   1 (sites)
  AUTHORS   Fujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y.,
            Kyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y.,
            Shinomiya,H., Suzuki,M., Takaichi,A., Takeda,S., Watanabe,T.,
            Maekawa,H., Nakamura,Y. and Takahashi,E.
  TITLE   Otsuka cDNA project
  JOURNAL   Unpublished (1996)
REFERENCE   2 (bases 1 to 478)
  AUTHORS   Fujiwara,T.
  TITLE   Direct Submission
  JOURNAL   Submitted (13-MAY-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu
            Fujiwara, Otsuka GEN Research Institute,Otsuka Pharmaceutical
            Co.,Ltd; 463-10 Kagasuno Kawauchi-cho, Tokushima 771-01,
            Japan (Tel:+81-886-65-2888, Fax:81-886-37-1035)
FEATURES   Location/Qualifiers
     source   1. .478
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="539G04"
                     /tissue_type="placenta"
BASE COUNT   125 a   113 c   96 g   144 t
ORIGIN

Query Match   24.28%;   Score 254;   DB 23;   Length 478;
Best Local Similarity   99.2%;   Pred. No. 0.00e+00;
Matches 256;   Conservative   0;   Mismatches 2;   Indels 0;   Gaps 0;

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Qy    1  CCAGAATGCACGCTACAGGAGAAAACCCATTCTTCTTCCCAGCGCCGGGGTGCCCCAATACTTCAG  60
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Db  791  CCAGAATGCACGCTACAGGAGAAAACCCATTCTTCTTCCCAGCGCCGGGGTGCCCCAATACTTCAG  850

Qy   61  TGCATGGGCGTCGCTGCTTCTCTGAGACCATATCCCACTCCAGCGCCGGGGTGCCCAAGAAGACGATG  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  851  TGCATGGGCGTCGCTGCTTCTCTGAGACCATATCCCACTCCAGCGCCGGGGTGCCCAAGAAGACGATG  910

Qy  121  TTGGGTCCAAAAGAAGGACGTCACCTCAGAGTCCACTTGTGTCGTGAGCTAAATCATTATAACAGG  180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  911  TTGGGTCCAAAAGAAGGACGTCACCTCAGAGTCCACTTGTGTCGTGAGCTAAATCATTATAACAGG  970

Qy  181  GTCACAGTATGGGGGGGGTTTCAAAGTGGAGAACCACACGGGGGCGTGCCACTGCAGTACTTGT  240
         |||||||| ||||||| ||||||||||||||||||||||||||| ||||||||||||||||||
Db  971  GTCACAGTCATGGGGGGGTTTCAAAGTGGAGAACCACACGGGGGTGCCACTGCAGTACTTGT  1030

Qy  241  TATTATCACAAATCTTAA  258
         ||||||||||||||||||
Db  241  TATTATCACAAATCTTAA  258
```

Qy   1031 TATTATCACAAATCTTAA 1048

RESULT 10

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LOCUS       C18403      330 bp    mRNA           EST        09-SEP-1996
DEFINITION  Human placenta cDNA 5'-end GEN-561H02.
ACCESSION   C18403
NID         g1580005
KEYWORDS    EST; EST(expressed sequence tag); Human placenta.
SOURCE      Homo sapiens placenta cDNA to mRNA, clone:561H02.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
            Homo.
REFERENCE   1 (sites)
  AUTHORS   Fujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y.,
            Kyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y.,
            Shinomiya,H., Suzuki,H., Takaichi,A., Takeda,S., Watanabe,T.,
            Maekawa,H., Nakamura,Y. and Takahashi,E.
  TITLE     Otsuka cDNA project
  JOURNAL   Unpublished (1996)
REFERENCE   2 (bases 1 to 330)
  AUTHORS   Fujiwara,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUN-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu
            Fujiwara, Otsuka GEN Research Institute,Otsuka Pharmaceutical
            Co.,Ltd; 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01,
            Japan (Tel:+81-886-65-2888, Fax:+81-886-37-1035)
FEATURES             Location/Qualifiers
     source          1..330
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="561H02"
                     /tissue_type="placenta"
BASE COUNT     82 a     87 c     73 g     88 t
ORIGIN
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Query Match   23.9%; Score 251; DB 23; Length 330;
Best Local Similarity   98.9%; Pred. No. 0.00e+00;
Matches   259; Conservative   0; Mismatches 2; Indels   1; Gaps   1;

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Qy   787 TTGCCCAGAATGCACGCTACAGGAAAACCCAATTCTTCTCCCAGCCCGGGGGTGCCCCAATACT 846
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Db    67 TTGCCCAGAATGCACGCTACAGGAAAAACCATTCTTCTCCCAGCCCGGGGGTGCCCCAATACT 126

Qy   847 TCAGTGCAATGGGCGTGCTGCTTCTCTTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAGAC 906
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Db   127 TCAGTGCAATGGGCGTGCTGCTTCTCTTCTAGAGACATATCCCACTCCACTAAGGTCCAAGAGAC 186

Qy   907 GATGTTGGTCCAAAAAGAACGTCACCTCACTTGCTGTGTGAGCTAAATCATATAA 966
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   187 GATGTTGGTCCAAAAAGAACGTCACCTCACTTGCTGTGTGAGCTAAATCATATAA 246

Qy   967 CAGGGTCACAGTAATGGGGGGGTTTCAAAGTGGAGA-CCACACGGGGTGCCCACTGCAGTAC 305
         |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db   247 CAGGGTCACAGTAATGGGGGGGTTTCAAAGTGGAGAACCACACGGGGTGCCCACTGCAGTAC 305

Qy  1027 TTGTTATTATCACAAATCTTAA 1048
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Db   306 TTGTTATTATCACAAATCTTAA 327
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RESULT 11

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LOCUS       R77385      458 bp    mRNA           EST        06-JUN-1995
DEFINITION  yf75d11.r1 Homo sapiens cDNA clone 145077 5' similar to gb:V00518
            GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (HUMAN);.
ACCESSION   R77385
NID         g852017
KEYWORDS    EST.
SOURCE      human clone-145077 library-Soares placenta Nb2HP vector-pT7T3D
            (Pharmacia) with a modified polylinker host=DH10B (ampicillin
            resistant) primer=M13RP1 Rsite1=Not I Rsite2=Eco RI Female placenta
            obtained at birth (full term). 1st strand cDNA was primed with a
            Not I - oligo(dT) primer (5'...
            AACTGGAAGAATTCGGCCGCCGAGGAATTTTTTTTTTTTTTTTTTT 3'), double-stranded
            cDNA was ligated to the Not I and Eco RI adaptors (Pharmacia), digested with Not
            I and cloned into the Not I and Eco RI sites of the modified pT7T3
            vector. Library went through one round of normalization. Library
            constructed by Bento Soares and M.Fatima Bonaldo.
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 458)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: estwatson.wustl.edu
            High quality sequence stops: 393
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES             Location/Qualifiers
     source          1..458
                     /organism="Homo sapiens"
                     /clone="145077"
BASE COUNT    119 a    109 c     97 g    133 t
ORIGIN
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Query Match   23.8%; Score 250; DB 11; Length 458;
Best Local Similarity   99.2%; Pred. No. 0.00e+00;
Matches   252; Conservative   0; Mismatches 2; Indels   0; Gaps   0;

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Qy   795 AATGCACGCTACAGGAAAACCCAATTCTTCTCCCAGCCCGGGGGTGCCCCAATACTTCAGTGCA 854
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Db    16 AATGCACGCTACAGGAAAAACCATTCTTCTCCCAGCCCGGGGGTGCCCCAATACTTCAGTGCA 75

Qy   855 TGGGCTGCTGCTTCTCTTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAGACGATGTTGG 914
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    76 TGGGCTGCTGCTTCTCTTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAGACGATGTTGG 135

Qy   915 TCCAAAAAGAACGTCACCTCACTTGCTGTGTGAGCTAAATCATATAACAGGGTCA 974
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   136 TCCAAAAAGAACGTCACCTCACTTGCTGTGTGAGCTAAATCATATAACAGGGTCA 195

Qy   975 CAGTCATGGGGGGGTTTCAAAGTGGAGAACCACACGGGGTGCCCACTGCAGTACTGTGTTATT 1034
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Db   196 CAGTCATGGGGGGGTTTCAAAGTGGAGAACCACACGGGGTGCCCACTGCAGTACTGTGTTATT 255

Qy  1035 ATCACAAATCTTAA 1048
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Db   256 ATCACAAATCTTAA 269
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RESULT 12

```
LOCUS       H03289      482 bp    mRNA           EST        20-JUN-1995
DEFINITION  yj44h10.r1 Homo sapiens cDNA clone 151651 5' similar to gb:V00518
            GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (HUMAN);.
ACCESSION   H03289
NID         g866222
KEYWORDS    EST.
```

Left column — RESULT 13

SOURCE   human clone~151651 library~Soares placenta N2bHP vector~pT73D
            (Pharmacia) with a modified polylinker host~M13RP1 Rsite2~Eco RI female placenta
            resistant) primer~M13RP1 Rsite1~Not I Rsite2~Eco RI female placenta
            obtained at birth (full term). 1st strand cDNA was primed with a
            Not I - oligo(dT) primer (5'-
            AACTGGAAGAATTCGGCGCGCCAGGAANTTTTTTTTTTTTTTTTTT 3'), double-stranded
            cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
            I and cloned into the Not I and Eco RI sites of the modified pT713
            vector. Library went through one round of normalization. Library
            constructed by Bento Soares and M.Fatima Bonaldo.
ORGANISM   Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 482)
AUTHORS   Hillier,L., Clark,N., Dubnick,M., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
TITLE   The WashU-Merck EST Project
JOURNAL   Unpublished (1995)
COMMENT   Contact: Wilson RK
            Washu-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High qality sequence stops: 301
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES   Location/Qualifiers
     source 1..482
            /organism="Homo sapiens"
            /clone="151651"
BASE COUNT   111 a   106 c   118 g   142 t   5 others
ORIGIN

Query Match   23.6%; Score 248; DB 12; Length 482;
  Best Local Similarity   98.9%; Pred. No. 0.00e+00;
  Matches 261; Conservative   0; Mismatches   1; Indels   2; Gaps   2;

Db   51 TTGCCCAGAANTGCACGCTACAGGAAAAACCCATTCTTCTCCCAGCCGGGGGTGCCCAATACT 110
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Qy   787 TTGCCCAGAATGCACGCTACAGGAAAAACCCATTCTTCTCCCAGCCGGGGGTGCCCAATACT 846

Db   111 TCAGTGCAATGGGCGTTGCTGCTTCTTCTAGAGACCATATCCCACTCCACTAAGGTCCAAGAAGAC 170
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Qy   847 TCAGTGCAATGGGCGTTGCTGCTTCTTCTAGAGACCATATCCCACTCCACTAAGGTCCAAGAAGAC 906

Db   171 GATGTTGGTCCAAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 230
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   907 GATGTTGGTCCAAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 966

Db   231 CAGGGTCACAGTAATGGGGGGTTTCAAAGTGGGAGAACCACACGGGCGTGCCACTGCAGT 290
            ||||||||||| |||||||||||||||||||| ||||||||||||| |||||||||||||
Qy   967 CAGGGTCACAGTCATGGGGGGTTTCAAAGTGG-AGAACCACACGGG-GTGCCACTGCAGT 1024

Db   291 ACTTGTTATTATTACACAAATCTTAA 314
            ||||||||||||||||||||||||||
Qy   1025 ACTTGTTATTATTACACAAATCTTAA 1048

RESULT 13
LOCUS   HUM530G10B   336 bp   mRNA   EST   13-DEC-1995
DEFINITION Human placenta cDNA 5'-end GEN-530G10.
ACCESSION   D79076
NID   g1180949

Right column — RESULT 14

KEYWORDS   EST; EST(expressed sequence tag); Human placenta.
SOURCE   Homo sapiens placenta cDNA to mRNA, clone_lib:human placenta
            polyA+.
ORGANISM   Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
            Homo.
REFERENCE   1 (bases 1 to 336)
AUTHORS   Fujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Nagata,M.,
            Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiya,H.,
            Takaichi,A., Takeda,S., Watanabe,T., Takahashi,E., Hirai,Y.,
            Maekawa,H., Shin,S. and Nakamura,Y.
TITLE   Direct Submission
JOURNAL   Submitted (07-NOV-1995) to the DDBJ/EMBL/GenBank databases. Tsutomu
            Fujiwara, Otsuka GEN Research Institute,Otsuka Pharmaceutical
            Co.,Ltd, 463-10 Kagasuno Kawauchi-cho, Tokushima 771-01,
            Japan
REFERENCE   2 (bases 1 to 336)
AUTHORS   Fujiwara,T.
TITLE   Large-scale sequencing project at Otsuka GEN Research Institute
JOURNAL   Unpublished (1995)
COMMENT   Submitted (7-Nov-1995) to DDBJ by:
            Tsutomu Fujiwara
            Otsuka GEN Research Institute
            Otsuka Pharmaceutical CO.,Ltd
            463-10 Kagasuno Kawauchi-cho
            Tokushima, Tokushima
            771-01
            Japan
            Phone:0886-65-2888
            Fax :0886-37-1035.
FEATURES   Location/Qualifiers
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            /db_xref="taxon:9606"
            /clone_lib="human placenta polyA+"
            /tissue_type="placenta"
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ORIGIN

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  Matches 250; Conservative   0; Mismatches   5; Indels   0; Gaps   0;

Db   47 TTGCCCAGAAATGCACGCTACAGGAAAAACCCATTCTTCTCTCCCAGCCGGGGGTGCCCAATACT 106
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Qy   787 TTGCCCAGAA-TGCACGCTACAGGAAAAACCCATTCTTCTCTCCCAGCCGGGGGTGCCCAATACT 846

Db   107 TCAGTGCAATGGGCGTTGCTGCTTCTTCTAGAGACCATATCCCACTCCACTAAGGTCCAAGAAGAC 166
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Qy   847 TCAGTGCAATGGGCGTTGCTGCTTCTTCTAGAGACCATATCCCACTCCACTAAGGTCCAAGAAGAC 906

Db   167 GATGTTGGTCCAAAAGAAGACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 226
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Qy   907 GATGTTGGTCCAAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAA 966

Db   227 CAGGGTCACAGTAATGGGGGGTTTCATAGTAGTGGGGGGACCCACACGGGCGTGCCACTGCAGTAC 286
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Qy   967 CAGGGTCACAGTCATGGGGGGTTTCAAAGTGGGAG-AACCACACGGG-GTGCCACTGCAGTAC 1026

Db   287 TTGTTATTATCACAA 301
            |||||||||||||||
Qy   1027 TTGTTATTATCACACA 1041

RESULT 14
LOCUS   C18044   519 bp   mRNA   EST   09-SEP-1996
DEFINITION Human placenta cDNA 5'-end GEN-556F06.
ACCESSION   C18044
NID   g1579646
KEYWORDS   EST; EST(expressed sequence tag); Human placenta.
SOURCE   Homo sapiens placenta cDNA to mRNA, clone:556F06.

ORGANISM   Homo sapiens
           Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
           Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
           Homo.
REFERENCE 1 (sites)
AUTHORS   Fujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y.,
           Kyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y.,
           Shinomiya,H., Suzuki,M., Takichi,A., Takeda,S., Watanabe,T.,
           Maekawa,H., Nakamura,Y. and Takahashi,E.
TITLE   Otsuka cDNA project
JOURNAL   Unpublished (1996)
REFERENCE 2 (bases 1 to 519)
AUTHORS   Fujiwara,T.
TITLE   Direct Submission
JOURNAL   Submitted (24-JUN-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu
           Fujiwara, Otsuka GEN Research Institute,Otsuka Pharmaceutical
           Co.,Ltd; 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01,
           Japan (Tel:+81-886-65-2888, Fax:+81-886-37-1035)
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BASE COUNT   103 a   140 c   153 g   119 t   4 others
ORIGIN

Query Match   22.5%;   Score 236; DB 23;   Length 519;
Best Local Similarity   88.9%;   Pred. No. 0.00e+00;
Matches 305; Conservative   0; Mismatches 31; Indels   7; Gaps   6;

Qy   1 ATGGCTGCAGGTAAGCGCCCCCTAAAANNNNNTTGGGCACAACGTGTCCTGAGGGAGAGG   99
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Db   40 ATGGCTACAGGTAAGCGCCCCTAAAATCCCTTGGGCACAATGTGTCCTTCTGAGGGAGAGG   65

Qy   66 CAGCGACCTGTAGATGGGACGGGGGCACTAACCCTCAGGTTTGTGGGGCTTCCAATCTCAC 125
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Db   100 CGGCGCCCTCCAGAATGGGAGGGGGGCACTAACC--TCAGGTTTGTGGGGCTTCTGAATGA 158

Qy   126 TATCCCCATGTAAGCCCAG-TATTTGGCCAATCTCAGAAAAGCTCTCCCCCCTGGAGGGA   184
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Db   159 TATCGGCCATCTAAGGCCAGATATTTGGCCAATCTCTGAATGTTCCTGGTGTCCCTGGAGGGA 218

Qy   185 TGGAGAGAGA---AAAACAAA-CAGCTCCTGGAGCAGGAGAGTGCTGGGCCTTCTTGGCTCTC 241
             ||||||||| ||| ||| |||||||||||||||| |||||||| |||| ||| ||||
Db   219 TGGAGAGAGAAGAAAAAGAAAACAGCTCCTGGAACAGGAGAGTACTGGGCCCTCTTGCTCTG   278

Qy   242 CGGCTCCCTCTGTTGCCCCTCTGGTTTTCTCCCCAGCCGTCCCCGACGGTCCCCTGCTCCCTGGCT 301
             ||||||||||||||| ||||||||||||||| |||||||||||||||||||||||||||||||
Db   279 CGGCTCCCT-TCTTGCCCTCCGGTTTCTCTCCCCAGCCGTCCCCGACGTCCCCTTCTCCTCGGGCT 337

Qy   302 TTTGCCTGCTCTCGCCTCGCCCTGGCTTCA-GAGGCTGGGGTGCCG 344
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Db   338 TTTGCCCTGCTCTCGCCTGCCCCTGGCTTCA-GAGGCTGGGGTGCCG 379

COMMENT   Contact: Wilson RK
           Washington University School of Medicine
           4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
           Tel: 314 286 1800
           Fax: 314 286 1810
           Email: est@watson.wustl.edu
           This clone is available royalty-free through LLNL ; contact the
           IMAGE Consortium (info@image.llnl.gov) for further information.
           High quality sequence stop: 316.
TITLE   Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
JOURNAL   Wash U-NCI human EST Project
           Unpublished (1997)
FEATURES   Location/Qualifiers
     source   1..519
                    /organism="Homo sapiens"
                    /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                    with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                    This is a subtracted version of the original Soares fetal
                    liver spleen 1NFLS S1 library. 1st strand cDNA was primed
                    with a Pac I - Oligo(dT) primer [5'
                    AACTGGAAGAATTAATACGACTCTTTTTTTTTTTTTTTTT 3'],
                    double-stranded cDNA was ligated to Eco RI adaptors
                    (Pharmacia), digested with Pac I and cloned into the Pac I
                    and Eco RI sites of the modified pT7T3 vector. Library
                    went through one round of normalization. Library
                    constructed by Bento Soares and M.Fatima Bonaldo."
                    /db_xref="GDB:1389737"
                    /db_xref="taxon:9606"
                    /clone="453381"
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                    /sex="male"
                    /dev_stage="20 week post conception fetus"
                    /lab_host="DH10B (ampicillin resistant)"
                    Seq primer: -40m13 fwd. ET from Amersham
BASE COUNT   156 a   98 c   127 g   138 t
ORIGIN

Query Match   22.3%;   Score 234; DB 31;   Length 519;
Best Local Similarity   95.9%;   Pred. No. 0.00e+00;
Matches 255; Conservative   0; Mismatches 9; Indels   2; Gaps   2;

Db   253 TTAAGATTTGGATAATAAACAAGTACTGCAGTGGCACGCCGGTGTGGTTCTCCACTTTGAA 312
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Cp   1048 TTAAGATTTGTGATAATAAACAAGTACTGCAGTGGCACCCCGTGTGGTTCTCCACTTTGAA   989

Db   313 ACCCCCATTACTGTGTGACCCTGTTATATNATGATTTAGNTNACACAGCAAGTGGACTCTGAGGT 372
             |||||| |||||||||||||||||||| | ||||||| | | |||||||||||||||||||
Cp   988 ACCCCCATGACTGTGACCCCGTTATATGATTTAGTTACACAGCAAGTGGACTCTGAGGT   929

Db   373 GACGTTCTTTTGGACCAAACATCGTCTTCTTCTTGGACCTTAGTGGAGTGGGGATANGCTCTAGA 432
             ||||||| ||||||||||||||||| | |||||||||||||||||||| |||||| ||||||||
Cp   928 GACGTTCTTTTGGACCAAACATCGTCTTCTTCTTGGACCTTAGTGGAGTGGGGATANGCTCTAGA   869

Db   433 GAAGCAGCAGCCCATGCACTGAAGTAGTGGGGCACCCGGTCCGTAGAAGAATGGGTTTC 492
             || ||||||||||||| |||||||||||||||||||| | || |||||| ||||||||
Cp   868 GAAGCAGCAGCCCATGCCACTGAAGTATTGGGGCACCCGGCTCGGGGAGAAGAATGGGTTTC   809

Db   493 CTG-AGGGTG-ANTTCTGGGGAATCTG 516
             ||| ||||| | |||||||||||||||
Cp   808 CTGTAGGGTGCGCAATTCTGGGCAACCTG 783

LOCUS   AA779136   519 bp   mRNA   EST   05-FEB-1998
DEFINITION z146h11.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA
           clone 453381 3' similar to gb:V00518 GLYCOPROTEIN HORMONES ALPHA
           CHAIN PRECURSOR (HUMAN);.
ACCESSION AA779136
NID   g2838467
KEYWORDS   EST.
SOURCE   human.
  ORGANISM Homo sapiens
           Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
           Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 519)
AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
           Kizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
           Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,

```
*************************************************

                    M P S R C H   (TM)

*************************************************
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          Distribution rights by Oxford Molecular Ltd
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 6 08:50:59 1998; MasPar time 8.51 Seconds
                                        449.440 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-2 from US08804166.pep
Description: (1-256) from US08804166.pep
Perfect Score: 1994
Sequence: 1 SRTSLLLAFGLLCLPWLQEG.........GFKVENHTGCHCSTCYHKS 256

Scoring table: PAM 150
                Gap 11

Searched: 12037 seqs, 14945562 residues

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database: a-geneseq31
                1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
                8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
                14:part14 15:part15 16:part16 17:part17 18:part18
                19:part19 20:part20 21:part21 22:part22 23:part23
                24:part24 25:part25 26:part26

Statistics: Mean 31.442; Variance 119.617; scale 0.263

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                           SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
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3	1321	66.2	319	26	W33358	TBP(20-161)/hCG-beta	6.46e-132
4	1291	64.7	307	26	W33360	TBP(20-190)/hCG-beta	1.46e-128
5	1124	56.4	336	26	R24496	Native 30 kD TNF inhi	1.19e-110
6	1124	56.4	161	4	R24080	Truncated TNF-alpha 5	1.19e-110
7	1124	56.4	199	4	R24000	TNF-alpha 55kD recept	1.19e-110
8	1124	56.4	309	13	R07108	TNF-R-GBPH fusion pro	1.19e-110
9	1124	56.4	371	2	R07449	Tumour Necrosis Facto	1.19e-110
10	1124	56.4	451	13	R07107	TNF-R-GBP 130 fusion	1.19e-110
11	1124	56.4	455	8	R42059	Lambda derived TNF-R.	1.19e-110
12	1124	56.4	455	2	R10986	30XD TNF inhibitor pr	1.19e-110
13	1124	56.4	455	2	R20787	TNF-alpha binding pro	1.19e-110
14	1124	56.4	455	14	R75084	p55 TNF-R.	1.19e-110
15	1124	56.4	455	2	R07451	Human Tumour Necrosis	1.19e-110
16	1124	56.4	547	4	R11082	Human 55kD TNF-bindin	1.19e-110
17	1124	56.4	547	13	R70104	TNF-alpha 55kD recept	6.19e-110
18	1124	56.4	884	13	R70109	TNF-R-GBP 130 fusion	6.19e-110
19	1124	56.4	900	13	R70103	TNF-R-GBP 130 fusion	6.19e-110
20	1124	56.4	1245	13	R70106	TNF-R-Pl, vivax Duffy	6.19e-110
21	1124	56.4	1604	13	R70105	TNF-R-EBA 175 fusion	6.19e-110
22	1118	56.1	433	8	R51032	Mutant p55 tumour nec	2.88e-109
23	1118	56.1	443	8	R51033	Mutant p55 tumour nec	2.88e-109
24	1118	56.1	455	8	R51034	Mutant p55 tumour nec	2.88e-109
25	1118	55.7	455	3	R42197	Type I TNF receptor.	2.24e-108
26	1110	55.7	461	2	R12550	p55 Tumour necrosis f	1.06e-95
27	996	49.9	168	4	R24084	Truncated TNF-alpha 5	1.13e-74
28	800	40.1	158	4	R24081	Truncated TNF-alpha 5	5.13e-74
29	788	39.5	461	2	R07450	Rat Tumour Necrosis F	1.08-72
30	672	33.7	96	1	R15182	hCG/bCG alpha subunit	5.96e-60
31	667	33.5	92	1	P92146	Beta subunit of urina	2.10e-59
32	667	33.5	96	1	R15195	hCG alpha subunit mut	2.10e-59
33	667	33.5	116	26	W31665	Secreted protein huma	2.10e-59
34	667	33.5	116	2	R10095	Engineered human alph	2.10e-59
35	667	33.5	116	19	R99417	Dimeric glycoprotein	2.10e-59
36	667	33.5	222	15	R86268	Partially deglycosyla	2.10e-59
37	667	33.5	222	15	R86256	Single chain gonadotr	2.10e-59
38	667	33.5	226	15	R86255	Single chain gonadotr	2.10e-59
39	667	33.5	226	15	R86250	Single chain gonadotr	2.10e-59
40	667	33.5	234	15	R86254	Single chain gonadotr	2.10e-59
41	667	33.5	234	15	R86249	Single chain gonadotr	2.10e-59
42	667	33.5	234	15	R86248	Single chain gonadotr	2.10e-59
43	667	33.5	234	15	R86253	Single chain gonadotr	2.10e-59
44	667	33.5	237	15	R86251	Single chain gonadotr	2.10e-59
45	667	33.5	265	15	R86247	Single chain gonadotr	2.10e-59

                           ALIGNMENTS

RESULT 1
W33357 standard; Protein; 256 AA.

```
ID   W33357;
AC   W33357;
DT   19-MAR-1998  (first entry)
DE   TBP(20-161)/hCG-alpha fusion protein.
KW   Fusion protein; thrombopoietin; TPO; human chorionic gonadotrophin;
KW   alpha subunit; hCG-alpha.
OS   Homo sapiens.
PN   WO9730161-A1.
PD   21-AUG-1997;
PF   20-FEB-1996; U02315.
PR   20-FEB-1996; US-011936.
PA   (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
PI   Campbell RK, Chappel SC, Jameson BA;
PT   WPI; 97-425036/39.
DR   N-PSDB; T94007.
PT   Hybrid dimeric protein comprising two co-expressed units - each
PT   based on receptor or ligand and a subunit of a heterodimeric
PT   hormone, especially FSH, for inducing follicular maturation
PS   Example; Pages 32-33; 60pp; English.
CC   A novel fusion protein comprises 2 dimer forming co-expressed amino
CC   acid sequences, each consisting of a homodimeric or heterodimeric
CC   receptor chain or ligand, with ligand-receptor binding activity,
CC   bound directly or via a peptide linker to a subunit of a
CC   heterodimeric protein hormone capable of forming a heterodimer with
CC   the hormone's other subunits. The fusion protein, e.g. the
CC   thrombopoietin (TPO)/human chorionic gonadotrophin-alpha subunit
CC   (hCG-alpha) fusion protein denoted by the present sequence,
CC   significantly increases the biological activity of the hormone
CC   component, reducing the requirement for hormone itself and the
CC   number of injections needed.
SQ   Sequence 256 AA;
```

Query Match   100.0%; Score 1994; DB 26; Length 256;
Best Local Similarity 100.0%;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy   1 srtsllllafgllclpwlqegsadsvcpqgkylhpqnnsicctkchkgtylyndcpgpgqd  60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 srtsllllafgllclpwlqegsadsvcpqgkylhpqnnsicctkchkgtylyndcpgpgqd  60

Qy  61 tdcrecesgsftasenhlrhclscskcrkemgveisscvvdtvcgcrknqyrhywse 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61 tdcrecesgsftasenhlrhclscskcrkemgveisscvdtvcgcrknqyrhywse 120
```

Left column

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Qy    61  TDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRTVCGGRKNQYRHYWSE 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  nlfqcfncslclngtvhlscqekqntvctchagfflrenecvscagapgcpectlqenp 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   121  NLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCAGAAPGCPECTLQENP 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  ffsgpgapilqcmgccfsrayptplirskktmlvqknvtsestccvaksynrvtvmggfkv 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   181  FFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSYNRVTVMGGFKV 240
          ||||||||||||||||||||||||||||||||||||||||||||
Db   241  enhtgchcstccyyhks 256
          |||||||||||||||||
Qy   241  ENHTGCHCSTCCYYHKS 256
```

RESULT 2

```
ID   W33359 standard; Protein; 285 AA.
AC   W33359;
DT   19-MAR-1998  (first entry)
DE   TBP(20-190)/hCG-alpha fusion protein.
KW   Fusion protein; thrombopoietin; TPO; human chorionic gonadotrophin;
KW   alpha subunit; hCG-alpha.
OS   Homo sapiens.
PN   WO9730161-A1.
PD   21-AUG-1997;
PF   20-FEB-1997; U02315.
PR   20-FEB-1996; US-011936.
PA   (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
PI   Campbell RK, Chappel SC, Jameson BA;
DR   WPI; 97-425036/39.
DR   N-PSDB; T94021.
PT   A novel fusion protein comprises 2 dimer forming co-expressed amino
PT   acid sequences, each consisting of a homodimeric or heterodimeric
PT   receptor chain or ligand, with ligand-receptor binding activity,
PT   bound directly or via a peptide linker to a subunit of a
PT   heterodimeric protein hormone capable of forming a heterodimer with
PT   the hormone's other subunits. The fusion protein, e.g. the
PT   thrombopoietin (TPO)/human chorionic gonadotrophin-alpha subunit
PT   (hCG-alpha) fusion protein denoted by the present sequence,
PT   significantly increases the biological activity of the hormone
PT   component, reducing the requirement for hormone itself and the
PT   number of injections needed.
PS   Example; Pages 37-38; 60pp; English.
SQ   Sequence 285 AA;

Query Match             83.6%;
Best Local Similarity   89.1%;
Matches  254;  Conservative   2;  Mismatches   0;  Indels  29;  Gaps   1;
                        Score 1667;  DB 26;  Length 285;
                        Pred. No. 1.11e-170;

Db    1  srtsllafgllclpwlqegsadsvcpggkyihpqnnsicctkchkgtylyndcpgpggd 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    1  SRTSLLAFGLLCLPWLQEGSADSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQD 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  TDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRTVCGGRKNQYRHYWSE 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   61  TDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRTVCGGRKNQYRHYWSE 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  nlfqcfnctlclngtvhlscqekqntvctchagfflrenecvscsncckslectklslpq 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  121  NLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSC------------- 164
         |||||||||||||||||||||||||||||||||||||||||||||||
Db  181  lenvkgtedsgttagaapgcpectlqenpffsgpgapilqcmgccfsrayptplirskktm 240
         |||||||||||||||||||||||||||||||||||||||||||||
Qy  165  -----------------AGAAPGCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTM 211
         ||||||||||||||||||||||||||||||||||||||||||||
Db  241  lvqknvtsestccvaksynrvtvmggfkvenhtachcstccyyhks 285
         ||||||||||||||||||||||||||||||||||||||||||||
Qy  212  LVQKNVTSESTCCVAKSYNRVTVMGGFKVENHTGCHCSTCCYYHKS 256
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Right column

RESULT 3

```
ID   W33358 standard; Protein; 307 AA.
AC   W33358;
DT   19-MAR-1998  (first entry)
DE   TBP(20-161)/hCG-beta fusion protein.
KW   Fusion protein; thrombopoietin; TPO; human chorionic gonadotrophin;
KW   beta subunit; hCG-beta.
OS   Homo sapiens.
PN   WO9730161-A1.
PD   21-AUG-1997;
PF   20-FEB-1997; U02315.
PR   20-FEB-1996; US-011936.
PA   (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
PI   Campbell RK, Chappel SC, Jameson BA;
DR   WPI; 97-425036/39.
DR   N-PSDB; T94008.
PT   A novel fusion protein comprises 2 dimer forming co-expressed amino
CC   acid sequences, each consisting of a homodimeric or heterodimeric
CC   receptor chain or ligand, with ligand-receptor binding activity,
CC   bound directly or via a peptide linker to a subunit of a
CC   heterodimeric protein hormone capable of forming a heterodimer with
CC   the hormone's other subunits. The fusion protein, e.g. the
CC   thrombopoietin (TPO)/human chorionic gonadotrophin-beta subunit
CC   (hCG-beta) fusion protein denoted by the present sequence,
CC   significantly increases the biological activity of the hormone
CC   component, reducing the requirement for hormone itself and the
CC   number of injections needed.
SQ   Sequence 307 AA;
FH   Key             Location/Qualifiers
FT   CDS             279..1202
FT                   /*tag= a

Query Match             66.2%;
Best Local Similarity   98.8%;
Matches  169;  Conservative   1;  Mismatches   1;  Indels   0;  Gaps   0;
                        Score 1321;  DB 26;  Length 307;
                        Pred. No. 6.46e-132;

Db    1  srtsllafgllclpwlqegsadsvcpggkyihpqnnsicctkchkgtylyndcpgpggd 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    1  SRTSLLAFGLLCLPWLQEGSADSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQD 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  tdcrecesgsftasenhlrhclscskcrkemgqveisssctvdrdtvcgcrknqyrhywse 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   61  TDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRTVCGGRKNQYRHYWSE 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  nlfqcfncslclngtvhlscqekqntvctchagfflrenecvscagagrc 171
         |||||||||||||||||||||||||||||||||||||||||||||::||
Qy  121  NLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCAGAAPGC 171
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RESULT 4

```
ID   W33360 standard; Protein; 336 AA.
AC   W33360;
DT   19-MAR-1998  (first entry)
DE   TBP(20-190)/hCG-beta fusion protein.
KW   Fusion protein; thrombopoietin; TPO; human chorionic gonadotrophin;
KW   beta subunit; hCG-beta.
OS   Homo sapiens.
PN   WO9730161-A1.
PD   21-AUG-1997;
PF   20-FEB-1997; U02315.
PR   20-FEB-1996; US-011936.
PA   (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
PI   Campbell RK, Chappel SC, Jameson BA;
DR   WPI; 97-425036/39.
DR   N-PSDB; T94022.
PT   A novel fusion protein comprising two co-expressed units - each
PT   based on receptor or ligand and a subunit of a heterodimeric
PT   hormone, especially FSH, for inducing follicular maturation
PS   Example; Pages 39-40; 60pp; English.
```

CC   A novel fusion protein comprises 2 dimer forming co-expressed amino
CC   acid sequences, each consisting of a homodimeric or heterodimeric
CC   receptor chain or ligand, with ligand-receptor binding activity,
CC   bound directly or via a peptide linker to a subunit of a
CC   heterodimeric protein hormone capable of forming a heterodimer with
CC   the hormone's other subunits. The fusion protein, e.g. the
CC   thrombopoietin (TPO)/human chorionic gonadotrophin-beta subunit
CC   (hCG-beta) fusion protein denoted by the present sequence,
CC   significantly increases the biological activity of the hormone
CC   component, reducing the requirement for hormone itself and the
CC   number of injections needed.
SQ   Sequence 336 AA;

Query Match   64.7%; Score 1291; DB 26; Length 336;
Best Local Similarity   99.4%;
Matches 164; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Qy   1 srtslllafgllclpwlgegsadsvcppggkyihpqnnsicctkchkgtylyndcpgpggd 60
         |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||| |
Db   1 SRTSLLLAFGLLCLPWLGEGSADSVCPGGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQD 60

Qy   61 tdcrecesgsftasenhlrhclscskckrkemgqveisscctvdrdtvcgcrknqyrhywse 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TDCRECESGSFTASENHLRHCLSCSKCKRKEMGQVEISSCCTVDRDTVCGCRKNQYRHYWSE 120

Qy 121 nlfqcfncslclngtvhlscqekqntvctchagfflrenecvscs 165
         |||||||||||||||||||||||||||||||||||||||||||||
Db 121 NLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCA 165

RESULT 5
ID   R27496 standard; protein; 161 AA.
AC   R27496;
DT   09-MAR-1993 (first entry)
DE   Native 30 kD TNF inhibitor.
KW   Tumour necrosis factor; ethylene glycol; pharmokinetic;
KW   adult respiratory distress syndrome; rheumatoid arthritis;
KW   septic shock; pulmonary fibrosis; spacer.
OS   Homo sapiens.
PN   WO9216221-A.
PD   01-OCT-1992.
PF   13-MAR-1992; U02122.
PR   15-MAR-1991; US-669862.
PR   17-JAN-1992; US-822296.
PA   (SYND) SYNERGEN INC.
PI   Armes LG, Brewer MT, Evans RJ, Kohno T, Thompson RC;
DR   WPI; 92-348933/42.
PT   New ethylene glycolated polypeptide(s) with improved
PT   pharmacokinetic properties - for treating e.g. TNF and IL-1
PT   mediated diseases, e.g. adult respiratory distress syndrome,
PT   rheumatoid arthritis, septic shock etc.
PS   Claim 54; Fig 2; 100pp; English.
CC   The sequence shows a native 30 kD TNF inhibitor which may be
CC   modified to contain at least one non-native cysteine residue, pref.
CC   at positions 1, 14, 105, 111 and/or 165. The non-native cysteine is
CC   joined to a non-peptidic polymer, pref. monomethoxy PEG via
CC   thio-ether bonds. Two such TNF inhibitor mols. may be linked via
CC   this non-peptidic spacer. The modified polypeptides show improved
CC   pharmokinetic properties, i.e. increased mol. wt. hence reduced
CC   clearance rate following s.c. or systemic administration, increased
CC   sol. of native TNF inhibitors, and reduced antigenicity. The
CC   polypeptides may be used for treatment of TNF mediated diseases such
CC   as adult respiratory distress syndrome, pulmonary fibrosis, rheumatoid
CC   arthritis, inflammatory bowel disease and septic shock. The same
CC   method may be applied to the interleukin-1 receptor antagonist
CC   IL-1ra. See also R27495.
SQ   Sequence 161 AA;

Query Match   56.4%; Score 1124; DB 5; Length 161;
Best Local Similarity   99.3%; Pred. No. 6.19e-110;
Matches 142; Conservative   1; Mismatches   0; Indels   0; Gaps   0;
Sequence

Qy   1 dsvcpggkyihpqnnsicctkchkgtylyndcpgpggdtdcrecesgsftasenhlrhcl 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 dsvcpggkyihpqnnsicctkchkgtylyndcpgpggdtdcrecesgsftasenhlrhcl 60

Qy   23 DSVCPGGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 scskckrkemgqveisscctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 120

Qy   83 SCSKCKRKEMGQVEISSCCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 kqntvctchagfflrenecvscs 143

Qy 143 KQNTVCTCHAGFFLRENECVSCA 165
         |||||||||||||||||||||||:
Db 121 nlfqcfncslclngtvhlscqekqntvctchagfflrenecvscs 165

RESULT 6
ID   R24080 standard; Protein; 199 AA.
AC   R24080;
DT   05-NOV-1992 (first entry)
DE   Truncated TNF-alpha 55kD receptor.
KW   tumour necrosis factor alpha; extracellular binding domain;
KW   treatment; pulmonary diseases; septic shock; HIV infection: AIDS;
KW   malaria; viral meningitis; graft versus host disease;
KW   autoimmune disease; rheumatoid arthritis.
OS   Homo sapiens.
PN   WO9207076-A.
PD   30-APR-1992.
PF   18-OCT-1991; G01826.
PR   18-OCT-1990; GB-022648.
PA   (CHAR-) CHARING CROSS SUNLEY RES CENT.
PI   Brennan FM, Feldmann M, Gray PW, Turner MJC;
DR   WPI; 92-167156/20.
DR   N-PSDB; Q24441.
PT   New polypeptide capable of binding human TNF alpha - comprises
PT   first three cysteine-rich subdomains of TNF alpha receptor for
PT   treating autoimmune disease, septic shock, HIV etc.
PS   Example: Fig 7; 43pp; English.
CC   This sequence is a truncated TNF-alpha receptor derivative, as encoded
CC   in pTNFrecd. This was produced as described in Q24440.
CC   This derivative lacks the 81 carboxyl terminal residues of the
CC   cytoplasmic domain. The derivative could be used in the
CC   regulation of TNF-alpha mediated responses by binding and
CC   sequestering human TNF-alpha e.g. in the treatment of pulmonary
CC   diseases, septic shock, HIV infection, malaria, viral meningitis,
CC   graft versus host disease and autoimmune diseases, esp. rheumatoid
CC   arthritis.
CC   See also Q24440-51, R24000, R24080-84, R27585, Q29236-8
SQ   Sequence 199 AA;

Query Match   56.4%; Score 1124; DB 4; Length 199;
Best Local Similarity   99.3%; Pred. No. 6.19e-110;
Matches 142; Conservative   1; Mismatches   0; Indels   0; Gaps   0;
Sequence

Qy   41 dsvcpggkyihpqnnsicctkchkgtylyndcpgpggdtdcrecesgsftasenhlrhcl 100
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 dsvcpggkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 60

Qy   23 DSVCPGGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 scskckemgqveisscctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160

Qy   83 SCSKCKRKEMGQVEISSCCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 161 kqntvctchagfflrenecvscs 183

Qy 143 KQNTVCTCHAGFFLRENECVSCA 165
         |||||||||||||||||||||||:

RESULT 7
ID   R70108 standard; Protein; 309 AA.
AC   R70108;
DT   10-NOV-1995 (first entry)
DE   TNF-R-GBPH fusion protein.
KW   Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;
KW   red blood cell; cytokine receptor; glycophorin binding peptide 130;
KW   GBP 130; GBPH; glycophorin binding peptide homologue; glycophorin A;
KW   tumour necrosis factor receptor; TNF-R.
OS   Chimeric Homo sapiens.

OS Chimeric Plasmodium falciparum.
FH Key   Location/Qualifiers
FT misc_difference 230..269
FT   /label= repeat_region
FT   /note= "can be repeated n times, where n is a real
FT   number"
PN WO9506737-A.
PD 09-MAR-1995.
PF 01-SEP-1994; G01900.
PF 03-SEP-1993; GB-018350.
PR 03-SEP-1993; GB-018350.
PR 23-AUG-1994; GB-017021.
PA (PREN/) PRENDERGAST K F.
PI Prendergast KF;
DR WPI; 95-115452/15.
PT New hybrid peptide(s) for binding cytokine(s) - comprising a
PT malaria parasite peptide capable of binding a red blood cell and
PT a receptor peptide.
PS Example A; Page 54-55; 93pp; English.
CC Hybrid peptides for binding cytokines, comprising a malaria parasite
CC (Plasmodium falciparum) peptide (capable of binding to a red blood
CC cell (RBC)) and a receptor peptide (capable of binding cytokine
CC of these hybrid peptides. R70108 is a fusion of tumour necrosis factor
CC receptor (in accordance with H Loetscher et al Cell, Vol. 61, 351-359)
CC and glycophorin binding protein (GBPH). The
CC use of cytokine receptors not normally found on RBCs means that the
CC cytokine can bind harmlessly to the
CC hybrid peptides from excretion from the kidney, and
CC due to steric hindrance prevents the cytokines binding to a receptor in
CC another cell. GBP 130 or GBPH are the prefd. malaria parasite peptides
CC used, others include EBA 175 (175 kDa erythrocyte binding antigen), PMMSA
CC (pre major merozoite surface antigen) and the Duffy binding receptor
CC molecule (eg. exhibited by Plasmodium vivax). These peptides bind to
CC pref. glycophorin A, B and C, sialo glycoproteins, found on the surface
CC of RBCs. The hybrid peptides are thus used to lower the levels of free
CC cytokines in the circulation to reduce pathological damage.
SQ Sequence 309 AA;

Query Match   56.4%; Score 1124; DB 13; Length 309;
Best Local Similarity 99.3%; Pred. No. 6.19e-110;
Matches 142; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db   20 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 79
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db   80 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 139
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db 140 kqntvctchagfflrenecvscs 162
         |||||||||||||||||||||||:
Qy 143 KQNTVCTCHAGFFLRENECVSCA 165

RESULT 8
ID R07449 standard; protein; 371 AA.
AC R07449;
DT 29-JAN-1991 (first entry)
DE Tumour Necrosis Factor-Binding Protein from pTNF-BP15 cDNA.
KW Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
KW pTNF-BP15; infectious disease; parasitic disease; cachexia;
KW autoimmune disease; shock.
OS Homo sapiens.
PN EP-393438-A.
PD 24-OCT-1990.
PF 06-APR-1990; 106624.
PF 21-APR-1989; DE-913101.
PR 21-JUN-1989; DE-920282.
PA (BOEH) BOEHRINGER INGELHEIMINT.
PI Hauptmann R, Himmler A, Maurer-Fogy I, Stratowa C;
DR WPI; 90-321987/43.
DR N-PSDB; Q06282.
PT DNA encoding TNF binding protein and TNF- receptor - used in
PT tumour treatment and to understand mechanismsm to TNF action
PS Disclosure; Fig 1(1-3); 51pp; German.
CC Clone pTNF-BP15 was used to contruct pADTNF-BP, for transfection of
CC e.g. COS7 cells. The expressed proteins are useful
CC prophylactically and therapeutically to control disorders which
CC involve the damaging effects of TNF-alpha or -beta (e.g. infectious or
CC parasitic diseases, shock, cachexia, autoimmune diseases, adult
CC respiratory distress syndrome etc., or side effects of treatment with
CC TNF-alpha). They can also be used as diagnostic reagents for
CC assaying TNF and in study of TNF-receptor interactions.
CC See also Q06282-Q006285.
SQ Sequence 371 AA;

Query Match   56.4%; Score 1124; DB 2; Length 371;
Best Local Similarity 99.3%; Pred. No. 6.19e-110;
Matches 142; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db   41 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db 101 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db 161 kqntvctchagfflrenecvscs 183
         |||||||||||||||||||||||:
Qy 143 KQNTVCTCHAGFFLRENECVSCA 165

RESULT 9
ID R70107 standard; Protein; 451 AA.
AC R70107;
DT 10-NOV-1995 (first entry)
DE TNF-R-GBP 130 fusion protein.
PA (PREN/) PRENDERGAST K F.
PI Prendergast KF;
DR WPI; 95-115452/15.
KW Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;
KW red blood cell; cytokine receptor; glycophorin binding protein 130;
GBP 130; GBPH; glycophorin binding peptide homologue; glycophorin A.
OS Chimeric Homo sapiens.
OS Chimeric Plasmodium falciparum.
PN WO9506737-A.
PD 09-MAR-1995.
PF 01-SEP-1994; G01900.
PF 03-SEP-1993; GB-018350.
PR 23-AUG-1994; GB-017021.
PA (PREN/) PRENDERGAST K F.
PI Prendergast KF;
DR WPI; 95-115452/15.
PT New hybrid peptide(s) for binding cytokine(s) - comprising a
PT malaria parasite peptide capable of binding a red blood cell and
PT a receptor peptide.
PS Example A; Page 53-54; 93pp; English.
CC Hybrid peptides for binding cytokines, comprising a malaria parasite
CC (Plasmodium falciparum) peptide (capable of binding to a red blood
CC cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples
CC of these hybrid peptides. R70107 is a fusion of tumour necrosis factor
CC receptor (in accordance with H Loetscher et al Cell, Vol. 61, 351-359)
CC and glycophorin binding protein (GBP) 130. The use of cytokine
CC receptors not normally found on RBCs means that the cytokine can bind
CC harmlessly to the RBC without deleterious effect. The RBC protects the
CC hybrid peptides from excretion from the kidney, and due to steric
CC hindrance prevents the cytokines binding to a receptor in another cell.
CC GBP130 or GBPH (GBP homologue) are the prefd. malaria parasite peptides
CC used, others include EBA 175 (175 kDa erythrocyte binding antigen),
CC PMSA (pre major merozoite surface antigen) and the Duffy binding
CC receptor molecule (eg. exhibited by Plasmodium vivax). These peptides
CC bind to pref. glycophorin A, B and C, sialo glycoproteins, found on
CC the surface of RBCs. The hybrid peptides are thus used to lower
CC the levels of free cytokines in the circulation to reduce pathological
CC damage.
SQ Sequence 451 AA;

Query Match   56.4%; Score 1124; DB 13; Length 451;

```
Qy  143 KQNTVCTCHAGFFLRENECVSCA 165

Qy  140 kqntvctchagfflrenecvscs 162
        |||||||||||||||||||||||:

Db  140 kqntvctchagfflrenecvscs 162

Db   83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142
Qy   83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db   80 scskcrkemgqvelssctvdrdtvcgcrknqyrhywsenlfgcfncslcngtvhlscqe 139
        ||||||||||||:|||||||||||||||||||||||:|:|||:|||||||:|||||||||

Qy   23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db   20 dsvcpqgkyihpqnnsicctkchkgtylyndcppgqdtdcrecesgsftasenhlrhcl 79
        |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
```

RESULT 10

```
ID   R42059 standard; Protein; 455 AA.
AC   R42059;
DT   29-APR-1994 (first entry)
DE   Lambda derived TNF-R.
KW   Human; tumour necrosis factor receptor; TNF-R;
KW   IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;
KW   rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;
KW   pulmonary fibrosis; silicosis; allograft; xenograft; rejection;
KW   graft verses host disease; sepsis; inflammation; allergy;
OS   Homo sapiens.
OS   Lambda-gt10-7ctnfbp.
FH   Key            Location/Qualifiers
FT   peptide        1..40
FT                  /note= "Signal peptide"
FT   protein        41..455
FT                  /note= "Mature hTNF-R"
```

```
WO9319777-A.
14-OCT-1993.
26-MAR-1993; U02938.
30-MAR-1992; US-860710.
(IMMV ) IMMUNEX CORP.
Smith CA;
WPI; 93-336592/42.
N-PSDB; Q4932.
```
New fusion protein tumour necrosis factor and human interleukin-1
receptor - useful in therapy, diagnosis and assays of e.g.
rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.
Disclosure; Page 57-59; 85pp; English.
The sequences given in R42058-59 represent human tumour necrosis
factor receptor (TNF-R) and the sequences in R42060-61 represent
human interleukin-1 receptor (IL-1R). These sequences were used in
the production of a fusion protein which conformed to one of the
formulae:
TNF-R-linker-TNF-R-linker-IL-1R
IL-1R-linker-TNF-R-linker-TNF-R or
TNF-R-linker-TNF-R
The linker may comprise 5-100 amino acids selected from Gly, Asp,
Ser, Thr and Ala. These linkers separate the individual moieties
by such a distance that each component of the fusion protein is
capable of folding into the secondary or tertiary structure required
for its biological activity. These fusion proteins may be used in
therapy, diagnosis and assays for conditions mediated by TNF or IL-1,
particularly in conditions in which both TNF and IL-1 play a causitive
role. They may be used to treat cachexia, rheumatoid arthritis,
diabetes, multiple sclerosis, pulmonary fibrosis and silicosis,
cerebral malaria, allograft and xenograft rejection in graft verses
host disease, sepsis, septic shock, inflammation, allergies and
autoimmune dysfunctions.
Sequence   455 AA;

```
Query Match    56.4%; Score 1124; DB 8; Length 455;
Best Local Similarity 99.3%; Pred. No. 6.19e-110;
Matches   142; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Db   41 dsvcpqgkyihpqnnsicctkchkgtylyndcppgqdtdcrecesgsftasenhlrhcl 100
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Qy   23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db  101 scskcrkemgqvelssctvdrdtvcgcrknqyrhywsenlfgcfncslcngtvhlscqe 160
Qy   83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db  161 kqntvctchagfflrenecvscs 183
Qy  143 KQNTVCTCHAGFFLRENECVSCA 165
```

RESULT 11

```
ID   R10986 standard; Protein; 455 AA.
AC   R10986;
DT   13-MAY-1991 (first entry)
DE   30KD TNF inhibitor precursor.
KW   Tumour necrosis factor; inhibitor.
OS   Homo sapiens.
FH   Key            Location/Qualifiers
FT   cleavage-site  40..41
FT                  /note= "cleavage gives active protein "
PN   AU9058976-A.
PD   24-JAN-1991.
PF   16-JUL-1990; 058976.
PF   18-JUL-1989; US-381080.
PR   11-DEC-1989; US-450329.
PR   07-FEB-1990; US-479661.
PA   (SYNE- ) SYNERGEN INC.
```
```
WPI; 91-073847/11.
N-PSDB; Q10883.
```
Tumour necrosis factor inhibitor - for suppression of TNF-alpha
and -beta, useful as therapeutic agent.
Disclosure; Fig 21; 14pp; English.
The sequence comprises the entire 30 kD TNF inhibitor. The clone
from which the sequence was deduced was isolated from a cDNA
library prepd. from RNA form U937 cells treated with PMA/PHA.
The whole gene can be inserted into expression vectors for prepn.
of TNF inhibitor for use in the treatment of inflammatory and
degenerative diseases. The active protein is claimed (Claim 8).
See also R10984 and R11001.
Sequence   455 AA;

```
Query Match    56.4%; Score 1124; DB 2; Length 455;
Best Local Similarity 99.3%; Pred. No. 6.19e-110;
Matches   142; Conservative   1; Mismatches   0; Indels   0; Gaps   0;
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Db  101 scskcrkemgqvelssctvdrdtvcgcrknqyrhywsenlfgcfncslcngtvhlscqe 160
Qy   83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db  161 kqntvctchagfflrenecvscs 183
Qy  143 KQNTVCTCHAGFFLRENECVSCA 165
```

RESULT 12

```
ID   R20787 standard; Protein; 455 AA.
AC   R20787;
DT   11-MAY-1992 (first entry)
DE   TNF-alpha binding protein.
KW   Tumour necrosis factor alpha; autoimmune diseases; cachectin;
KW   extracellular domain.
OS   Homo sapiens.
FH   Key            Location/Qualifiers
FT   peptide        1..40
FT                  /note= "signal peptide"
FT   peptide        41..455
FT                  /note= "mature peptide"
```

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Query Match    56.4%; Score 1124; DB 2; Length 455;
Best Local Similarity 99.3%; Pred. No. 6.19e-110;
Matches   142; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Db   41 dsvcpqgkyihpqnnsicctkchkgtylyndcppgqdtdcrecesgsftasenhlrhcl 100
```

```
FT   domain            30..199
FT                     /note= "extracellular domain"
FT   domain            212..234
FT                     /note= "transmembrane domain"
FT   modified_site     145..147
FT                     /note= "potential N-glycosylation site"
FT   modified_site     151..153
FT                     /note= "potential N-glycosylation site"
PN   GB2246569-A.
PD   05-FEB-1992;
PF   15-JUN-1990;
PR   15-JUN-1990; 013410.
PA   (CHAR-) CHARING CROSS SUNLE.
PI   Feldman M, Gray P, Turner M, Brennan F;
DR   WPI; 92-043613/06.
DR   N-PSDB; Q20973.
PT   New tumour necrosis factor alpha binding protein and polypeptide
PT   - useful in treating cachexia, sepsis and auto immune diseases
PT   e.g. rheumatoid arthritis
PS   Disclosure; Fig 1; 25pp; English.
CC   The amino acid sequence is that of tumour necrosis factor alpha
CC   binding protein which contains the extracellular domain of human TNF
CC   alpha receptor. It is soluble and can be used in the regulation of
CC   TNF-mediated responses by binding and sequestering the cytokine. It
CC   can therefore be used therapeutically to treat disorders such as
CC   cachexia, sepsis and autoimmune diseases, specifically rheumatoid
CC   arthritis.
SQ   Sequence     455 AA;

Query Match              56.4%;    Score 1124;  DB 4;   Length 455;
Best Local Similarity    99.3%;    Pred. No. 6.19e-110;
Matches   142;  Conservative   1;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      41 dsvcpggkylhpqnnslcctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      41 dsvcpggkylhpqnnslcctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100

Qy      23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGQDTDCRECESGSFTASENHLRHCL 82

Db     101 scskcrkemgqvelsscctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      83 SCSKCRKEMGQVEISSCCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db     161 kqntvctchagffllrenecvscs 183
           |||||||||||||||||||||:|
Qy     143 KQNTVCTCHAGFFLRENECVSCA 165
```

```
RESULT   13
ID   R75084 standard; Protein; 455 AA.
AC   R75084;
DT   19-JAN-1996  (first entry)
DE   P55 TNF-R.
KW   P55; tumour necrosis factor receptor; TNF-R; human; murine; chimera;
KW   epidermal growth factor receptor; EGF-R; protease; inhibitor;
KW   phorbol myristate acetate; PMA.
OS   Homo sapiens.
FH   Key              Location/Qualifiers
FT   peptide           41..53
FT                     /note= "N terminus of soluble p55 TNF-R"
FT   modified_site     54..56
FT                     /note= "glycosylation site"
FT   modified_site     145..147
FT                     /note= "glycosylation site"
FT   modified_site     161..163
FT                     /note= "glycosylation site"
FT   peptide           193..210
FT                     /note= "peptide used in creation of chimeras"
FT   region            198..210
FT                     /note= "spacer region"
FT   region            201
FT                     /note= "major C terminus for soluble p55 TNF-R"
FT   misc_difference   202
FT                     /note= "essential for shedding reaction"
FT   misc_difference   203
```

```
FT   region            212..234
FT                     /note= "minor C terminus for soluble p55 TNF-R"
FT                     /note= "transmembrane region"
PN   AU9475742-A.
PD   04-MAY-1995;
PF   11-OCT-1994; 075742.
PR   12-OCT-1993; II-107268.
PA   (YEDA) YEDA RES & DEV CO LTD.
PA   Batkin M, Brakebusch C, Varfolomeev E, Wallach D;
DR   WPI; 95-194342/26.
DR   N-PSDB; Q90513.
PT   New protease capable of cleaving soluble tumour necrosis factor
PT   (TNF) receptor - from cell-bound TNF- receptor, useful for
PT   antagonising deleterious effects of TNF.
PS   Disclosure; Fig 1; 40pp; English.
CC   This sequence represents human p55 tumour necrosis factor (TNF-R).
CC   Expression of this receptor is regulated by shedding of the extracellular
CC   receptor fragment. The p55 TNF-R can be shed in response to different
CC   inducing agents, e.g. phorbol myristate acetate (PMA), depending on cell
CC   type. The only region of the receptor whose structure affects the
CC   shedding response is the spacer region (see R75012) in the extracellular
CC   domain. This region is located close to a site of cleavage of the
CC   molecule, and links the Cys rich module to the transmembrane domain. The
CC   spacer region of the encoded protein was used to create the chimeras
CC   between human p55 TNF-R and murine epidermal growth factor receptor
CC   (EGF-R) that are represented by R75007-11. This spacer region was
CC   subjected to deletion mutations (R75013-25) and substitutions
CC   (R75026-47). Of the spacer region, the most important residues are
CC   Asn 172, Val 173, Lys 174 and Gly 175, with Val 173 being the most
CC   important of these. The shedding of the receptor is independent of the
CC   side chain identity of these residues, with the exception of a limited
CC   dependence on the identity of Val 173. Mutations which alter the
CC   conformation of the protein adversely affect the shedding process.
CC   The mutations shown in R75013-47 were introduced in order to create an
CC   inhibitor of a protease that is capable of cleaving the soluble TNF-R
CC   from the cell bound TNF-R. Fragments of these inhibitors can be seen in
CC   R75017-9, R75025, R75033-5 and R75042-3. These protease inhibitors can
CC   be used for enhancing TNF function.
SQ   Sequence     455 AA;

Query Match              56.4%;    Score 1124;  DB 14;  Length 455;
Best Local Similarity    99.3%;    Pred. No. 6.19e-110;
Matches   142;  Conservative   1;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      41 dsvcpggkylhpqnnslcctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGQDTDCRECESGSFTASENHLRHCL 82

Db     101 scskcrkemgqvelsscctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      83 SCSKCRKEMGQVEISSCCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db     161 kqntvctchagffllrenecvscs 183
           |||||||||||||||||||||:|
Qy     143 KQNTVCTCHAGFFLRENECVSCA 165
```

```
RESULT   14
ID   R07451 standard; protein; 455 AA.
AC   R07451;
DT   29-JAN-1991  (first entry)
DE   Human Tumour Necrosis Factor-Receptor from lambdaTNF-R2 cDNA insert.
KW   Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
KW   infectious disease; parasitic disease; cachexia;
KW   autoimmune disease; shock; lambdaTNF-R2; raTNF-R8.
OS   Homo sapiens.
PN   EP-393438-A.
PD   24-OCT-1990.
PF   06-APR-1990; 106624.
PR   24-OCT-1990;
PR   06-APR-1990; 106624.
PR   21-APR-1989; DE-913101.
PR   21-JUN-1989; DE-920282.
PA   (BOEH ) BOEHRINGER INGELHEIMINT.
PA   Hauptmann R, Himmler A, Maurer-Fogy I, Stratowa C;
PI   
```

DR   WPI; 90-321987/43.
DR   N-PSDB; Q06285.
PT   DNA encoding TNF binding protein and TNF- receptor - used in
PT   tumour treatment and to understand mechanism to TNF action
PS   Disclosure; Fig 91(1-2); 51pp; German.
CC   raTNF-R8 (Q06284) was used to screen the HS913T cDNA library.
CC   LambdaTNF-R2 encodes the complete human TNF-R2 and was used to
CC   construct a plasmid (pADTNF-R) expressing the product the same way
CC   as pADTNF-BP (see Q06282). The expressed proteins are useful
CC   prophylactically and therapeutically to control disorders which
CC   involve the damaging effects of TNF-alpha or -beta (e.g. infectious or
CC   parasitic diseases, shock, cachexia, autoimmune diseases, adult
CC   respiratory distress syndrome etc., or side effects of treatment with
CC   TNG-alpha). They can also be used as diagnostic reagents for
CC   assaying TNF and in study of TNF-receptor interactions.
CC   See also Q06282-Q06285.
SQ   Sequence   455 AA;

Query Match   56.4%; Score 1124; DB 2; Length 455;
Best Local Similarity   99.3%; Pred. No. 6.19e-110;
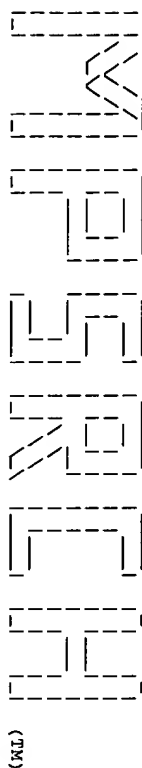Matches   142; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Qy   41 dsvcpqgkylhpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
         ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db   23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Qy 101 scskcrkemgqveissctvdrdtvccgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   83 SCSKCRKEMGQVEISSCTVDRDTVCCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Qy 161 kqntvctchagfflrenecvscs 183
         ||||||||||||||||||||||:
Db 143 KQNTVCTCHAGFFLRENECVSCA 165

RESULT 15
ID   R11082 standard; Protein; 455 AA.
AC   R11082;
DT   24-MAY-1991 (first entry)
DE   Human 55kD TNF-binding protein.
KW   Tumour Necrosis Factor; binding proteins; septic shock;
KW   autoimmune glomerulonephritis; lymphokine; cytokine.
FH   Key   Location/Qualifiers
FT   modified_site 54
FT   /label= putative N-glycosylation site
FT   modified_site 145
FT   /label= putative N-glycosylation site
FT   modified_site 151
FT   /label= putative N-glycosylation site
FT   modified_site 270
FT   /label= putative N-glycosylation site
FT   region   212..230
FT   /label= putative N-glycosylation site
FT   region
FT   /label= transmembrane region
FT   peptide   1..28
FT   /label= signal peptide
PN   EP-417563-A.
PD   20-MAR-1991.
PF   31-AUG-1990; 116707.
PR   12-SEP-1989; CH-003319.
PR   08-MAR-1990; CH-000746.
PR   20-APR-1990; CH-001347.
PA   (HOFF) HOFFMANN-LA ROCHE AG.
PI   Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;
PI   Schlaeger EJ;
DR   WPI; 91-081851/12.
DR   N-PSDB; Q10955.
PT   Insoluble tumour necrosis factor binding proteins - and DNA
PT   encoding them, useful in pharmaceutical prods. and for antibody
PT   prodn.
PS   Claim 1; Fig 1; 26pp; German.
CC   Partial amino acid sequences were determined for the 55 and 75kD
CC   TNF-BPs (see R11072-R11081) and oligonucleotide primers were
CC   synthesised based on these partial sequences. The primers were used

CC   to produce a cDNA fragment for use as aprobe to screen a human
CC   placental cDNA bank constructed in lambda gt11. Positive clones were
CC   identified and sequenced. DNA constructs comprising the TNF-BP coding
CC   sequence may also contain a fragment encoding a human Ig domain.
CC   Recombinant constructs are used to transform cells to confer
CC   improved TNF-binding properties.
CC   See also Q10956.
SQ   Sequence   455 AA;

Query Match   56.4%; Score 1124; DB 2; Length 455;
Best Local Similarity   99.3%; Pred. No. 6.19e-110;
Matches   142; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Qy   41 dsvcpqgkylhpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
         ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db   23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Qy 101 scskcrkemgqveissctvdrdtvccgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   83 SCSKCRKEMGQVEISSCTVDRDTVCCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Qy 161 kqntvctchagfflrenecvscs 183
         ||||||||||||||||||||||:
Db 143 KQNTVCTCHAGFFLRENECVSCA 165

Search completed: Wed May 6 08:52:53 1998
Job time : 114 secs.

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  MM MM  P   P S     R   R  C     H   H
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  M   M  P         S R  R   C     H   H
  M   M  P      SSS  R   R   CCC  H   H   (TM)
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        Distribution rights by Oxford Molecular Ltd
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```

MPsrch_pp   protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 6 08:50:01 1998; MasPar time 11.89 Seconds
                                         786.633 Million cell updates/sec

Tabular output not generated.

Title:
Description:
Perfect Score:
Sequence: 1 SRTSLLAFGLLCLPWLQEG..........GFKVENHTGCHCSTCYHKS 256

Scoring table: PAM 150
               Gap 11
Searched: 120446 seqs, 36531193 residues
Post-processing: Minimum Match 0%
                 Listing first 45 summaries
Database: pir56
               1:pir1 2:pir2 3:pir3 4:pir4 5:nr13d

Statistics: Mean 40.411; Variance 71.735; scale 0.563

               Pred. No. is the number of results predicted by chance to have a
               score greater than or equal to the score of the result being printed,
               and is derived by analysis of the total score distribution.

Title: >US-08-804-166-2
Description: (1-256) from US08804166.pep
Sequence: 1994

SUMMARIES

Result NO.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1124	56.4	158	5	1EXTB	tumor necrosis factor	2.23e-230
2	1124	56.4	455	1	GQHUT1	tumor necrosis factor	2.23e-230
3	1118	56.1	160	5	1EXTA	tumor necrosis factor	5.83e-229
4	1114	55.9	142	5	1NCFB	tumor necrosis factor	5.14e-228
5	1105	55.4	139	5	1TNRR	tumor necrosis factor	6.85e-226
6	1098	55.1	140	5	1NCFA	tumor necrosis factor	3.08e-224
7	962	48.2	461	2	JC4302	tumor necrosis factor	3.26e-192
8	841	42.2	454	2	I57826	tumor necrosis factor	7.05e-164
9	841	42.2	454	2	GQMST1	tumor necrosis factor	7.05e-164
10	809	40.6	461	1	GORTT1	tumor necrosis factor	2.05e-156
11	667	33.5	116	5	TTHUAP	glycoprotein hormones	1.71e-123
12	647	32.4	85	5	1HRPA	chorionic gonadotropi	6.89e-119
13	645	32.3	86	5	1XULA	chorionic gonadotropi	1.99e-118
14	645	32.3	85	5	1HCNA	Human chorionic gonad	1.99e-118
15	551	27.6	120	1	A39555	glycoprotein hormones	6.48e-97
16	548	27.5	120	1	TTBOA	glycoprotein hormones	3.12e-96
17	548	27.5	120	1	UTSHA	glycoprotein hormones	3.12e-96
18	546	27.4	96	2	A05096	glycoprotein hormones	8.89e-96
19	544	27.3	120	1	TTRTA	glycoprotein hormones	2.53e-95
20	541	27.1	96	2	PN0138	glycoprotein hormones	1.22e-94
21	541	27.1	120	1	UTPGA	glycoprotein hormones	1.22e-94
22	541	27.1	120	1	TTMSA	glycoprotein hormones	1.22e-94
23	539	27.0	120	2	G00021	chorionic gonadotropi	3.47e-94
24	537	26.9	120	2	A45585	glycoprotein hormones	9.87e-94
25	537	26.9	120	2	I51241	pituitary glycoprotei	9.87e-94
26	507	25.4	118	2	A40554	glycoprotein hormones	6.20e-87
27	503	25.2	120	2	S55062	glycoprotein hormones	4.97e-86
28	501	25.1	96	1	TTHOA	gonadotropin hormones	1.41e-85
29	500	25.1	118	2	S16762	glycoprotein alpha ch	2.37e-85
30	500	25.1	118	1	UTCAA	glycoprotein hormones	2.37e-85
31	500	25.1	118	2	A60626	glycoprotein hormones	2.37e-85
32	478	24.0	93	2	S07091	glycoprotein hormones	2.15e-80
33	476	23.9	97	2	S20287	lutropin alpha chain	6.06e-80
34	474	23.8	117	2	A37198	glycoprotein hormones	1.71e-79
35	451	22.6	119	2	I51229	gonadotropin alpha 1	2.46e-74
36	448	22.5	114	2	B60627	gonadotropin alpha 1	1.15e-73
37	447	22.4	108	2	A60627	glycoprotein hormones	1.93e-73
38	446	22.4	114	2	I51230	gonadotropin alpha 2	3.23e-73
39	440	22.1	117	2	I50992	gonadotropin alpha-su	7.08e-72
40	231	11.6	435	2	I54182	tumor necrosis factor	8.52e-27
41	228	11.4	38	2	A60583	glycoprotein hormones	3.48e-26
42	225	11.3	325	2	B43692	T2 protein - rabbit f	1.42e-25
43	221	11.1	326	1	GQV2ML	T2 protein - myxoma v	9.18e-25
44	214	10.7	349	2	D36858	gene G4R protein - va	2.37e-23
45	212	10.6	474	2	B38634	tumor necrosis factor	5.96e-23

ALIGNMENTS

RESULT   1

ENTRY   1EXTB   #type complete
TITLE   tumor necrosis factor receptor extracellular domain, chain B
PDB_TITLE   extracellular domain of the 55kda tumor necrosis factor
            receptor. crystallized at ph3.7 in p 21 21 21.
ORGANISM   #formal_name Homo sapiens #common_name man
#note   expressed in Escherichia coli. the construct contains
            residues 12 to 172 of the mature sequence of the entire
            receptor. residue 11 is mutated to met as a result of the
            expression system
REFERENCE   A65560
#authors   Naismith, J.H.; Sprang, S.R.
#submission submitted to the Brookhaven Protein Data Bank, July 1996
#cross-references PDB:1EXT
REFERENCE   TN026251
#authors   Naismith, J.H.; Devine, T.Q.; Brandhuber, B.J.; Sprang, S.R.
#journal   J. Biol. Chem. (1995) 270:13303
#title   Crystallographic evidence for dimerization of unliganded
            tumor necrosis factor receptor.
REFERENCE   TN026252
#authors   Rodseth, L.E.; Brandhuber, B.; Devine, T.Q.; Eck, M.J.; Hale,
            K.; Naismith, J.H.; Sprang, S.R.
#journal   J. Mol. Biol. (1994) 239:332
#title   Two crystal forms of the extracellular domain of type 1 tumor
            necrosis factor receptor.
REFERENCE   A40737
#authors   Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
            H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
#journal   Cell (1993) 73:431-445
#title   Crystal structure of the soluble human 55 kd TNF
            receptor-human TNFbeta complex: implications for TNF
            receptor activation.
COMMENT   Resolution: 1.85 angstroms
COMMENT   Determination: X-ray diffraction
COMMENT   R-value: no refinement
KEYWORDS   binding protein; cytokine; signalling protein
FEATURE
    68-70   #region helix (right hand 3-10)\
    143-145   #region helix (right hand 3-10)\
    9-11,19-21   #region beta sheet\
    133-136,139-142 #region beta sheet\
    27-31,41-44   #region beta sheet\
    73-76,85-87   #region beta sheet\
    92-98,101-106   #region beta sheet\
    113-117,126-129 #region beta sheet\
    5-19   #disulfide_bonds\

```
          20-33    #disulfide_bonds\\
          23-42    #disulfide_bonds\\
          45-60    #disulfide_bonds\\
          63-78    #disulfide_bonds\\
          66-86    #disulfide_bonds\\
          88-104   #disulfide_bonds\\
          107-119  #disulfide_bonds\\
          110-127  #disulfide_bonds\\
          129-140  #disulfide_bonds\\
          143-156  #disulfide_bonds\\
          146-152  #disulfide_bonds\\
SUMMARY            #length 158  #molecular-weight 17827  #checksum 5022

Query Match  56.4%;  Score 1124; DB 5; Length 158;
Best Local Similarity 99.3%;  Pred. No. 2.23e-230;
Matches 142;  Conservative 1;  Mismatches 0;  Indels 0;  Gaps 0;

Qy   2  DSVCPQGKYIHPQNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL  61
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  23  DSVCPQGKYIHPQNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL  82

Qy  62  SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 121
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  83  SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Qy 122  KQNTVCTCHAGFFLRENECVSCS 144
        |||||||||||||||||||||||
Db 143  KQNTVCTCHAGFFLRENECVSCA 165
```

```
RESULT  2

ENTRY     GQHUT1    #type complete
TITLE     tumor necrosis factor receptor type 1 precursor - human
CONTAINS  tumor necrosis factor alpha inhibitor; tumor necrosis factor
          binding protein 1 (TNF blocking factor)
ORGANISM  #formal_name Homo sapiens #common_name man
DATE      30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
          24-Oct-1997
ACCESSIONS A38208; A34899; A34900; A36555; C36555; A38281; S12057;
           JT0758; A60231; A38258; A60594; A35010; JC2404
REFERENCE A38208
 #authors Fuchs, P.; Strehl, S.; Dworzak, M.; Himmler, A.; Ambros, P.F.
 #journal Genomics (1992) 13:219-224
 #title   Structure of the human TNF receptor 1 (p60) gene (TNFR1) and
          localization to chromosome 12p13.
 #accession A38208
   ##molecule_type DNA
   ##residues 1-455 ##label FUC
   ##cross-references GB:M75864; GB:M75865; GB:M75866; NID:g339748;
                      PID:g339750
REFERENCE A34899
 #authors Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus,
          M.; Tabuchi, H.; Lesslauer, W.
 #journal Cell (1990) 61:351-359
 #title   Molecular cloning and expression of the human 55 kd tumor
          necrosis factor receptor.
 #accession A34899
   ##molecule_type mRNA
   ##residues 1-455 ##label LOE
   ##cross-references GB:M58286; GB:M33480; NID:g339753; PID:g339754
REFERENCE A34900
 #authors Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.;
          Wong, G.H.W.; Gatanaga, T.; Granger, G.A.; Lentz, R.; Raab,
          H.; Kohr, W.J.; Goeddel, D.V.
 #journal Cell (1990) 61:361-370
 #title   Molecular cloning and expression of a receptor for human
          tumor necrosis factor.
 #cross-references MUID:90235285
```

```
 #accession A34900
   ##molecule_type mRNA
   ##residues 1-455 ##label SCH
   ##cross-references GB:M33294; NID:g339744; PID:g339745
REFERENCE A36555
 #authors Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.;
          Pfizenmaier, K.; Lantz, M.; Olsson, I.; Hauptmann, R.;
          Stratowa, C.; Adolf, G.R.
 #journal DNA Cell Biol. (1990) 9:705-715
 #title   Molecular cloning and expression of human and rat tumor
          necrosis factor receptor chain (p60) and its soluble
          derivative, tumor necrosis factor-binding protein.
 #cross-references MUID:91090841
 #accession A36555
   ##molecule_type mRNA
   ##residues 1-455 ##label HIM
   ##cross-references GB:M63121; NID:g339755; PID:g339756
 #accession C36555
   ##molecule_type protein
   ##residues 30-38;41-53,'X',55-79,'XX',82-94,'NK','XX',100-104;
              107-128;162-167,'X',169-201 ##label HI2
   ##note the purified protein, called tumor necrosis factor
          binding protein, is a soluble derivative of the
          receptor
REFERENCE A38281
 #authors Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann,
          M.
 #journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:7380-7384
 #title   Cloning of human tumor necrosis factor (TNF) receptor cDNA
          and expression of recombinant soluble TNF-binding protein.
 #cross-references MUID:91017509
 #accession A38281
   ##molecule_type mRNA
   ##residues 1-455 ##label GRA
   ##cross-references GB:M37764
   ##note the authors translated the codon TGG for residue 371 as
          Thr, AAG for residue 372 as Leu, and GAC for residue
          427 as Asn
REFERENCE S12057
 #authors Nophar, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang,
          R.; Aderka, D.; Holtmann, H.; Wallach, D.
 #journal EMBO J. (1990) 9:3269-3278
 #title   Soluble forms of tumor necrosis factor receptors (TNF-Rs).
          The cDNA for the type I TNF-R, cloned using amino acid
          sequence data of its soluble form, encodes both the cell
          surface and a soluble form of the receptor.
 #cross-references MUID:91006021
 #accession S12057
   ##molecule_type mRNA
   ##residues 1-455 ##label NOP
   ##cross-references EMBL:X55313; NID:g37223; PID:g37224
   ##note parts of soluble TNF binding protein 1, including its
          amino and carboxyl ends, were confirmed by protein
          sequencing
REFERENCE JT0758
 #authors Kemper, O.; Wallach, D.
 #journal Gene (1993) 134:209-216
 #title   Cloning and partial characterization of the promoter for the
          human p55 tumor necrosis factor (TNF) receptor.
 #accession JT0758
   ##molecule_type DNA
   ##residues 1-13 ##label KEM
REFERENCE A60231
 #authors Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer,
          J.M.
 #journal Eur. J. Immunol. (1990) 20:1167-1174
 #title   Tumor necrosis factor inhibitor: purification, NH-2-terminal
          amino acid sequence and evidence for anti-inflammatory and
          immunomodulatory activities.
 #cross-references MUID:90292116
 #accession A60231
   ##molecule_type protein
   ##residues 41-43,'X',45-53,'X',55-57 ##label SEC
```

REFERENCE
#authors   Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci III,
           J.A.; Jeffes, E.W.B.; Lentz, R.; Tomich, J.; Yamamoto,
           R.S.; Granger, G.A.
#journal   Proc. Natl. Acad. Sci. U.S.A. (1990) 87:8781-8784
#title   Purification and characterization of an inhibitor (soluble
           tumor necrosis factor receptor) for tumor necrosis factor
           and lymphotoxin obtained from the serum ultrafiltrates of
           human cancer patients.
#cross-references MUID:91062364
#accession A38258
          ##molecule_type protein
          ##residues 41-60 ##label GAT
REFERENCE
#authors   Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thysell, H.;
           Grubb, A.; Adolf, G.
#journal   Eur. J. Haematol. (1989) 42:270-275
#title   Isolation and characterization of a tumor necrosis factor
           binding protein from urine.
#accession A60594
          ##molecule_type protein
          ##residues 41-43,'X',45-53,'V',55-57,'XK',60 ##label OLS
          ##experimental_source renal failure patient urine
REFERENCE
#authors   Engelmann, H.; Novick, D.; Wallach, D.
#journal   J. Biol. Chem. (1990) 265:1531-1536
#title   Two tumor necrosis factor-binding proteins purified from
           human urine. Evidence for immunological cross-reactivity
           with cell surface tumor necrosis factor receptors.
#cross-references MUID:90110215
#accession A35010
          ##molecule_type protein
          ##residues 41-45 ##label ENG
          ##experimental_source normal urine
#authors   Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.
#journal   Biosci. Biotechnol. Biochem. (1994) 58:2266-2268
#title   Amino acid sequence of natural tumor necrosis factor alpha
           inhibitor purified from human urine.
#accession JC2404
          ##molecule_type protein
          ##residues 41-53,'X',55-144,'X',146-150,'X',152-186,'X',188-201
          ##label KAJ
COMMENT   This protein is one of two known receptors for both TNF-alpha
           (cachectin) and TNF-beta (lymphotoxin).
          ##experimental_source urine
GENETICS
#gene   GDB:TNFR1
          ##cross-references GDB:125913; OMIM:191190
          ##map_position 12p13.2-12p13.2
#introns   13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
CLASSIFICATION
#superfamily tumor necrosis factor receptor type 1; NGF
             receptor repeat homology
KEYWORDS   duplication; glycoprotein; receptor; transmembrane protein
FEATURE
     1-21 #domain signal sequence #status predicted #label SIG\
    22-455 #product tumor necrosis factor receptor type 1 #status
           predicted #label MAT\
    30-211 #domain extracellular #status predicted #label EXT\
    41-201 #product TNF binding protein 1 (tumor necrosis factor
           alpha inhibitor) #status experimental #label TBP1\
    44-82 #domain NGF receptor repeat homology #label NG1\
    84-126 #domain NGF receptor repeat homology #label NG2\
   127-167 #domain NGF receptor repeat homology #label NG3\
   168-196 #domain NGF receptor repeat homology #label NG4\
   212-234 #domain transmembrane #status predicted #label MEM\
   235-455 #domain intracellular #status predicted #label INT\
54,145,151 #binding-site carbohydrate (Asn) (covalent) #status
           predicted
SUMMARY   #length 455   #molecular-weight 50494   #checksum 153
Query Match 56.48;   Score 1124;   DB 1;   Length 455;

Best Local Similarity 99.3%;   Pred. No. 2.23e-230;   Indels 0;   Gaps 0;
Matches 142;   Conservative 1;   Mismatches 0;

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Db  41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL  82

Db 101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db 161 KQNTVCTCHAGFFLRENECVSCS 183
        |||||||||||||||||||||||:
Qy 143 KQNTVCTCHAGFFLRENECVSCA 165
```

RESULT 3
ENTRY   1EXTA   #type complete
TITLE   tumor necrosis factor receptor extracellular domain, chain A
PDB_TITLE extracellular domain of the 55kda tumor necrosis factor
          receptor: crystallized at ph3.7 in p 21 21 21.
ORGANISM #formal_name Homo sapiens #common_name man
#note   expressed in Escherichia coli, the construct contains
          residues 12 to 172 of the mature sequence of the entire
          receptor. residue 11 is mutated to met as a result of the
          expression system
REFERENCE
#authors   Naismith, J.H.; Sprang, S.R.
#submission submitted to the Brookhaven Protein Data Bank, July 1996
#cross-references PDB:1EXT
REFERENCE
#authors   Naismith, J.H.; Devine, T.Q.; Brandhuber, B.J.; Sprang, S.R.
#journal   J. Biol. Chem. (1995) 270:13303
#title   Crystallographic evidence for dimerization of unliganded
           tumor necrosis factor receptor.
REFERENCE
#authors   Rodseth, L.E.; Brandhuber, B.J.; Devine, T.Q.; Eck, M.J.; Hale,
           K.; Naismith, J.H.; Sprang, S.R.
#journal   J. Mol. Biol. (1994) 239:332
#title   Two crystal forms of the extracellular domain of type 1 tumor
           necrosis factor receptor.
REFERENCE
#authors   Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
           H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
#journal   Cell (1993) 73:431-445
#title   Crystal structure of the soluble human 55 kd TNF
           receptor-human TNFbeta complex: implications for TNF
           receptor activation.
COMMENT   Resolution: 1.85 angstroms
COMMENT   Determination: X-ray diffraction
COMMENT   R-value: no refinement
KEYWORDS   binding protein; cytokine; signalling protein
FEATURE
    66-68 #region helix (right hand 3-10)\
   141-143 #region helix (right hand 3-10)\
   151-154 #region helix (right hand alpha)\
   7-9,17-19 #region beta sheet\
   131-134,137-140 #region beta sheet\
   25-29,39-42 #region beta sheet\
   71-74,83-85 #region beta sheet\
   90-96,99-104 #region beta sheet\
   111-115,124-127 #region beta sheet\
     3-17 #region beta sheet\
    18-31 #region beta sheet\
    21-40 #region beta sheet\
    43-58 #region beta sheet\
    61-76 #region beta sheet\
    64-84 #region beta sheet\
    86-102 #disulfide_bonds\
   105-117 #disulfide_bonds\
   108-125 #disulfide_bonds\
   127-138 #disulfide_bonds\

SUMMARY

| 141-154 | #disulfide_bonds\ |
| 144-150 | #disulfide_bonds |

Query Match   56.1%;   Score 1118; DB 5;   Length 160;
Best Local Similarity 99.3%;   Pred. No. 5.83e-229;
Matches 141;   Conservative 1;   Mismatches 0;   Indels 0;   Gaps 0;

Qy 1 SVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLS 60
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQ 120

Qy 24 SVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLS 83
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 CSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEK 120

Qy 84 CSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEK 143
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 QNTVCTCHAGFFLRENECVSCS 142

Qy 144 QNTVCTCHAGFFLRENECVSCA 165

RESULT 4

ENTRY   1NCFB   #type complete

TITLE   tumor necrosis factor receptor 55 extracellular domain
         contains residues 12 172 of the mature receptor sequence,
         chain B - hu

ALTERNATE_NAMES   stnfrl: type 1 receptor
ORGANISM   #formal_name Homo sapiens #common_name man
#note   expressed in Escherichia coli, residue 11 is mutated to met
                  as a result of the expression system

REFERENCE   A66195
#authors   Naismith, J.H.; Sprang, S.R.
#submission submitted to the Brookhaven Protein Data Bank, October 1994
#cross-references PDB:1NCF

REFERENCE   TN029041
#authors   Rodseth, L.E.; Brandhuber, B.; Devine, T.Q.; Eck, M.J.; Hale,
            K.; Naismith, J.H.; Sprang, S.R.
#journal   J. Mol. Biol. (1994) 239:332
#title   Two crystal forms of the extracellular domain of type 1 tumor
            necrosis factor receptor.

REFERENCE   A40737
#authors   Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
            H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
#journal   Cell (1993) 73:431-445
#title   Crystal structure of the soluble human 55 kd TNF
            receptor-human TNFbeta complex: implications for TNF
            receptor activation.

COMMENT   Resolution 2.25 angstroms
COMMENT   Determination: X-ray diffraction
COMMENT   R-value: no refinement
KEYWORDS binding protein; cytokine; signalling protein
FEATURE

2-16	#disulfide_bonds\
17-30	#disulfide_bonds/
20-39	#disulfide_bonds\
42-57	#disulfide_bonds/
60-75	#disulfide_bonds\
63-83	#disulfide_bonds/
85-101	#disulfide_bonds\
104-116	#disulfide_bonds/
107-124	#disulfide_bonds\
126-137	#disulfide_bonds/

SUMMARY   #length 142   #molecular-weight 16046   #checksum 1225

Query Match   55.9%;   Score 1114; DB 5;   Length 142;
Best Local Similarity 99.3%;   Pred. No. 5.14e-228;
Matches 140;   Conservative 1;   Mismatches 0;   Indels 0;   Gaps 0;

Qy 1 VCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC 60
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 25 VCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC 84

Db 61 SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQ 120
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 85 SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQ 144

Db 121 NTVCTCHAGFFLRENECVSCS 141
       ||||||||||||||||||||:
Qy 145 NTVCTCHAGFFLRENECVSCA 165

RESULT 5

ENTRY   1TNRR   #type complete

TITLE   tumor necrosis factor receptor type 1 (P55 extracellular
ORGANISM   #formal_name Homo sapiens #common_name man
#note   recombinant form expressed in Baculovirus SF9

REFERENCE   A52442
#authors   Banner, D.W.
#submission submitted to the Brookhaven Protein Data Bank, May 1994
#cross-references PDB:1TNR

REFERENCE   A40737
#authors   Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
            H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
#journal   Cell (1993) 73:431-445
#title   Crystal structure of the soluble human 55 kd TNF
            receptor-human TNFbeta complex: implications for TNF
            receptor activation.

COMMENT   Resolution: 2.85 angstroms
COMMENT   Determination: X-ray diffraction
KEYWORDS Complex(lymphokineRECEPTOR)
FEATURE

1-15	#disulfide_bonds\
16-29	#disulfide_bonds/
19-38	#disulfide_bonds\
41-56	#disulfide_bonds/
59-74	#disulfide_bonds\
62-82	#disulfide_bonds/
84-100	#disulfide_bonds\
103-115	#disulfide_bonds/
106-123	#disulfide_bonds\
125-136	#disulfide_bonds/

SUMMARY   #length 139   #molecular-weight 15746   #checksum 5235

Query Match   55.4%;   Score 1105; DB 5;   Length 139;
Best Local Similarity 100.0%; Pred. No. 6.85e-226;
Matches 139;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy 1 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCS 60
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQ 120

Qy 26 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCS 85
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 KCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQN 120

Qy 86 KCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQN 145
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 TVCTCHAGFFLRENECVSC 139
       |||||||||||||||||||
Qy 146 TVCTCHAGFFLRENECVSC 164

RESULT 6

ENTRY   1NCFA   #type complete

TITLE   tumor necrosis factor receptor 55 kd extracellular domain
         contains residues 12 172 of the mature receptor sequence,
         chain A - hu
ALTERNATE_NAMES   stnfrl; type 1 receptor

ORGANISM #formal_name Homo sapiens #common_name man
          #note expressed in Escherichia coli, residue 11 is mutated to met
          as a result of the expression system
REFERENCE
          #authors Naismith, J.H.; Sprang, S.R.
          #submission submitted to the Brookhaven Protein Data Bank, October 1994
          #cross-references PDB:1NCF
REFERENCE
          #authors Rodseth, L.E.; Brandhuber, B.; Devine, T.O.; Eck, M.J.; Hale,
          K.; Naismith, J.H.; Sprang, S.R.
          #journal J. Mol. Biol. (1994) 239:332
          #title Two crystal forms of the extracellular domain of type 1 tumor
          necrosis factor receptor.
REFERENCE
          #authors Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
          H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
          #journal Cell (1993) 73:431-445
          #title Crystal structure of the soluble human 55 kd TNF
          receptor-human TNFbeta complex: implications for TNF
          receptor activation.
COMMENT   Resolution: 2.25 angstroms
COMMENT   Determination: X-ray diffraction
COMMENT   R-value: no refinement
KEYWORDS binding protein; cytokine; signalling protein
FEATURE
   5-19   #disulfide_bonds\
   20-33   #disulfide_bonds\
   23-42   #disulfide_bonds\
   45-60   #disulfide_bonds\
   63-78   #disulfide_bonds\
   66-86   #disulfide_bonds\
   88-104   #disulfide_bonds\
   107-119   #disulfide_bonds\
   110-127   #disulfide_bonds\
   129-140   #disulfide_bonds
SUMMARY   #length 140 #molecular-weight 15889 #checksum 6622

Query Match   55.1%; Score 1098; DB 5; Length 140;
Best Local Similarity   100.0%; Pred. No. 3.08e-224;
Matches   139; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db   2 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 61
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db   62 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVVHLSCQE 121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVVHLSCQE 142

Db 122 KQNTVCTCHAGFFLRENEC 140
          |||||||||||||||||||
Qy 143 KQNTVCTCHAGFFLRENEC 161

RESULT 7
ENTRY   JCA302   #type complete
TITLE   tumor necrosis factor receptor p55 - pig   #formal_name s
DATE   29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change
          12-Dec-1997
ACCESSIONS JCA302; PC4093
REFERENCE
          #authors Suter, B.; Pauli, U.
          #journal Gene (1995) 163:263-266
          #title Cloning of the cDNA encoding the porcine p55 tumor necrosis
          factor receptor.
          #accession JCA302
          ##molecule_type mRNA
          ##residues 1-461 ##label SUT
          #cross-references GB:U19994; NID:g1141752; PID:g1141753
          #accession PC4093
          ##molecule_type protein
          ##residues 1-7 ##label SU2

GENETICS ##experimental_source kidney cell line 15
          #gene tnfr
CLASSIFICATION #superfamily tumor necrosis factor receptor type 1; NGF
          receptor repeat homology
KEYWORDS glycoprotein; kidney; receptor; transmembrane protein; tumor
FEATURE
   1-29   #domain signal sequence #status predicted #label SIG\
   30-461   #product tumor necrosis factor receptor p55 #status
             predicted #label MAT\
   44-194   #domain extracellular cysteine rich #status predicted
             #label EXT\
   44-82   #domain NGF receptor repeat homology #label NG1\
   211-231   #domain transmembrane #status predicted #label TMM\
   361-447   #domain signal transduction #status predicted #label
             SIN\
   54,145,151 #binding_site carbohydrate (Asn) (covalent) #status
             predicted
SUMMARY   #length 461 #molecular-weight 50696 #checksum 8079

Query Match   48.2%; Score 962; DB 2; Length 461;
Best Local Similarity   69.8%; Pred. No. 3.26e-192;
Matches   120; Conservative   22; Mismatches   26; Indels   4; Gaps   4;

Db   41 ESLCPQGKYIHPQNRSICCTKCHKGTYLHHDCLGPGLDTDCRECDNGTFTASENHLTQCL 100
          :|:|||||| ||||||||||| ||||||||:||:|||| |||||:|||::|||||||||:||
Qy   23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db 101 SCSKCRSEMSQVEISPCTVDRDTVCGCRKNQYRKYWSETLFQCLNCSLCPNGTVQLPCLE 160
          |||||| ||.|||| |||||||||||||||||||:||||:|||:||||||||:||: ||
Qy   83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVVHLSCQE 142

Db 161 KQDTICNCHSGFFLRDKECVSCVNCKNADCKNICPATSETRNDFQDTGTTVL 212
          ||:.|:|||:|||||.:||||| | | :| ||||:|:|: |: |:|
Qy 143 KQNTVCTCHAGFFLRENECVSCAG-AAPGCPE-C-TLQENPF-FSQPGAPIL 190

RESULT 8
ENTRY   I57826   #type complete
TITLE   tumor necrosis factor receptor - mouse
DATE   02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
          23-May-1997
ACCESSIONS I57826
REFERENCE
          #authors Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.;
          Steinmetz, M.
          #journal Mol. Immunol. (1993) 30:165-176
          #title Genomic organization and promoter function of the murine
          tumor necrosis factor receptor beta gene.
          #accession I57826
          #cross-references MUID:93156721
          ##molecule_type DNA
          ##residues 1-454 ##label RES
          ##status preliminary; translated from GB/EMBL/DDBJ
          ##cross-references GB:M76656; NID:g202100; PID:g202102
GENETICS
          #gene TNFR-2
          #introns 13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; 353/1
CLASSIFICATION #superfamily tumor necrosis factor receptor type 1; NGF
          receptor repeat homology
KEYWORDS cytokine receptor
SUMMARY   #length 454 #molecular-weight 50030 #checksum 4267

Query Match   42.2%; Score 841; DB 2; Length 454;
Best Local Similarity   70.6%; Pred. No. 7.05e-164;
Matches   101; Conservative   23; Mismatches   19; Indels   0; Gaps   0;

Db   41 DSLCPQGKYVHSKNNSICCTKCHKGTYLVSDCPSPGRDTVCRECEKGTFTASQNYLRQCL 100
          |:|||||| |..:||||||||||||||||:.||| | || |||:|:|:||||:| |.||
Qy   41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db 101 SCKTCRKEMSQVEISPCQADKDTVCGCKENQFQRYLSETHFQCVDCSPCFNGTVTIPCKE 160

```
Qy   83  SCSKCRKEMGQVEISSCCTVDRDTVCGCRRNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142
         ||||| ||||||||||||||||||||||||||||||||||| :|||
Db  161  TQNTVCNCHAGFFLRESECVPCS 183
         || : ||||| | :|:| ||||||||||| :|:|:| :| |
Qy  143  KQNTVCTCHAGFFLRENECVSCA 165

RESULT  9

ENTRY   GOMST1          #type complete
TITLE           tumor necrosis factor receptor type 1 precursor - mouseALTERNATE_NAMES
ORGANISM        #formal_name Mus musculus #common_name house mouse
DATE            30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
                05-Sep-1997
ACCESSIONS      A38634; B40254; S16677; S19021; I54532
REFERENCE       A38634
#authors        Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice,
                G.C.; Wong, G.H.W.; Chen, E.Y.; Goeddel, D.V.
#journal        Proc. Natl. Acad. Sci. U.S.A. (1991) 88:2830-2834
#title          Cloning and expression of cDNAs for two distinct murine tumor
                necrosis factor receptors demonstrate one receptor is
                species specific.
#cross-references MUID:91187885
##accession     A38634
##molecule_type mRNA
##residues      1-454       ##label LEW
REFERENCE       A40254
#authors        Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan,
                C.I.; Copeland, N.G.; Jenkins, N.A.; Smith, C.A.
#journal        Mol. Cell. Biol. (1991) 11:3020-3026
#title          Molecular cloning and expression of the type 1 and type 2
                murine tumor necrosis factor receptors for tumor necrosis factor.
#cross-references MUID:91246168
##accession     B40254
##molecule_type mRNA
##residues      1-454       ##label GO2
REFERENCE       S16677
#authors        Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissonerghis,
                A.M.; Gray, P.W.; Feldmann, M.; Foxwell, B.M.J.
#journal        Eur. J. Immunol. (1991) 21:1649-1656
#title          Cloning, expression and cross-linking analysis of the murine
                p55 tumor necrosis factor receptor.
#cross-references MUID:91285014
##accession     S16677
##molecule_type mRNA
##residues      1-454       ##label BAR
REFERENCE       S19021
#authors        Rothe, J.; Brockhaus, M.; Gentz, R.; Lesslauer, W.
#journal        Immunogenetics (1991) 34:338-340
#title          Molecular cloning and expression of the mouse Tnf receptor
                type b.
#cross-references MUID:92039815
##accession     S19021
##molecule_type mRNA
##residues      1-454       ##label ROT
REFERENCE       I54532
#authors        Bebo, B.F.
#journal        Immunogenetics (1994) 39:450-451
#title          Nucleotide sequence of the TNF type I receptor from a mouse
                endothelioma cell line.
#cross-references MUID:94245292
##accession     I54532
##status        translated from GB/EMBL/DDBJ
##molecule_type mRNA
##residues      1-454       ##label RES
##cross-references GB:L26349; NID:g430732; PID:g430733
COMMENT         This protein is one of two distantly related receptors for both
                TNF-alpha (cachectin) and TNF-beta (lymphotoxin).
```

```
CLASSIFICATION  #superfamily tumor necrosis factor receptor type 1; NGF
                receptor repeat homology; receptor; transmembrane protein
                duplication; glycoprotein; receptor; transmembrane protein
KEYWORDS        #product tumor necrosis factor receptor type 1 #status
FEATURE
      1-29      #domain signal sequence #status predicted #label MAT\
     30-454     #product #label MAT\
                predicted #label MAT\
     30-212     #domain extracellular #status predicted #label EXT\
     44-82      #domain NGF receptor repeat homology #label NG1\
     84-126     #domain NGF receptor repeat homology #label NG2\
    127-167     #domain NGF receptor repeat homology #label NG3\
    168-204     #domain NGF receptor repeat homology #label NG4\
    213-235     #domain transmembrane #status predicted #label MEM\
    236-454     #domain intracellular #status predicted #label INT\
     54,151,202 #binding_site carbohydrate (Asn) (covalent) #status
                predicted
SUMMARY         #length 454   #molecular-weight 50129   #checksum 4839

Db   41  DSLCPGGKIVYHSKNNSICCTKCHKGTYLVSDCPSPGRDTVCRECEKGTFTASQNYIRQCL 100
         |:||:|||||||||||||::| |||||||||||||||||:||||||||:||||::||
Qy   23  DSVCPGGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENLRHCL 82
Db  101  SCKTCRKEMSQVEISPCQADKDTVCGCKENQFQRILSETHFQCVDCSPCFNGTVTIPCKE 160
         |:|| |||||||||||| ||||||:|||||| ||||||||||||||| :|||:|||:|
Qy   23  SCSKCRKEMGQVEISSCCTVDRDTVCGCRRNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142
Db  161  TQNTVCNCHAGFFLRESECVPCS 183
         || : ||||| | :|:| |||||||||| :|:|:| :| |
Qy  143  KQNTVCTCHAGFFLRENECVSCA 165
```

```
RESULT  10

ENTRY   GQRTT1          #type complete
TITLE           tumor necrosis factor receptor type 1 precursor - ratCONTAINS
ORGANISM        #formal_name Rattus norvegicus #common_name Norway rat
DATE            30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change
                05-Sep-1997
ACCESSIONS      B36555
REFERENCE       A36555
#authors        Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.;
                Pfizenmaier, K.; Lantz, M.; Olsson, I.; Hauptmann, R.;
                Stratowa, C.; Adolf, G.R.
#journal        DNA Cell Biol. (1990) 9:705-715
#title          Molecular cloning and expression of human and rat tumor
                necrosis factor receptor chain (p60) and its soluble
                derivative, tumor necrosis factor-binding protein.
#cross-references MUID:91090841
##accession     B36555
##molecule_type mRNA
##residues      1-461       ##label HIM
##cross-references GB:M63122; NID:g207361; PID:g207362
COMMENT         This protein is one of two known receptors for both TNF-alpha
                (cachectin) and TNF-beta (lymphotoxin).
CLASSIFICATION  #superfamily tumor necrosis factor receptor type 1; NGF
                receptor repeat homology
KEYWORDS        #product tumor necrosis factor receptor type 1; NGF
                duplication; glycoprotein; receptor; transmembrane protein
FEATURE
      1-29      #domain signal sequence #status predicted #label SIG\
     30-461     #product tumor necrosis factor receptor type 1 #status
                predicted #label MAT\
     30-211     #domain extracellular #status predicted #label EXT\
     44-82      #domain NGF receptor repeat homology #label NG1\
     84-126     #domain NGF receptor repeat homology #label NG2\
    127-167     #domain NGF receptor repeat homology #label NG3\
    168-204     #domain NGF receptor repeat homology #label NG4\
    212-234     #domain tumor necrosis factor binding protein #status
    30-201      #product tumor necrosis factor receptor type 1 #status
    30-211      #domain extracellular #status predicted #label EXT\
     44-82      #domain NGF receptor repeat homology #label NG1\
     84-126     #domain NGF receptor repeat homology #label NG2\
    127-167     #domain NGF receptor repeat homology #label NG3\
    168-204     #domain NGF receptor repeat homology #label NG4\
    212-234     #domain transmembrane #status predicted #label MEM\
```

```
SUMMARY
235-461        #domain intracellular #status predicted #label INT\
54,151,201     #binding_site carbohydrate (Asn) (covalent) #status
               predicted

Query Match     #length 461 #molecular-weight 50969 #checksum 1617
Best Local Similarity 40.6%;    Score 809; DB 1; Length 461;
Matches  98;  Conservative  21;  Mismatches  24;  Indels  0;  Gaps  0;

Db  41  DNLCPQGKYAHPKNNSICCTKCHKGTYLVSDCPSPGQEVTCVEVGDKGTFTASQNHVRQCL 100
        |:::|||||| ||||||||||||||||:||||||| ||||:|||:||::|:||:|
Qy  23  DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECEGSGSFTASENLRHCL 82

Db 101  SCKTCRKEMFQVEISPCKADMDTVCGCKKNQFQRYLSETHFQCVDCSPCFNGTVTIPCKE 160
        || |||||| ||||:::||||||||:||||||||||:||||  :||||| ::||
Qy  83  SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVVHLSCQE 142

Db 161  KQNTVCNCHAGFFLSGNECTPCS 183
        ||||| |||||||| ||| :|:
Qy 143  KQNTVCTCHAGFFLRENECVSCA 165


RESULT  11
ENTRY   TTHUAP      #type complete
TITLE   glycoprotein hormones alpha chain precursor - human ALTERNATE_NAMES cho
          alpha chain; follitropin alpha chain; interstitial
          cell-stimulating hormone alpha chain; luteinizing hormone
          alpha chain; lutropin alpha chain; thyroid-stimulating
          hormone alpha chain; thyrotropin alpha chain
          #formal_name Homo sapiens #common_name man
ORGANISM
DATE    13-Jul-1981 #sequence_revision 23-Oct-1981 #text_change
        05-Sep-1997
ACCESSIONS A93213; A92832; B92303; A90751; A90179; A91461; A92184;
           A94552; B92181; A92141; I58200; A01481
REFERENCE
   #authors  Fiddes, J.C.; Goodman, H.M.
   #journal  Nature (1979) 281:351-356
   #title    Isolation, cloning and sequence analysis of the cDNA for the
             alpha-subunit of human chorionic gonadotropin.
   #cross-references MUID:80011660
   #accession A93213
     ##molecule_type mRNA
     ##residues 1-116 ##label FID
   #cross-references GB:V00518; NID:g31868; PID:g31869
REFERENCE
   #authors  Fiddes, J.C.; Goodman, H.M.
   #journal  J. Mol. Appl. Genet. (1981) 1:3-18
   #title    The gene encoding the common alpha subunit of the four human
             glycoprotein hormones.
   #cross-references MUID:82267643
   #accession A92832
     ##molecule_type DNA
     ##residues 1-98 #label FI2
   #cross-references GB:V00484
REFERENCE
   #authors  Birken, S.; Fetherston, J.; Canfield, R.; Bolme, I.
   #journal  J. Biol. Chem. (1981) 256:1816-1823
   #title    The amino acid sequences of the prepeptides contained in the
             alpha and beta subunits of human choriogonadotropin.
   #cross-references MUID:81117268
   #accession B92303
     ##molecule_type protein
     ##residues 1-24 ##label BIR
   #note     restriction endonuclease evidence indicates that a
             single gene codes for the alpha chain common to the
             four dimeric hormones: thyrotropin, lutropin,
             follitropin, and choriogonadotropin
   ##note    previously the mature alpha chain (residues 25-116) was
             isolated from each of the hormones and its sequence
             was determined, as documented below
REFERENCE
   #authors  Sairam, M.R.; Li, C.H.
```

```
   #journal  Can. J. Biochem. (1977) 55:755-760
   #title    Human pituitary thyrotropin. The primary structure of the
             alpha and beta subunits.
   #cross-references MUID:77243687
   #accession A90751
     ##molecule_type protein
     ##residues 28-107,'SC',110-116 ##label SAI
REFERENCE
   #authors  Sairam, M.R.; Papkoff, H.; Li, C.H.
   #journal  Biochem. Biophys. Res. Commun. (1972) 48:530-537
   #title    Human pituitary interstitial cell stimulating hormone:
             primary structure of the alpha subunit.
   #cross-references MUID:72242988
   #accession A90179
     ##molecule_type protein
     ##residues 28-107,'SC',110-116 ##label SA2
REFERENCE
   #authors  Keutmann, H.T.; Williams, R.M.; Bishop, W.H.; Ryan, R.J.
   #journal  Fed. Proc. (1978) 37:1828
   #title    Structure of human luteinizing hormone.
   #accession A91461
     ##molecule_type protein
     ##residues 28-116 ##label KEU
REFERENCE
   #authors  Rathnam, P.; Saxena, B.B.
   #journal  J. Biol. Chem. (1975) 250:6735-6746
   #title    Primary amino acid sequence of follicle-stimulating hormone
             from human pituitary glands.
   #cross-references MUID:76005558
   #accession A92184
     ##molecule_type protein
     ##residues 25-28,'E',30-116 ##label RAT
REFERENCE
   #authors  Shome, B.; Parlow, A.F.
   #submission submitted to the Atlas, April 1975
   #accession A94552
     ##molecule_type protein
     ##residues 28-116 ##label SHO
REFERENCE
   #authors  Morgan, F.J.; Birken, S.; Canfield, R.E.
   #journal  J. Biol. Chem. (1975) 250:5247-5258
   #title    The amino acid sequence of human chorionic gonadotropin. The
             alpha subunit and beta subunit.
   #cross-references MUID:75211304
   #accession B92181
     ##molecule_type protein
     ##residues 25-116 ##label MOR
   #note     heterogeneity is found at the amino end. Approximately
             10 and 30% of the chains lack residues 1-2 and 1-3,
             respectively
REFERENCE
   #authors  Bellisario, R.; Carlsen, R.B.; Bahl, O.P.
   #journal  J. Biol. Chem. (1973) 248:6796-6809
   #title    Human chorionic gonadotropin. Linear amino acid sequence of
             the alpha subunit.
   #cross-references MUID:74011266
   #accession A92141
     ##molecule_type protein
     ##residues 25-116 ##label BEL
REFERENCE
   #authors  Shome, B.; Parlow, A.F.
   #journal  J. Clin. Endocrinol. Metab. (1974) 39:199-202
   #title    Human follicle stimulating hormone (hFSH): first proposal for
             the amino acid sequence of the alpha-subunit (hFSHalpha)
             and first demonstration of its identity with the
             alpha-subunit of human luteinizing hormone (hLRalpha).
   #accession A92760
     ##molecule_type protein
     ##residues 25-116
REFERENCE
   #authors  Fujiki, Y.; Rathnam, P.; Saxena, B.B.
   #journal  Biochim. Biophys. Acta (1980) 624:428-435
   #title    Studies on the disulfide bonds in human pituitary
             follicle-stimulating hormone.
   #cross-references MUID:74262937
   #contents annotation
```

COMMENT
  #cross-references MUID:81021713
  #contents annotation: preliminary disulfide bonds
REFERENCE A44674
  #authors Lapthorn, A.J.; Harris, D.C.; Littlejohn, A.; Lustbader, J.W.; Canfield, R.E.; Machin, K.J.; Morgan, F.J.; Isaacs, N.W.
  #journal Nature (1994) 369:455-461
  #title Crystal structure of human chorionic gonadotropin.
  #contents annotation: X-ray crystallography, 3.0 angstroms; correction of disulfide bonds
REFERENCE I58200
  #authors Miyoshi, I.; Kasai, N.; Hayashizaki, Y.
  #journal Nippon Rinsho (1994) 52:940-947
  #title [Structure and regulation of human thyroid-stimulating hormone (TSH) gene].
  #cross-references MUID:94254248
  #accession I58200
  ##status preliminary; translated from GB/EMBL/DDBJ
  ##molecule_type DNA
  ##residues 1-116 ##label RES
  #cross-references GB:S70585; NID:g546844; PID:g546845
GENETICS
  #gene GDB:CGA
  #cross-references GDB:119774; OMIM:118850
  #map_position 6q14-6q21
  #introns 30/1; 91/3
CLASSIFICATION #superfamily glycoprotein hormones alpha chain
KEYWORDS glycoprotein; heterodimer; hormone; pituitary
FEATURE
  1-24 #domain signal sequence experimental #label SIG\
  25-116 #product glycoprotein hormones alpha chain #status experimental #label MAT\
  31-55,34-84,52-106, #disulfide_bonds experimental\
  56-108,83-111
  76,102 #binding_site carbohydrate (Asn) (covalent) #status experimental
SUMMARY #length 116 #molecular-weight 13075 #checksum 1664

Query Match 33.5%; Score 667; DB 1; Length 116;
Best Local Similarity 93.5%; Pred. No. 1.7e-123;
Matches 86; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Db   25 APDVQDCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCC 84
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   165 AGAAPGCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCC 224

Db   85 VAKSYNRVTVMGGFKVENHTACHCSTCYYHKS 116
          ||||||||||||||||||||:|||||||||||
Qy   225 VAKSYNRVTVMGGFKVENHTGCHCSTCYYHKS 256

RESULT 12
ENTRY 1HRPA #type complete
TITLE chorionic gonadotropin, chain A - humanORGANISM
  #note placental origin, urinary extracted
REFERENCE A52806
  #authors Lapthorn, A.J.; Harris, D.C.; Isaacs, N.W.
  #submission submitted to the Brookhaven Protein Data Bank, August 1994
  #cross-references PDB:1HRP
REFERENCE TN022062
  #authors Lapthorn, A.J.; Harris, D.C.; Littlejohn, A.; Lustbader, J.W.; Canfield, R.E.; Machin, K.J.; Morgan, F.J.; Isaacs, N.W.
  #journal Nature (1994) 369:455
  #title Crystal structure of human chorionic gonadotropin.
REFERENCE TN022063
  #authors Harris, D.C.; Machin, K.J.; Evin, G.M.; Morgan, F.J.; Isaacs, N.W.
  #journal J. Biol. Chem. (1989) 264:6705
  #title Preliminary x-ray diffraction analysis of human chorionic gonadotropin.
COMMENT Resolution: 3.0 angstroms

COMMENT Determination: X-ray diffraction
KEYWORDS hormone
FEATURE
  4-28 #disulfide_bonds\
  7-57 #disulfide_bonds\
  25-79 #disulfide_bonds\
  29-81 #disulfide_bonds\
  56-84 #disulfide_bonds\
SUMMARY #length 86 #molecular-weight 9572 #checksum 1371

Query Match 32.4%; Score 647; DB 5; Length 86;
Best Local Similarity 95.3%; Pred. No. 6.89e-119;
Matches 82; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db   1 TQDCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAK 60
          :|||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   168 APGCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAK 227

Db   61 SYNRVTVMGGFKVENHTACHCSTCYY 86
          ||||||||||||||||||:|||||||
Qy   228 SYNRVTVMGGFKVENHTGCHCSTCYY 253

RESULT 13
ENTRY 1XULA #type complete
ORGANISM chorionic gonadotropin, chain A - humanPDB_TITLE
TITLE receptor complexed with human chorionic gonadotropin
  #formal_name Homo sapiens #common_name man
REFERENCE A66957
  #authors Jiang, X.; Dreano, M.; Buckler, D.R.; Cheng, S.; Ythier, A.; Wu, H.; Hendrickson, W.A.; El Tayar, N.
  #journal Structure (London) (1996) 3:1341
  #title Structural predictions for the ligand-binding region of glycoprotein hormone receptors and the nature of hormone-receptor interactions structure.
REFERENCE TN032624
  #authors Wu, H.; Lustbader, J.W.; Liu, Y.; Canfield, R.E.; Hendrickson, W.A.
  #journal Structure (London) (1994) 2:545
  #title Structure of human chorionic gonadotropin at 2.6 a resolution from mad analysis of the selenomethionyl protein.
REFERENCE TN032623
  #authors Jiang, X.; Dreano, M.; Buckler, D.R.; Cheng, S.; Ythier, A.; Wu, H.; Hendrickson, W.A.; El Tayar, N.
  #submission submitted to the Brookhaven Protein Data Bank, December 1996
  #cross-references PDB:1XUL
COMMENT Determination: theoretical model
COMMENT Resolution: not applicable
COMMENT complex: glycoprotein hormone receptor glycoprotein; hormone; phosphorylation; receptor
KEYWORDS
FEATURE
  37-41 #region helix (right hand alpha)\
  7-10,22-25 #region beta sheet\
  49-53,26-34 #region beta sheet\
  61-65,71-75 #region beta sheet\
  55-60,77-81 #region beta sheet\
  3-27 #disulfide_bonds\
  6-56 #disulfide_bonds\
  24-78 #disulfide_bonds\
  28-80 #disulfide_bonds\
  55-83 #disulfide_bonds\
SUMMARY #length 85 #molecular-weight 9471 #checksum 9656

Query Match 32.3%; Score 645; DB 5; Length 85;
Best Local Similarity 98.8%; Pred. No. 1.99e-118;
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db   3 CPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSYN 62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   171 CPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSYN 230

Db   63 RVTVMGGFKVENHTACHCSTCYY 85

```
Qy    231  RVTVMGGFKVENHTGCHCSTCYY 253
           |||||||||||||:|||||||:|
Db     35  CPECKPRENKFFSRPGAPIYQCMGCCFSRAYPTPVRSKKTMLVQKNVTSESTCCVAKSLT 94
Matches    71; Conservative    4; Mismatches   10; Indels    0; Gaps    0;
Best Local Similarity 83.5%;   Pred. No. 6.48e-97;
Query Match                    Score 551; DB 2; Length 120;
SUMMARY         #length 120    #molecular-weight 13785   #checksum 5074
KEYWORDS        glycoprotein
CLASSIFICATION  #superfamily glycoprotein hormones alpha chain
           ##residues 1-120  ##label GOL
           ##molecule_type DNA
           ##status preliminary; not compared with conceptual translation
           #accession A39555
           #cross-references MUID:91321740
Qy         alpha-subunit gene.
           #title Molecular cloning of the rhesus glycoprotein hormone
           #journal DNA Cell Biol. (1991) 10:367-380
           #authors Golos, T.G.; Durning, M.; Fisher, J.M.
REFERENCE  A39555
ACCESSIONS A39555
DATE       13-Jan-1995
           08-Nov-1991 #sequence_revision 08-Nov-1991 #text_change
TITLE      glycoprotein hormones alpha chain precursor - rhesus macaqueORGANISM
ENTRY      A39555         #type complete

RESULT     15
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Qy    231  RVTVMGGFKVENHTGCHCSTCYY 253
           ||||||||||||||||||||||
Db     63  RVTVMGGFKVENHTACHCSTCYY 85
Qy    171  CPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSYN 230
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3  CPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSYN 62
Matches    82; Conservative    1; Mismatches    0; Indels    0; Gaps    0;
Best Local Similarity 98.8%;   Pred. No. 1.99e-118;
Query Match                    Score 645; DB 5; Length 85;
SUMMARY         #length 85    #molecular-weight 9471   #checksum 9656
           55-83    #disulfide_bonds\
           28-80    #disulfide_bonds/
           24-78    #disulfide_bonds\\
           6-56     #disulfide_bonds/
           3-27     #disulfide_bonds/
           29-35,48-54  #region beta sheet\
           4-11,21-28   #region beta sheet\
           36-43    #region helix (right hand alpha)\
FEATURE
KEYWORDS   Hormone
COMMENT    Determination: X-ray diffraction
COMMENT    Resolution: 2.6 angstroms
           protein.
           resolution from mad analysis of the selenomethionyl
           Structure of human chorionic gonadotropin at 2.6 angstroms
           #title Structure (1994) 2:545
           #journal
           Hendrickson, W.A.
           #authors Wu, H.; Lustbader, J.W.; Liu, Y.; Canfield, R.E.;
REFERENCE  TN020262
           #cross-references PDB:1HCN
           submitted to the Brookhaven Protein Data Bank, July 1994
           #submission
           Hendrickson, W.A.
           #authors Wu, H.; Lustbader, J.W.; Liu, Y.; Canfield, R.E.;
REFERENCE  A52587
TITLE      Human chorionic gonadotropin, chain A - humanORGANISM
ENTRY      1HCNA          #type complete

RESULT     14
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Qy    231  RVTVMGGFKVENHTGCHCSTCYY 253
           ||||||||||||||:|||||||:||
Db     95  RVMVMGSVRVENHTECHCSTCYY 119
           |||: :|||||| ||||||||||
Qy    171  CPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSYN 230
           |||| :|| |||| |||||| |||||||||||:|||||||||||||||||||||||||||
Db      3  CPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSYN 62
Qy    231  RVTVMGGFKVENHTGCHCSTCYY 255
Db     95  RVMVMGSVRVENHTECHCSTCYYHK 119
Qy    171  CPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSYN 230

Search completed: Wed May  6 08:50:40 1998
Job time : 39 secs.
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FT   DOMAIN          43    195       4 X TNFR-CYS.
FT   REPEAT          43     82       TNFR-CYS 1.
FT   REPEAT          83    125       TNFR-CYS 2.
FT   REPEAT         126    166       TNFR-CYS 3.
FT   REPEAT         167    195       TNFR-CYS 4.
FT   DOMAIN         362    447       DEATH DOMAIN.
FT   DISULFID        44     58       BY SIMILARITY.
FT   DISULFID        59     72       BY SIMILARITY.
FT   DISULFID        62     81       BY SIMILARITY.
FT   DISULFID        84     99       BY SIMILARITY.
FT   DISULFID       102    117       BY SIMILARITY.
FT   DISULFID       105    125       BY SIMILARITY.
FT   DISULFID       127    143       BY SIMILARITY.
FT   DISULFID       146    158       BY SIMILARITY.
FT   DISULFID       149    166       BY SIMILARITY.
FT   DISULFID       168    179       BY SIMILARITY.
FT   DISULFID       182    190       BY SIMILARITY.
FT   DISULFID       185    194       BY SIMILARITY.
FT   CARBOHYD        54     54       POTENTIAL.
FT   CARBOHYD        86     86       POTENTIAL.
FT   CARBOHYD       145    145       POTENTIAL.
FT   CARBOHYD       151    151       POTENTIAL.
SQ   SEQUENCE       461 AA;  50696 MW;  8E2C350A CRC32;
```

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RESULT 3

ID   TNR1_MOUSE     STANDARD;      PRT;    454 AA.
AC   P25118;
DT   01-MAY-1992 (REL. 22, CREATED)
DT   01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
GN   TNFR1 OR TNFR-1.
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91187885.
RA   LEWIS M., TARTAGLIA L.A., LEE A., BENNETT G.L., RICE G.C.,
RA   WONG G.H., CHEN E.Y., GODDEL D.V.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 88:2830-2834(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91246168.
RA   GOODWIN R.G., ANDERSON D., JERZY R., DAVIS T., BRANNAN C.I.,
RA   COPELAND N.G., JENKINS N.A., SMITH C.A.;
RL   MOL. CELL. BIOL. 11:3020-3026(1991).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91285014.
RA   BARRETT K., TAYLOR-FISHWICK D.A., COPE A.P., KISSONERGHIS A.M.,
RA   GRAY P.W., FELDMANN M., FOXWELL B.M.J.;
RL   EUR. J. IMMUNOL. 21:1649-1656(1991).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=SPLEEN;
```

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Qy   Query Match     48.2%;  Score 962;  DB 1;  Length 461;
     Best Local Similarity  69.8%;  Pred. No. 3.53e-226;
Matches   120;  Conservative  22;  Mismatches  26;  Indels  4;  Gaps  4;

Db    41 ESLCPQGKYSHPQNRSICCTKCHKGTYLHNDCLGPGLDTDCRECDNGTFTASENHLTQCL 100
         :|:||||||:|| ||||:|| |||||||:||:|||  ||| |||||||||||||||||| :||
Qy    23 DSVCPQGKYIHPQNNSICCTKCHRGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db   101 SCSKCRSEMSQVEISPCTVDRDTVCGCRKNQYRKYWSETLFQCLNCSLCPNGTVQLPCLE 160
         ||||| :|  :||| ||||||| ||||||||:||| |||:::|||:||||||||:||  ||
Qy    83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db   161 KQDTICNCHSGFFLRDKECVSCVYNCKNADCKNLCPATSETRNDEQDTGTTVL 212
         :|:|:|  |||||||:|::||:|||||||||||||:|| |  |||:||::|||
Qy   143 KQNTVCTCHAGFFLRENECVSCAG-AAPGCPE-C-TLQENPF-FSQPGAPIL 190
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DR   EMBL; M60468; G199826; -.
DR   EMBL; M59377; G202097; -.
DR   EMBL; X59238; G53579; -.
DR   EMBL; X57796; G54849; -.
DR   EMBL; L26349; G430733; -.
DR   EMBL; M76656; G2021021; -.
DR   EMBL; M88067; G2021022; JOINED.
DR   EMBL; M76655; G2021022; JOINED.
DR   PIR; A38634; GOMSTI.
DR   PIR; S16677; S16677.
DR   PIR; S19021; S19021.
DR   HSSP; P19438; ITNR.
DR   MGD; MGI:98781; TNFR1.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS00050; TNFR_NGFR_2; 3.
DR   PROSITE; PS00017; DEATH_DOMAIN; 1.
KW   RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS.
FT   SIGNAL           1     21
FT   CHAIN           22    454       TUMOR NECROSIS FACTOR RECEPTOR 1.
FT   DOMAIN          22    212       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM       213    235       POTENTIAL.
FT   DOMAIN         236    454       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN          43    196       4 X TNFR-CYS.
FT   REPEAT          43     82       TNFR-CYS 1.
FT   REPEAT          83    125       TNFR-CYS 2.
FT   REPEAT         126    166       TNFR-CYS 3.
FT   REPEAT         167    196       TNFR-CYS 4.
FT   DOMAIN         356    441       DEATH DOMAIN.
FT   DISULFID        44     58       BY SIMILARITY.
FT   DISULFID        59     72       BY SIMILARITY.
FT   DISULFID        62     81       BY SIMILARITY.
FT   DISULFID        84     99       BY SIMILARITY.
FT   DISULFID       102    117       BY SIMILARITY.
FT   DISULFID       105    125       BY SIMILARITY.
FT   DISULFID       127    143       BY SIMILARITY.
FT   DISULFID       146    158       BY SIMILARITY.
FT   DISULFID       149    166       BY SIMILARITY.
FT   DISULFID       168    179       BY SIMILARITY.
FT   DISULFID       182    191       BY SIMILARITY.
FT   DISULFID       185    195       BY SIMILARITY.
FT   CARBOHYD        54     54       POTENTIAL.
FT   CARBOHYD       202    202       POTENTIAL.
FT   CONFLICT       394    394       R -> G (IN REF. 6).
```

```
RX   MEDLINE; 92039815.
RA   ROTHE J.G., BROCKHAUS M., GENTZ R., LESSLAUER W.;
RL   IMMUNOGENETICS 34:338-340(1991).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 94245292.
RA   BEBO B.F., LINTHICUM D.S.;
RL   IMMUNOGENETICS 39:450-451(1994).
RN   [6]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 93156721.
RA   ROTHE J., BLUETHMANN H., GENTZ R., LESSLAUER W., STEINMETZ M.;
RL   MOL. IMMUNOL. 30:165-175(1993).
CC   -!-  FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC        RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC        AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC        PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC        SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC        PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC   -!-  SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC        HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC        PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC        WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC        PROTEINS SUCH AS TRAF2, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC        TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC        ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC        NF-KAPPA B SIGNALING (BY SIMILARITY).
CC   -!-  SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!-  SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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RESULT 4

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ID   TNR1_RAT     STANDARD;     PRT;     461 AA.
AC   P22934;
DT   01-AUG-1991 (REL. 19, CREATED)
DT   01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
GN   TNFR1 OR TNFR-1.
OS   RATTUS NORVEGICUS (RAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91090841.
RA   HIMMLER A., MAURER-FOGY I., KRONKE M., SCHEURICH P., PFIZENMAIER K.,
RA   LANTZ M., OLSSON I., HAUPTMANN R., STRATOWA C., ADOLF G.R.;
RL   DNA CELL BIOL. 9:705-715(1990).
-!-  FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
     RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
     AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
     PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
     SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
     PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
-!-  SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
     HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
     PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
     WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
     PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
     TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
     ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
     NF-KAPPA B SIGNALING (BY SIMILARITY).
-!-  SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!-  SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR   EMBL; M63122; G207362; -.
DR   PIR; B36555; B36555.
DR   HSSP; P19438; 1TNR.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS00050; TNFR_NGFR_2; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS.
FT   SIGNAL         1     21
FT   CHAIN         22    455     TUMOR NECROSIS FACTOR RECEPTOR 1.
FT   DOMAIN        22    211     EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     212    234
FT   DOMAIN       235    461     CYTOPLASMIC (POTENTIAL).
FT   DOMAIN        43    196     4 X TNR-CYS.
FT   REPEAT        43     82     TNFR-CYS 1.
FT   REPEAT        83    125     TNFR-CYS 2.
FT   REPEAT       126    166     TNFR-CYS 3.
FT   REPEAT       167    196     TNFR-CYS 4.
FT   DOMAIN       363    448     DEATH DOMAIN.
FT   DISULFID      44     58     BY SIMILARITY.
FT   DISULFID      59     72     BY SIMILARITY.
FT   DISULFID      62     81     BY SIMILARITY.
```

```
Query Match          42.2%;   Score 841; DB 1; Length 454;
Best Local Similarity 70.6%;  Pred. No. 8.77e-193;
Matches 101;  Conservative 23;  Mismatches 19;  Indels 0;  Gaps 0;

Qy   41 DSLCPQGKYVHSKNNSICCTKCHKGTYLVSDCPSPGRDTVCRECEKGTFTASQNYLRQCL 100
         |:||||||||:||||| |||||||||||||| || |:|||||||||||||| || ||:||
Db  101 SCKTCRKEMSQVEISPCQADKDTVCGCKENQFQRYLSETHFQCCVDCSPCFNGTVTIPCKE 160

Qy   23 DSVCPQGKYIHPQNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL  82
         ||:|||||| |::||| |||||||||:| | :||| ||| |::|  ||:||| ::|:||
Db   83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCCE 142

Db  161 TQNTVCNCHAGFFLRESECVPCS 183
         |||||| |||||||||::|| |
Qy  143 KQNTVCTCHAGFFLRENECVSCA 165
```

RESULT 5

```
ID   GLHA_HUMAN    STANDARD;    PRT;    116 AA.
AC   P01215;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR.
GN   CGA.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 80011660.
RA   FIDDES J.C., GOODMAN H.M.;
RL   NATURE 281:351-356(1979).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 94254248.
RA   MIYOSHI I., KASAI N., HAYASHIZAKI Y.;
RL   NIPPON RINSHO 52:940-947(1994).
RN   [3]
RP   SEQUENCE OF 1-98 FROM N.A.
RX   MEDLINE; 82267643.
RA   FIDDES J.C., GOODMAN H.M.;
RL   J. MOL. APPL. GENET. 1:3-18(1981).
RN   [4]
RP   SEQUENCE OF 1-24.
RX   MEDLINE; 81117268.
RA   BIRKEN S., FETHERSTON J., CANFIELD R.E., BOIME I.;
RL   J. BIOL. CHEM. 256:1816-1823(1981).
RN   [5]
RP   SEQUENCE OF 28-116.
RX   MEDLINE; 77243687.
RA   SAIRAM M.R., LI C.H.;
RL   CAN. J. BIOCHEM. 55:755-760(1977).
RN   [6]
RP   SEQUENCE OF 28-116.
RX   MEDLINE; 72242988.
RA   SAIRAM M.R., PAPKOFF H., LI C.H.;
RL   BIOCHEM. BIOPHYS. RES. COMMUN. 48:530-537(1972).
RN   [7]
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Query Match          40.6%;   Score 809; DB 1; Length 461;
Best Local Similarity 68.5%;  Pred. No. 5.45e-184;
Matches 98;  Conservative 21;  Mismatches 24;  Indels 0;  Gaps 0;
SQ   SEQUENCE 461 AA; 50969 MW; 82F68B08 CRC32;

Qy   41 DNLCPQGKYAHRKNNSICCTKCHKGTYLVSDCPSPGQETVCEVCDKGTFTASQNHVRQCL 100
         |:|||||||| :||||| |||||||||||||| || :|:||| ||:|||||||:|:|||
Db  101 SCKTCRKEMFQVEISPCKADMDTVCGCKKNQFQRYLSETHFQCCVDCSPCFNGTVTIPCKE 160

Qy   23 DSVCPQGKYIHPQNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL  82
         ||:||||||:|::||| |||||||||:| |:|| ||| ::||: | |:||| ::|::|
Db   83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCCE 142

Db  161 KQNTVCNCHAGFFLSGNECTPCS 183
         |||||| |||||||::|:| |
Qy  143 KQNTVCTCHAGFFLRENECVSCA 165
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RP   SEQUENCE, AND REVISIONS.
RA   KEUTMANN H.T., WILLIAMS R.M., BISHOP W.H., RYAN R.J.;
RL   FED. PROC. 37:1828-1828(1978).
RN   [8]
RP   SEQUENCE OF 25-116.
RX   MEDLINE; 7605558.
RA   MORGAN F.J., BIRKEN S., CANFIELD R.E.;
RL   J. BIOL. CHEM. 250:5247-5258(1975).
RN   [9]
RP   SEQUENCE OF 25-116.
RA   RATHNAM P., SAXENA B.B.;
RL   J. BIOL. CHEM. 250:6735-6746(1975).
RN   [10]
RP   SEQUENCE OF 28-116.
RX   MEDLINE; 74262937.
RA   SHOME B., PARLOW A.F.;
RL   J. CLIN. ENDOCRINOL. METAB. 39:199-202(1974).
RN   [11]
RP   SEQUENCE OF 25-116.
RX   MEDLINE; 7601266.
RA   BELLISARIO R., CARLSEN R.B., BAHL O.P.;
RL   J. BIOL. CHEM. 248:6796-6809(1973).
RN   [12]
RP   PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.
RX   MEDLINE; 81021713.
RA   FUJIKI Y., RATHNAM P., SAXENA B.B.;
RL   BIOCHIM. BIOPHYS. ACTA 624:428-435(1991).
RN   [13]
RP   PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.
RX   MEDLINE; 81006887.
RA   MORGAN F.J., BAHL O.P.;
RL   MISE T.,
RN   [14]
RP   STRUCTURE OF CARBOHYDRATES.
RX   MEDLINE; 9112088.
RA   WEISSHAAR G., HIYAMA J., RENWICK A.G.C., NIMTZ M.;
RL   EUR. J. BIOCHEM. 195:257-268(1991).
RN   [15]
RP   X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RX   MEDLINE; 94261179.
RA   LAPTHORN A.J., HARRIS D.C., LITTLEJOHN A., LUSTBADER J.W.,
RA   CANFIELD R.E., MACHIN K.J., MORGAN F.J., ISAACS N.W.;
RL   NATURE 369:455-461(1994).
RN   [16]
RP   STRUCTURE BY NMR.
RX   MEDLINE; 97054614.
RA   DE BEER T., VAN ZUYLEN C.W.E.M., LEEFLANG B.R., HARD K., BOELENS R.,
RA   KAPTEIN R., KAMERLING J.P., VLIEGENTHART J.F.G.;
RL   EUR. J. BIOCHEM. 241:229-242(1996).
-!-  SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC   CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC   LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
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FT   DISULFID     31     55
FT   DISULFID     34     84
FT   DISULFID     52    106
FT   DISULFID     56    108
FT   DISULFID     83    111
FT   CARBOHYD     63     63
FT   CARBOHYD     76     76
FT   CONFLICT    102    102
FT   CONFLICT     29     29       Q -> E (IN REF. 8).
FT   CONFLICT    108    109       CS -> SC (IN REF. 5 AND 6).
SQ   SEQUENCE   116 AA;  13075 MW;  3BA19E2F CRC32;

Query Match          33.5%;   Score 667;  DB 1;  Length 116;
Best Local Similarity 93.5%;
Matches   86;  Conservative   1;  Pred. No. 3.28e-145;  Indels   5;  Gaps   0;

Db    25  APDVQDCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCC  84
          ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   165  AGAAPGCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCC 224

Db    85  VAKSYNRVTVMGGFKVENHTACHCSTCYYHKS 116
          |||||||||||||||||||| ||||||||||||
Qy   225  VAKSYNRVTVMGGFKVENHTGCHCSTCYYHKS 256
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RESULT 6
ID   GLHA_MACMU    STANDARD;    PRT;    120 AA.
AC   P22762;
DT   01-AUG-1991 (REL. 19, CREATED)
DT   01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR.
GN   CGA.
OS   MACACA MULATTA (RHESUS MACAQUE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91321740.
RA   GOLOS T.G., DURNING M., FISHER J.M.;
RL   DNA CELL BIOL. 10:367-380(1991).
-!-  SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC   CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC   LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   PIR; A39555; A39555.
DR   HSSP; P01215; 1HCN.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL        1     24       BY SIMILARITY.
FT   CHAIN        25    120       GLYCOPROTEIN HORMONES ALPHA CHAIN.
FT   DISULFID     35     59       BY SIMILARITY.
FT   DISULFID     38     88       BY SIMILARITY.
FT   DISULFID     56    110       BY SIMILARITY.
FT   DISULFID     60    112       BY SIMILARITY.
FT   DISULFID     87    115       BY SIMILARITY.
FT   CARBOHYD     67     67       BY SIMILARITY.
FT   CARBOHYD     80     80       BY SIMILARITY.
SQ   SEQUENCE   120 AA;  13785 MW;  85E1F974 CRC32;

Query Match          27.6%;   Score 551;  DB 1;  Length 120;
Best Local Similarity 83.5%;
Matches   71;  Conservative   4;  Mismatches  10;  Indels   0;  Gaps   0;

Db    35  CPECKPRENKFESKPGAPIYQCMGCCFSRAYPPPVRSKKTMLVQKNVTSESTCCVAKSLT  94
          || : |||||||||||||  ||||| |||||||::|||||||||||||||||||:|||||
Qy   171  CPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSYN 230

Db    95  RVNMVGSVRVENHTECHCSTCYYHK 119
          :|| ||| |||||||| |||||||||
Qy   231  RVTVMGGFKVENHTGCHCSTCYYHK 255
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RESULT 7

ID   GLHA_BOVIN   STANDARD;   PRT;   120 AA.
AC   P01217;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   23-OCT-1986 (REL. 02, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR.
GN   CGA.
OS   BOS TAURUS (BOVINE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; ARTIODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 84041490.
RA   GOODWIN R.G., MONCMAN C.L., ROTTMAN F.M., NILSON J.H.;
RL   NUCLEIC ACIDS RES. 11:6873-6882(1983).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 84024633.
RA   ERWIN C., CROYLE M.L., DONELSON J., MAURER R.;
RL   BIOCHEMISTRY 22:4856-4860(1983).
RN   [3]
RP   SEQUENCE OF 8-133 FROM N.A.
RX   MEDLINE; 83161058.
RA   NILSON J.H., THOMASON A.R., CSERBAK M.T., MONCMAN C.L., WOYCHIK R.P.;
RL   J. BIOL. CHEM. 258:4679-4682(1983).
RN   [4]
RP   SEQUENCE OF 25-120.
RX   MEDLINE; 71111428.
RA   LIAO T.-H., PIERCE J.G.;
RL   J. BIOL. CHEM. 246:850-865(1971).
RN   [5]
RP   PRELIMINARY PARTIAL SEQUENCE.
RX   MEDLINE; 71111429.
RA   PIERCE J.G., LIAO T.-H., CARLSEN R.B., REIMO T.;
RL   J. BIOL. CHEM. 246:866-872(1971).
RN   [6]
RP   SEQUENCE OF 80-91 AND 100-120.
RX   MEDLINE; 72012932.
RA   MAGHUIN-ROGISTER G., HENNEN G.P.;
RL   EUR. J. BIOCHEM. 21:489-497(1971).
RN   [7]
RP   PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.
RX   MEDLINE; 74307752.
RA   CORNELL J.S., PIERCE J.G.;
RL   J. BIOL. CHEM. 249:4166-4174(1974).
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC   CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC   LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   EMBL; X00003; E274391; -.
DR   EMBL; X00004; E274391; JOINED.
DR   EMBL; X00050; G607; -.
DR   PIR; A01483; TTBOA.
DR   PIR; A05132; A05132.
DR   HSSP; P01215; 1HCN.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL   1   24
FT   CHAIN   25   120   GLYCOPROTEIN HORMONES ALPHA CHAIN.
FT   CONFLICT   35   59   BY SIMILARITY.
FT   DISULFID   38   88   BY SIMILARITY.
FT   DISULFID   56   110   BY SIMILARITY.
FT   DISULFID   60   112   BY SIMILARITY.
FT   DISULFID   87   115   BY SIMILARITY.
FT   CARBOHYD   80   80   BY SIMILARITY.
FT   CARBOHYD   106   106
FT   CONFLICT   13   13   A -> T (IN REF. 2).
FT   CONFLICT   37   37   E -> Q (IN REF. 4).
FT   CONFLICT   52   52   P -> A (IN REF. 2).
FT   CONFLICT   84   87   EATC -> A2CT (IN REF. 6).
SQ   SEQUENCE   120 AA; 13616 MW; 99C153C5 CRC32;

RESULT 8

ID   GLHA_SHEEP   STANDARD;   PRT;   120 AA.
AC   P01218;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR.
GN   CGA.
OS   OVIS ARIES (SHEEP).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; ARTIODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 90098887.
RA   BELLO P.A., MOUNTFORD P.S., BRANDON M.R., ADAMS T.E.;
RL   NUCLEIC ACIDS RES. 17:10494-10494(1989).
RN   [2]
RP   SEQUENCE OF 25-120.
RX   MEDLINE; 72211144.
RA   LIU W.-K., NAHM H.S., SWEENEY C.M., LAMKIN W.M., BAKER H.N.,
RA   WARD D.N.;
RL   J. BIOL. CHEM. 247:4351-4364(1972).
RN   [3]
RP   SEQUENCE OF 25-120.
RX   MEDLINE; 73190034.
RA   SAIRAM M.R., PAPKOFF H., LI C.H.;
RL   ARCH. BIOCHEM. BIOPHYS. 153:554-571(1972).
RN   [4]
RP   SEQUENCE OF 25-120.
RX   MEDLINE; 82113052.
RA   SAIRAM M.R.;
RL   BIOCHEM. J. 197:535-539(1981).
RN   [5]
RP   PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.
RA   CHUNG D., SAIRAM M.R., LI C.H.;
RL   ARCH. BIOCHEM. BIOPHYS. 159:678-682(1973).
RN   [6]
RP   STRUCTURE OF CARBOHYDRATES.
RA   WEISSHAAR G., HIYAMA J., RENWICK A.G.C.;
RL   EUR. J. BIOCHEM. 192:741-751(1990).
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91006170.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC   CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC   LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   EMBL; X16977; G1366; -.
DR   PIR; A01483; TTBOA.
DR   PIR; A01484; UTSHA.
DR   PIR; S06935; S06935.
DR   PIR; S13200; S13200.
DR   HSSP; P01215; 1HCN.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL   1   24
FT   CHAIN   25   120   GLYCOPROTEIN HORMONES ALPHA CHAIN.
FT   CONFLICT   35   59   BY SIMILARITY.
FT   DISULFID   38   88   BY SIMILARITY.
FT   DISULFID   56   110   BY SIMILARITY.
FT   DISULFID   60   112   BY SIMILARITY.

Query Match   27.5%; Score 548; DB 1; Length 120;
Best Local Similarity   77.0%; Pred. No. 4.06e-113;
Matches   67; Conservative   7; Mismatches 13; Indels   0; Gaps   0;

Qy   170 GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSY 229
           || ||| ||| || |||| ||||| || ||| |||| || ||||| | | |||||||
Db   34 GCPECKLKENKYFSKDAPIYQCMGCCFSRAYPTPARSKKTMLVPKNITSEATCCVAKAF 93

Qy   230 NRVTVMGGFKVENHTGCHCSTCYYHKS 256
           | ||| |||| | |||||||||||||||
Db   94 TKATVMGNVRVENHTECHCSTCYYHKS 120

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FT   DISULFID         87        115         BY SIMILARITY.
FT   CARBOHYD         80         80
FT   CARBOHYD        106        106
FT   CONFLICT         27         27         D -> N (IN REF. 2).
FT   CONFLICT         27         27         D -> Q (IN REF. 2).
FT   CONFLICT         29         29         E -> Q (IN REF. 2).
FT   CONFLICT         37         37         E -> Q (IN REF. 2 TO 4).
FT   CONFLICT        112        113         CS -> SC (IN REF. 3).
SQ   SEQUENCE        120 AA;  13588 MW;  13BA4DE1 CRC32;

Qy   230 NRVTVMGGFKVENHTGCHCSTCYYHKS 256
        |||| |||||||||||||||||||||||
Db   170 GCPECTLQENPFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVISESTCCVAKSY 229

Db    94 TKATVMGNVRVENHTECHCSTCYYHKS 120

Qy   170 GCPECTLQENPFSQPGAPILQCMGCCFSRAYPTPARSKKTMLVPKNITSEATCCVAKAF 93
        |||||| ||||||| ||||||||||| |||||||||||||| |:|||:||||||||||::
Db    34 GCPECKLKENKYFSKPDAPIYQCMGCCFSRAYPTPARSKKTMLVPKNITSEATCCVAKAF 93

Matches   67;  Conservative  77;  Pred. No. 7;  Mismatches 13;  Indels   0;  Gaps   0;
Best Local Similarity  77.0%;         Pred. No. 4.06e-113;
Query Match            27.5%;   Score 548;  DB 1;  Length 120;

RX   RA
RA
RP   SEQUENCE.
RN   [1]
OC   EUTHERIA; LAGOMORPHA.
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OS   ORYCTOLAGUS CUNICULUS (RABBIT).
GN   CGA.
DE   GLYCOPROTEIN HORMONES ALPHA CHAIN.
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DT   01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
DT   01-APR-1988 (REL. 07, CREATED)
AC   P07474;
ID   GLHA_RABIT          STANDARD;      PRT;   96 AA.

RESULT 9

RP   SEQUENCE.
RN   [1]
PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
HSSP; P01233; 1HRP.
PIR; A05096; A05096.
LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
J. PROTEIN CHEM. 3:143-156(1984).
RL   GLENN S.D., NAHM H.S., WARD D.N.;

SQ   SEQUENCE        96 AA;  10663 MW;  CD56D255 CRC32;
FT   CARBOHYD         82         82
FT   CARBOHYD         56         56
FT   DISULFID         63         91         BY SIMILARITY.
FT   DISULFID         36         88         BY SIMILARITY.
FT   DISULFID         32         86         BY SIMILARITY.
FT   DISULFID         14         64         BY SIMILARITY.
FT   DISULFID         11         35         BY SIMILARITY.
KW   HORMONE; GLYCOPROTEIN.

RESULT 10
ID   GLH1_RAT            STANDARD;      PRT;  120 AA.
AC   P11962; P70516;
DT   01-OCT-1989 (REL. 12, CREATED)
DT   01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

Qy   227 KSYNRVTVMGGFKVENHTGCHCSTCYYHKS 256
        |::  |||||||||||||||||||||||||
Db    67 KAFTKATVMGNAKVENHTECHCSTCYYHKS 96

Db   167 AAPGGCPECTLQENPFSQPGAPILQCMGCCFSRAYPTPARSKKTMLVPKNITSEATCCVA 226
        |   |:||||||||||| |||  |:||||||||||||||||||
Qy     7 AMQGGCPECTLKENKYFSKLGAPIYQCMGCCFSRAYPTPARSKKTMLVPKNITSEATCCVA 66
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Right column:

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DE   GLYCOPROTEIN HORMONES ALPHA CHAIN 1 PRECURSOR.
OS   RATTUS NORVEGICUS (RAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=PITUITARY;
RX   MEDLINE; 82214055.
RA   GODINE J.E., CHIN W.W., HABENER J.F.;
RL   J. BIOL. CHEM. 257:8368-8371(1982).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 89196918.
RA   BURNSIDE J., BUCKLAND P.R., CHIN W.W.;
RL   GENE 70:67-74(1988).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=WISTAR-IMAMICHI; TISSUE=ANTERIOR PITUITARY;
RA   KATO Y., EZASHI T., HIRAI T., KATO T.;
RL   ZOOL. SCI. 7:877-885(1990).
PIR; JT0408; TTRTA.
PIR; S27385; S27385.
HSSP; P01233; 1HRP.
PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL            1         24
FT   CHAIN            25        120         GLYCOPROTEIN HORMONES ALPHA CHAIN 1.
FT   DISULFID         35         59         BY SIMILARITY.
FT   DISULFID         38         88         BY SIMILARITY.
FT   DISULFID         56        110         BY SIMILARITY.
FT   DISULFID         60        112         BY SIMILARITY.
FT   DISULFID         87        115         BY SIMILARITY.
FT   CARBOHYD         80         80         PROBABLE.
FT   CARBOHYD        106        106         PROBABLE.
FT   CONFLICT         84         84         E -> Q (IN G206111).
SQ   SEQUENCE        120 AA;  13453 MW;  5E507A0D CRC32;

Qy   230 NRVTVMGGFKVENHTGCHCSTCYYHKS 256
        |||| |||||||||||||||||||||||
Db   170 GCPECTLQENPFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVISESTCCVAKSY 229

Db    94 TKATVMGNARVENHTDCHCSTCYYHKS 120

Matches   68;  Conservative  6;  Pred. No. 4.78e-112;
Best Local Similarity  78.2%;     Pred. No. 6;  Mismatches 13;  Indels   0;  Gaps   0;
Query Match            27.3%;   Score 544;  DB 1;  Length 120;

RESULT 11
ID   GLHA_BALAC          STANDARD;      PRT;   96 AA.
AC   P37036;
DT   01-JUN-1994 (REL. 29, CREATED)
DT   01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   GLYCOPROTEIN HORMONES ALPHA CHAIN.
GN   CGA.
OS   BALAENOPTERA ACUTOROSTRATA (MINKE WHALE) (LESSER RORQUAL).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; CETACEA.
RN   [1]
RP   SEQUENCE.
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EMBL references (middle block):

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CC   LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
EMBL; V01252; G55580; -.
EMBL; J00757; G206111; -.
EMBL; M22829; -; NOT_ANNOTATED_CDS.
EMBL; M25543; G204470; -.
EMBL; M25544; G204471; -.
EMBL; D00575; G220842; -.
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RA   KARASEV V.S., PANKOV Y.A.;
RL   BIOKHIMIA 50:1972-1986(1985).
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   PIR; PN0138; PN0138.
DR   HSSP; P01215; 1HCN.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW   HORMONE; GLYCOPROTEIN.
FT   DISULFID      11     35       BY SIMILARITY.
FT   DISULFID      14     64       BY SIMILARITY.
FT   DISULFID      32     86       BY SIMILARITY.
FT   DISULFID      36     88       BY SIMILARITY.
FT   DISULFID      63     91       BY SIMILARITY.
FT   CARBOHYD      56             BY SIMILARITY.
FT   CARBOHYD      82             BY SIMILARITY.
SQ   SEQUENCE   96 AA;  10720 MW;  E2CD30DF CRC32;

Qy    10  GCP2CKLKZBKYFSKLGAPIYCYCMGCCFSRAYPTPARSKKTMLVPKNITSZ4CCVAKAF  69
          ||:||::||||:||||||:|||| || |||||||||||||||||||:|||:||:||
Qy   170  GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSY  229

Db

Qy    70  TKATVMGBAARVZNHTZCHCSTCYYHKS  96
          :||||:||||||||||||||||||||||
Qy   230  NRVTVMGGFKVENHTGCHCSTCYYHKS  256

Db


RESULT  12
ID   GLH2_RAT                STANDARD;      PRT;   120 AA.
AC   P11963;
DT   01-OCT-1989 (REL. 12, CREATED)
DT   01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
DT   01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE   GLYCOPROTEIN HORMONES ALPHA CHAIN 2 PRECURSOR.
OS   RATTUS NORVEGICUS (RAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 82214055.
RA   GODINE J.E., CHIN W.W., HABENER J.F.;
RL   J. BIOL. CHEM. 257:8368-8371(1982).
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   EMBL; V01253; G55583; -.
DR   PIR; S27386; S27386.
DR   HSSP; P01215; 1HCN.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL         1     24
FT   CHAIN         25    120       GLYCOPROTEIN HORMONES ALPHA CHAIN 2.
FT   DISULFID      35     59       BY SIMILARITY.
FT   DISULFID      38     88       BY SIMILARITY.
FT   DISULFID      56    110       BY SIMILARITY.
FT   DISULFID      60    112       BY SIMILARITY.
FT   DISULFID      87    115       BY SIMILARITY.
FT   CARBOHYD      80             PROBABLE.
FT   CARBOHYD     106             PROBABLE.
SQ   SEQUENCE  120 AA;  13565 MW;  4E4FAB2E CRC32;

Query Match             27.1%;  Score 541;  DB 1;  Length 120;
Best Local Similarity   77.0%;  Pred. No. 3.03e-111;
Matches   67;  Conservative  7;  Mismatches  13;  Indels  0;  Gaps  0;

Qy    34  GCPECKLKENKYFSKLGAPIYQCMGCCFSRAYPTPARSKKTMLVPKNITSEATCCVAKAF  93
          |||| | ||:|| ||||||| | ::||||||||||||||||||||||||  ||:||||||
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Qy   170  GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSY  229

Db

Qy    94  TKAITVMGNARVENHTECHCSTCYYHKS  120
          :||||:||||||||||||||||||||||
Qy   230  NRVTVMGGFKVENHTGCHCSTCYYHKS  256


RESULT  13
ID   GLHA_MOUSE              STANDARD;      PRT;   120 AA.
AC   P01216;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR.
GN   CGA.
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 82060239.
RA   CHIN W.W., KRONENBERG H.M., DEE P.C., MALOOF F., HABENER J.F.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 78:5329-5333(1981).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 89170115.
RA   GORDON D.F., WOOD W.M., RIDGWAY E.C.;
RL   DNA 7:679-690(1988).
DR   MGD; MGI:88390; CGA.
DR   HSSP; P01215; 1HCN.
DR   PIR; A31598; A31598.
DR   EMBL; A01482; TTMSA.
DR   EMBL; M22992; G575520; -.
DR   EMBL; M22991; -; NOT_ANNOTATED_CDS.
DR   EMBL; V00852; G54799; -.
DR   EMBL; J00643; G202180; -.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
KW   HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL         1     24
FT   CHAIN         25    120       GLYCOPROTEIN HORMONES ALPHA CHAIN.
FT   DISULFID      35     59       BY SIMILARITY.
FT   DISULFID      38     88       BY SIMILARITY.
FT   DISULFID      56    110       BY SIMILARITY.
FT   DISULFID      60    112       BY SIMILARITY.
FT   DISULFID      87    115       BY SIMILARITY.
FT   CARBOHYD      80             PROBABLE.
FT   CARBOHYD     106             PROBABLE.
SQ   SEQUENCE  120 AA;  86F1F31A CRC32;

Query Match             27.1%;  Score 541;  DB 1;  Length 120;
Best Local Similarity   77.0%;  Pred. No. 3.03e-111;
Matches   67;  Conservative  7;  Mismatches  13;  Indels  0;  Gaps  0;

Qy    34  GCPECKLKENKYFSKLGAPIYQCMGCCFSRAYPTPARSKKTMLVPKNITSEATCCVAKAF  93
          |||| | ||:|| ||||||| | ::||||||||||||||||||||||||  ||:||||||
Qy   170  GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSY  229

Db

Qy    94  TKAITVMGNARVENHTECHCSTCYYHKS  120
          :||||:||||||||||||||||||||||
Qy   230  NRVTVMGGFKVENHTGCHCSTCYYHKS  256


RESULT  14
ID   GLHA_PIG               STANDARD;      PRT;   120 AA.
AC   P01219;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR.
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GN   CGA.
OS   SUS SCROFA (PIG).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; ARTIODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 89325834.
RA   HIRAI T., TAKIKAWA H., KATO Y.;
RL   MOL. CELL. ENDOCRINOL. 63:209-217(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 74075725.
RA   KATO Y., EZASHI T., HIRAI T., KATO T.;
RL   SUBMITTED (MAR-1992) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN   [3]
RP   SEQUENCE OF 31-120.
RX   MEDLINE; 74075725.
RA   MAGHUIN-ROGISTER G., COMBARNOUS Y., HENNEN G.;
RL   EUR. J. BIOCHEM 39:255-263(1973).
RN   [4]
RP   PRELIMINARY SEQUENCE OF 25-120.
RA   CLOSSET J., MAGHUIN-ROGISTER G., HENNEN G.;
RL   ENDOCRINOL. EXP. 8:164(1974).
RN   [5]
RP   PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.
RX   MEDLINE; 75099922.
RA   COMBARNOUS Y., HENNEN G.;
RL   BIOCHEM. SOC. TRANS. 2:915-917(1974).
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
     EMBL; D00768; G217699; -
     EMBL; D00767; G217699; JOINED.
     PIR; A01485; UTPGA.
     PIR; A30339; A30339.
     HSSP; P01215; 1HCN.
     PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
     PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL      1     24
FT   CHAIN      25    120       GLYCOPROTEIN HORMONES ALPHA CHAIN.
FT   DISULFID   25     59       BY SIMILARITY.
FT   DISULFID   35     88       BY SIMILARITY.
FT   DISULFID   38    110       BY SIMILARITY.
FT   DISULFID   56    112       BY SIMILARITY.
FT   DISULFID   60    115       BY SIMILARITY.
FT   DISULFID   87    115       BY SIMILARITY.
FT   CARBOHYD   80              BY SIMILARITY.
FT   CARBOHYD  106              BY SIMILARITY.
SQ   SEQUENCE  120 AA;  13532 MW;  8749DBA5 CRC32;
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RP   SEQUENCE.
RX   MEDLINE; 97025333.
RA   KOIDE Y., PAPKOFF H., KAWAUCHI H.;
RL   EUR. J. BIOCHEM. 240:262-267(1996).
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
     PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
     PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW   HORMONE; GLYCOPROTEIN.
FT   DISULFID   11     35       BY SIMILARITY.
FT   DISULFID   14     64       BY SIMILARITY.
FT   DISULFID   32     86       BY SIMILARITY.
FT   DISULFID   36     88       BY SIMILARITY.
FT   DISULFID   63     91       BY SIMILARITY.
FT   CARBOHYD   56              POTENTIAL.
FT   CARBOHYD   82              POTENTIAL.
SQ   SEQUENCE  96 AA;  10781 MW;  DDF7B4BB CRC32;
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Query Match             27.0%;  Score 538;  DB 1;  Length 96;
Best Local Similarity   74.7%;  Pred. No. 1.92e-110;
Matches      65;  Conservative  10;  Mismatches 12;  Indels  0;  Gaps  0;

Db      10 GCPECKLGENRFFSKPGAPVYQCTGCCFSRAYPTPLRSKKTMLVPKNITSEATCCVAKAF 69
           |||| ||| || ||| |||| |||||||||||||||||||| ||:|||:|:|||||||::
Qy     170 GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSY 229

Db      70 TKITLKDNVKIENHTECHCSTCYYHKS 96
           ::|:|  |||||:||||||||||||||
Qy     230 NRVTVWGGFKVENHTGCHCSTCYYHKS 256
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Query Match             27.1%;  Score 541;  DB 1;  Length 120;
Best Local Similarity   77.0%;  Pred. No. 3.03e-111;
Matches      67;  Conservative   7;  Mismatches 13;  Indels  0;  Gaps  0;

Db      34 GCPECKLKENKYFSKLGAPIYQCMGCCFSRAYPTPARSKKTMLVPKNITSEATCCVAKAF 93
           ||||| | ||: ||| ||||||||:|||||||||||  |:|||||:|||:||||||||::
Qy     170 GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSY 229

Db      94 TKATVMGNARVENHIECHCSTCYYHKS 120
           || | ||:|| |||| |||||||||||
Qy     230 NRVTVWGGFKVENHTGCHCSTCYYHKS 256
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RESULT  15
ID   GLHA_STRCA     STANDARD;       PRT;   96 AA.
AC   P80665;
DT   01-OCT-1996 (REL. 34, CREATED)
DT   01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   GLYCOPROTEIN HORMONES ALPHA CHAIN.
OS   STRUTHIO CAMELUS (OSTRICH).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES;
OC   PALAEOGNATHAE; STRUTHIONIFORMES.
RN   [1]
```

Search completed: Wed May 6 08:48:07 1998
Job time : 35 secs.

MPSRCH (TM)

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MPsrch.pp   protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 6 08:47:32 1998; MasPar time 7.91 Seconds
          811.687 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-2
Description: (1-256) from US08804166.pep
Perfect Score: 1994
Sequence: 1 SRTSLLLAFGLLCLPWLQEG........GFKVENHTGCHCSTCYHKS 256

Scoring table: PAM 150
                 Gap 11

Searched: 69112 seqs, 25083644 residues

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database: swiss-prot35
                 1:swiss1

Statistics: Mean 42.029; Variance 63.165; scale 0.665

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1124	56.4	455	1	TNR1_HUMAN	TUMOR NECROSIS FACTOR	3.58e-271
2	962	48.2	461	1	TNR1_PIG	TUMOR NECROSIS FACTOR	3.53e-226
3	841	42.2	454	1	TNR1_MOUSE	TUMOR NECROSIS FACTOR	8.77e-193
4	809	40.6	461	1	TNR1_RAT	TUMOR NECROSIS FACTOR	5.45e-184
5	667	33.5	116	1	GLHA_HUMAN	GLYCOPROTEIN HORMONES	3.28e-145
6	551	27.6	120	1	GLHA_MACMU	GLYCOPROTEIN HORMONES	6.39e-114
7	548	27.5	120	1	GLHA_BOVIN	GLYCOPROTEIN HORMONES	4.06e-113
8	548	27.5	120	1	GLHA_SHEEP	GLYCOPROTEIN HORMONES	4.06e-113
9	546	27.4	96	1	GLHA_RABIT	GLYCOPROTEIN HORMONES	1.39e-112
10	544	27.3	120	1	GLHA_RAT	GLYCOPROTEIN HORMONES	1.39e-112
11	541	27.1	96	1	GLHA_BALAC	GLYCOPROTEIN HORMONES	3.03e-111
12	541	27.1	120	1	GLHA_MOUSE	GLYCOPROTEIN HORMONES	3.03e-111
13	541	27.1	120	1	GLHA_PIG	GLYCOPROTEIN HORMONES	3.03e-111
14	541	27.1	96	1	GLHA_STRCA	GLYCOPROTEIN HORMONES	3.03e-111
15	538	27.0	120	1	GLHA_CALJA	GLYCOPROTEIN HORMONES	1.92e-110
16	539	27.0	120	1	GLHA_MELGA	GLYCOPROTEIN HORMONES	3.55e-110
17	537	26.9	120	1	GLHA_PHYCA	GLYCOPROTEIN HORMONES	1.22e-109
18	535	26.8	96	1	GLH2_CYPCA	GLYCOPROTEIN HORMONES	1.04e-110
19	507	25.4	118	1	GLHA_EQUAS	GLYCOPROTEIN HORMONES	3.54e-102
20	507	25.4	120	1	GLHA_HORSE	GLYCOPROTEIN HORMONES	4.10e-101
21	503	25.2	120	1	GLHA_HYPMO	GLYCOPROTEIN HORMONES	1.39e-100
22	501	25.1	96	1	GLH1_CYPCA	GLYCOPROTEIN HORMONES	2.57e-100
23	500	25.1	118	1	GLH1_CYPCA	GLYCOPROTEIN HORMONES	2.57e-100
24	500	25.1	118	1	GLHA_CTEID	GLYCOPROTEIN HORMONES	2.57e-100
25	499	25.0	116	1	GLHA_CLAGA	GLYCOPROTEIN HORMONES	4.73e-100
26	478	24.0	93	1	GLHA_MURCI	GLYCOPROTEIN HORMONES	1.74e-94
27	476	23.9	97	1	GLHA_RANCA	GLYCOPROTEIN HORMONES	5.90e-94
28	474	23.8	117	1	GLHA_ANGAN	GLYCOPROTEIN HORMONES	1.99e-93
29	448	22.5	114	1	GLH2_ONCKE	GLYCOPROTEIN HORMONES	1.43e-86
30	447	22.4	108	1	GLH1_ONCKE	GLYCOPROTEIN HORMONES	2.62e-86
31	427	21.4	94	1	GLHA_THUOB	GLYCOPROTEIN HORMONES	4.60e-81
32	424	21.3	117	1	GLHA_ACALA	GLYCOPROTEIN HORMONES	2.80e-80
33	377	18.9	125	1	GLHA_FUNHE	GLYCOPROTEIN HORMONES	4.56e-68
34	273	13.7	417	1	WSL1_HUMAN	WSL-1 PROTEIN PRECURSOR	8.97e-42
35	231	11.6	435	1	TNRC_HUMAN	LYMPHOTOXIN-BETA RECEP	1.40e-31
36	225	11.3	325	1	TNRC_MOUSE	TUMOR NECROSIS FACTOR	3.76e-30
37	221	11.1	326	1	VT2_SFVKA	TUMOR NECROSIS FACTOR	3.33e-29
38	215	10.8	415	1	VT2_MYXVL	LYMPHOTOXIN-BETA RECEP	8.65e-28
39	214	10.7	349	1	VC22_VARV	PROTEIN C22/B28 HOMOLO	1.49e-27
40	212	10.6	474	1	TNR2_MOUSE	TUMOR NECROSIS FACTOR	4.37e-27
41	207	10.4	425	1	NGFR_RAT	LOW-AFFINITY NERVE GRO	6.44e-26
42	207	10.4	427	1	NGFR_HUMAN	LOW-AFFINITY NERVE GRO	6.44e-26
43	204	10.2	260	1	CD27_HUMAN	CD27L RECEPTOR PRECURS	4.10e-25
44	188	9.4	323	1	CD27L_HUMAN	CD27L RECEPTOR PRECURS	3.21e-25
45	183	9.2	595	1	FASA_BOVIN	FASL RECEPTOR PRECURSO	1.52e-21
					FASL_HUMAN	FASL RECEPTOR PRECURS	
					CD30_HUMAN	CD30L RECEPTOR PRECURS	2.06e-20

ALIGNMENTS

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RESULT 1

ID   TNR1_HUMAN     STANDARD;     PRT;   455 AA.
AC   P19438;
DT   01-FEB-1991 (REL. 17, CREATED)
DT   01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (TUMOR NECROSIS FACTOR
DE   BINDING PROTEIN 1) (TBPI) (P60) (TNF-R1) (P55) (CD120A).
GN   TNFR1 OR TNFAR.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PLACENTA;
RX   MEDLINE; 90235285.
RA   SCHALL T.J., LEWIS M., KOLLER K.J., LEE A., RICE G.C., WONG G.H.W.,
RA   GETANAGA T., GRANGER G.A., LENTZ R., RAAB H., KOHR W.J., GOEDDEL D.V.;
RL   CELL 61:361-370(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 90235284.
RA   LOETSCHER H., PAN Y.-C.E., LAHM H.-W., GENTZ R., BROCKHAUS M.,
RA   TABUCHI H., LESSLAUER W.;
RL   CELL 61:351-359(1990).
RN   [3]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 41-53; 110-124 AND 199-201.
RX   MEDLINE; 91006021.
RA   NOPHAR Y., KEMPER O., BRAKEBUSCH C., ENGELMANN H., ZWANG R.,
RA   ADERKA D., HOLTMANN H., WALLACH D.;
RL   EMBO J. 9:3269-3278(1990).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91090841.
RA   HIMMLER A., MAURER-FOGY I., KROENKE M., SCHEURICH P., PFIZENMAIER K.,
RA   LANTZ M., OLSSON I., HAUPTMANN R., STRATOWA C., ADOLF G.R.;
RL   DNA CELL BIOL. 9:705-715(1990).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PLACENTA;
RX   MEDLINE; 91017509.
RA   GRAY P.W., BARRETT K., CHANTRY D., TURNER M., FELDMAN M.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 87:7380-7384(1990).
RN   [6]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 92250049.
RA   FUCHS P., STREHL S., DWORZAK M., HIMMLER A., AMBROS P.F.;
```

RL   GENOMICS 13:219-224(1992).
RN   [7]
RP   SEQUENCE OF 41-45.
RX   MEDLINE; 90110215.
RA   ENGELMANN H., NOVICK D., WALLACH D.;
RL   J. BIOL. CHEM. 265:1531-1536(1990).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211.
RX   MEDLINE; 93258809.
RA   BANNER D.W., D'ARCY A., JANES W., GENTZ R., SCHOENFELD H.-J.,
RA   BROGER C., LOETSCHER H., LESSLAUER W.;
RL   CELL 73:431-445(1993).
RN   [9]
RP   X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.
RX   MEDLINE; 97094982.
RA   NAISMITH J.H., DEVINE T.Q., KHONO H., SPRANG S.R.;
RL   STRUCTURE 4:1251-1262(1996).
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC   RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC   AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC   PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC   SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC   PROTEASES) MEDIATING APOPTOSIS.
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC   HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC   PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC   WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC   PROTEINS SUCH AS TRAF5, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC   TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC   ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC   NF-KAPPA B SIGNALING.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
EMBL; X55313; G37224; -.
EMBL; M33294; G339745; -.
EMBL; M58286; G339754; -.
EMBL; M63121; G339756; -.
EMBL; M75866; G339750; -.
EMBL; M75864; G339750; JOINED.
EMBL; M75865; G339750; JOINED.
EMBL; M60275; G339760; -.
EMBL; A21522; G579600; -.
PIR; A34899; GQHUT1.
PIR; A35010; A35010.
PIR; S12057; S12057.
PIR; A38208; A38208.
ITNR; 31-JUL-94.
PDB; 1TNR; 07-DEC-95.
PDB; 1NCF; 07-DEC-95.
PDB; 1EXT; 11-JAN-97.
MIM; 191190.
PROSITE; PS00652; TNFR_NGFR_1; 3.
PROSITE; PS50050; TNFR_NGFR_2; 3.
PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS;
KW   3D-STRUCTURE.
FT   SIGNAL   1   21
FT   CHAIN   22   455   TUMOR NECROSIS FACTOR RECEPTOR 1.
FT   CHAIN   41   291   TUMOR NECROSIS FACTOR BINDING PROTEIN 1.
FT   DOMAIN   22   211   EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   212   234   POTENTIAL.
FT   DOMAIN   235   455   CYTOPLASMIC (POTENTIAL).
FT   DOMAIN   43   196   4 X TNFR-CYS.
FT   REPEAT   43   82   TNFR-CYS 1.
FT   REPEAT   83   125   TNFR-CYS 2.
FT   REPEAT   126   166   TNFR-CYS 3.
FT   REPEAT   167   196   TNFR-CYS 4.
FT   DOMAIN   356   441   DEATH DOMAIN.
FT   DISULFID   44   58
FT   DISULFID   59   72
FT   DISULFID   62   81
FT   DISULFID   84   99
FT   DISULFID   102   117
FT   DISULFID   105   125

FT   DISULFID   127   143
FT   DISULFID   146   158
FT   DISULFID   149   166
FT   DISULFID   168   179
FT   DISULFID   182   191
FT   DISULFID   185   195
FT   CARBOHYD   54   54   POTENTIAL.
FT   CARBOHYD   145   145   POTENTIAL.
FT   CARBOHYD   151   151   POTENTIAL.
FT   CONFLICT   412   412   MISSING (IN REF. 4).
FT   CONFLICT   443   446   GPAA -> APP (IN REF. 4).
SQ   SEQUENCE   455 AA; 50494 MW; CE0EA06F CRC32;

Query Match   56.4%;   Score 1124;   DB 1;   Length 455;
Best Local Similarity   99.3%;   Pred. No. 3.58e-271;
Matches 142;   Conservative   1;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Qy   101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHWSENLFQCFNCSLCLNGTVHLSCQE 160
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHWSENLFQCFNCSLCLNGTVHLSCQE 142

Qy   161 KQNTVCTCHAGFFLRENECVSCS 183
           |||||||||||||||||||||||
Db   143 KQNTVCTCHAGFFLRENECVSCA 165

RESULT 2
ID   TNR1_PIG   STANDARD;   PRT;   461 AA.
AC   P50555;
DT   01-OCT-1996 (REL. 34, CREATED)
DT   01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
GN   TNFR1.
OS   SUS SCROFA (PIG).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; ARTIODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=KIDNEY;
RX   MEDLINE; 96011645.
RA   SUTER B., PAULI U.H.;
RL   GENE 163:263-266(1995).
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC   RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC   AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC   PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC   SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC   PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC   HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC   PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC   WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC   PROTEINS SUCH AS TRAF5, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC   TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC   ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC   NF-KAPPA B SIGNALING (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
EMBL; U19994; G1141753; -.
PROSITE; PS00652; TNFR_NGFR_1; 3.
PROSITE; PS50050; TNFR_NGFR_2; 2.
PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS.
FT   SIGNAL   1   21
FT   CHAIN   22   461   TUMOR NECROSIS FACTOR RECEPTOR 1.
FT   DOMAIN   22   210   EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   211   233   POTENTIAL.
FT   DOMAIN   234   461   CYTOPLASMIC (POTENTIAL).

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*                                                            *
*    M P S R C H    (TM)                                      *
*                                                            *
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MPsrch_pp   protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 6 08:48:26 1998; MasPar time 13.91 Seconds
                                           775.210 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-2
Description: (1-256) from US08804166.pep
Perfect Score: 1994
Sequence: 1 SRTSLLAFGLLCLPWLQEG............GFKVEHHTGHCHCSTCYHKS 256

Scoring table: PAM 150
                 Gap 11

Searched: 140555 seqs, 42109429 residues

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database: sptrembl5
                 1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
                 5:sp_mnc 6:sp_organelle 7:sp_phage 8:sp_plant
                 9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
                 13:sp_unclassified

Statistics: Mean 41.143; Variance 64.343; scale 0.639

                 Pred. No. is the number of results predicted by chance to have a
                 score greater than or equal to the score of the result being printed,
                 and is derived by analysis of the total score distribution.

                                  SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description	Pred. No.
1	945	47.4	180	4	Q95185	TUMOR NECROSIS FACTOR	3.15e-213
2	895	44.9	471	4	Q19131	TUMOR NECROSIS FACTOR-	6.13e-200
3	454	22.8	108	12	Q90287	GONADOTROPIN ALPHA SUB	6.53e-85
4	453	22.7	107	12	Q90286	GONADOTROPIN ALPHA SUB	1.17e-84
5	451	22.6	119	12	Q91370	GONADOTROPHIN ALPHA 1	3.76e-84
6	446	22.4	114	12	Q91371	GONADOTROPHIN ALPHA 2	6.95e-83
7	433	21.7	117	12	Q91119	GLYCOPROTEIN HORMONES	1.34e-79
8	333	16.7	55	10	Q06589	ALPHA SUBUNIT OF GLYCO	1.06e-54
9	273	13.7	253	2	Q00276	LYMPHOCYTE ASSOCIATED	1.06e-40
10	273	13.7	380	2	Q00280	LYMPHOCYTE ASSOCIATED	3.29e-40
11	273	13.7	418	2	Q00275	LYMPHOCYTE ASSOCIATED	3.29e-40
12	257	12.9	277	2	Q14866	SOLUBLE DEATH RECEPTOR	2.00e-36
13	257	12.9	426	2	Q14865	DEATH RECEPTOR 3 BETA,	2.00e-36
14	214	10.7	348	11	Q89118	HOMOLOG OF VACCINIA VI	1.76e-26
15	214	10.7	349	11	Q89119	SOMALIA-1977 RIGHT NEA	1.76e-26
16	214	10.7	349	11	Q89098	GARCIA-1966 RIGHT NEAR	1.76e-26
17	210	10.5	459	11	Q89308	SECRETED RECEPTOR BIND	1.42e-25
18	206	10.3	459	10	Q62327	TUMOR NECROSIS FACTOR	1.13e-24
19	187	9.4	267	4	Q02764	OX40 PRECURSOR (FRAGME	1.89e-20
20	182	9.1	259	2	Q14755	TRAIL RECEPTOR 3.	2.34e-19
21	180	9.0	283	2	Q92956	HERPESVIRUS ENTRY MEDI	6.38e-19
22	180	9.0	299	2	Q14798	CYTOTOXIC TRAIL RECEPT	6.38e-19
23	180	9.0	425	2	Q16042	TUMOR NECROSIS FACTOR	6.38e-19
24	179	9.0	324	10	Q63199	FAS ANTIGEN PRECURSOR.	1.05e-18
25	178	8.9	411	2	Q15508	P53-REGULATED DNA DAMA	1.73e-18
26	174	8.7	411	2	Q15517	CYTOTOXIC TRAIL RECEPT	1.27e-17
27	174	8.7	411	2	Q14720	DEATH RECEPTOR 5.	1.27e-17
28	174	8.7	440	2	Q15531	CYTOTOXIC TRAIL RECEPT	1.27e-17
29	174	8.7	440	2	Q14763	APOPTOSIS INDUCING PRO	1.27e-17
30	174	8.7	202	2	Q14405	APOPTOSIS INDUCING REC	1.27e-17
31	167	8.4	202	2	Q16631	SOMATOTROPIN PRECURSOR	3.98e-16
32	161	8.1	468	2	Q00220	CYTOTOXIC LIGAND TRAIL	7.40e-15
33	160	8.0	202	2	Q14643	PLACENTAL GROWTH HORMO	1.20e-14
34	160	8.0	245	2	Q14644	PLACENTAL GROWTH HORMO	1.20e-14
35	160	8.0	217	2	Q14407	CHORIONIC SOMATOMAMMOT	1.33e-13
36	156	7.8	372	2	Q00279	CHORIONIC SOMATOMAMMOT	2.14e-13
37	154	7.7	199	2	Q14406	CHORIONIC SOMATOMAMMOT	2.14e-13
38	153	7.7	401	10	Q00300	OSTEOPROTEGERIN.	3.45e-13
39	153	7.7	625	10	Q35305	OSTEOPROTEGERIN.	3.45e-13
40	152	7.6	401	10	Q08712	OSTEOPROTEGERIN.	3.45e-13
41	150	7.5	274	2	Q13663	RANK.	5.55e-13
42	150	7.5	217	2	Q08727	CELL SURFACE ANTIGEN O	5.55e-13
43	148	7.4	401	10	Q07367	SOMATOTROPIN 1 PRECURS	5.90e-12
44	146	7.3	217	4	Q07369	SOMATOTROPIN 3 PRECURS	9.42e-12
45	143	7.2	212	4	Q07368	SOMATOTROPIN 2 PRECURS	3.82e-11
```

                                  ALIGNMENTS

RESULT  1
ID    Q95185                         PRELIMINARY;      PRT;    180 AA.
AC    Q95185;
DT    01-FEB-1997 (TREMBLREL. 02, CREATED)
DT    01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
DT    01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE    TUMOUR NECROSIS FACTOR RECEPTOR P60 (FRAGMENT).
GN    TNFR-1.
OS    FELIS SILVESTRIS CATUS (CAT).
OC    EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC    EUTHERIA; CARNIVORA.
RN    [1]
RP    SEQUENCE FROM N.A.
RA    DUTHIE S., NASIR L., ECKERSALL P.D.;
RL    SUBMITTED (OCT-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR    EMBL; U72344; G1613880; -.
DR    PROSITE; PS00652; TNFR_NGFR_1; 3.
FT    NON_TER          1      1
FT    NON_TER        180    180
SQ    SEQUENCE FROM N.A.
      SEQUENCE        180 AA;   20399 MW;   5452A6B2 CRC32;

Query Match          47.4%;    Score 945;  DB 4;  Length 180;
Best Local Similarity 86.0%;   Pred. No. 3.15e-213;
Matches  117; Conservative   9; Mismatches  10;  Indels  0;  Gaps  0;

Qy   45  CPQGKYIHPQDNSICCTKCHKGTYLYNDCAGPGLDTDCRECENGTFTASENYLRQCLSCS  104
             ||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||
Db   45  CPQGKYIHPQDNSICCTKCHKGTYLYNDCAGPGLDTDCRECENGTFTASENYLRQCLSCS  104

Qy  105  KCRKEMTQVEISPCTVYRDTVCGGCRKNQYRYWSETHPQCLNCSLCLNGTVQISCKETQN  164
             |||| |||||:||:|||| |||||||||||||:|||||||||||||||:|||||||||
Db  105  KCRKEMGQVEISSCTVRDTVCGGCRKNQYRHWSENLPQCFNCSLCLNGTVHLSCQEKQN  145

Qy   26  CPQGKYIHPQDNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCS  85
             |||||||:||||||||||:|||||||||||:||::||||||::|:||||||||:||||||
Db   86  KCRKEMGQVEISSCTVRDTVCGGCRKNQYRHWSENLPQCFNCSLCLNGTVHLSCQEKQN  145

Qy  146  TVCTCHAGFFLRGNEC  161
             |||||||||||||||
Db  165  TVCTCHAGFFLRENEC  180

RESULT  2
ID    Q19131                         PRELIMINARY;      PRT;    471 AA.
AC    Q19131;
DT    01-JAN-1998 (TREMBLREL. 05, CREATED)

```
DT   01-JAN-1998 (TREMBLREL, 05, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL, 05, LAST ANNOTATION UPDATE)
DE   TUMOR NECROSIS FACTOR-RECEPTOR I.
GN   TNF-RI.
OS   BOS TAURUS (BOVINE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; ARTIODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=AORTA;
RA   LEE E.-K., TAYLOR M.J., KEHRLI M.E.;
RL   SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U90937; G2290398; -.
DR   PROSITE; PS00552; TNFR_NGFR_1; 3.
SQ   SEQUENCE   471 AA;   51368 MW;  1D60FF4A CRC32;
ID   Q90287         PRELIMINARY;      PRT;   108 AA.
RESULT 3

Query Match     44.9%;  Score 895;  DB 4;  Length 471;
Best Local Similarity   73.2%;
Matches  104;  Conservative  21;  Pred. No. 6.13e-200;  Mismatches 17;  Indels  0;  Gaps  0;

Qy   143 KQNTVCTCHAGFFLRENECVSC 164
         |:|| |||| |||||| |:||
Db   161 RQDTICHCHMGFFLKGAKCISC 182

Qy    83 SCSKCRKEMQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142
         |:||:| ||:|:::|| |||||:||||||:|||:|:||||: ::|:| ||| ::::|||
Db   101 SCSRCRDEMFQVEISPCVVDRDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQE 160

Qy    23 DSVCPQGKYIHPQNNSICCTKCHRGTYLIYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82
         : |||| | :| ||:||||||||:|| |||||:|||| | | |:| :|::::|::|||:||
Db    41 ESPCPQGKYNHPQNSTICCTKCHKGTYLIYNDCPGPGRDTDCRVCAPGTVTALENHLRCL 100
```

ID   Q90286   PRELIMINARY;   PRT;   107 AA.
RESULT 4

Query Match   22.8%; Score 454; DB 12; Length 108;
Best Local Similarity   72.0%;
Matches 59; Conservative 7; Pred. No. 6.53e-85; Mismatches 15; Indels 1; Gaps 1;

```
Qy   230 NRVTVMGGFKVENHTGCHCSTC 251
         ||||| |||||:|||||
Db    88 KRVLV-DDVRLVNHTDCHCSTC 108

Qy   170 GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVPKRDIITSEATCCVAKEV 229
         ||:||||:||| ||||||:|||:|||||||||||||||||||||||||||||||||||||
Db    28 GCEECKLKENNIFSKPGAPVYQCMGCCFSRAYPTPLRSKKTMLVPKRDIITSEATCCVAKEV 87
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DE   GONADOTROPIN ALPHA SUBUNIT (FRAGMENT).
OS   CARASSIUS AURATUS (GOLDFISH).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OC   OSTEICHTHYES; ACTINOPTERYGII; CYPRINIFORMES.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   KOBAYASHI M., KATO Y., YOSHIURA Y., AIDA K.;
RL   SUBMITTED (AUG-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; D86551; G1469836; -.
SQ   SEQUENCE   107 AA;   11959 MW;  880C6840 CRC32;
ID   Q91370         PRELIMINARY;      PRT;   107 AA.
RESULT 5

Query Match     22.7%;  Score 453;  DB 12;  Length 107;
Best Local Similarity   72.0%;
Matches  59;  Conservative  7;  Pred. No. 1.17e-84;  Mismatches 15;  Indels  1;  Gaps  1;

Qy   230 NRVTVMGGFKVENHTGCHCSTC 251
         ||||| |||||:|||||
Db    87 KRVLV-NDVRLVNHIDCHCSTC 107

Qy   170 GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVPKRDIITSEATCCVAKEV 229
         ||:||||:||| ||||||:|||:|||||||||||||||||||||||||||||||||||||
Db    27 GCEECKLKENNIFSKPGAPVYQCMGCCFSRAYPTPLRSKKTMLVPKRDIITSEATCCVAKEV 86
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DE   GONADOTROPIN ALPHA 1 SUBUNIT.
OS   ONCORHYNCHUS MASOU (CHERRY SALMON) (MASU SALMON).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OC   OSTEICHTHYES; ACTINOPTERYGII; SALMONIFORMES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 94197992.
RA   MARUYAMA O., KATO T., TOMIZAWA K., WAKABAYASHI K., KATO Y.;
RL   J. MOL. ENDOCRINOL. 11:265-273(1993).
DR   EMBL; S69273; G546258; -.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
SQ   SEQUENCE   119 AA;   13131 MW;  2EEF28F4 CRC32;
ID   Q91371         PRELIMINARY;      PRT;   114 AA.
RESULT 6

Query Match     22.6%;  Score 451;  DB 12;  Length 119;
Best Local Similarity   67.8%;
Matches  59;  Conservative  11;  Pred. No. 3.76e-84;  Mismatches 16;  Indels  1;  Gaps  1;

Qy   230 NRVTVMGGFKVENHTGCHCSTCYHKS 256
         ||||| |||||:||||||| |||
Db    94 ERV-VVDNIKLTNHIECWNTCYHHKS 119

Qy   170 GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVPKRDIITSEATCCVAKSY 229
         ||:||||:||| ||||||:|||:|||||||||||||||||||::||||||||||||||||
Db    34 GCEECKLKENRLFSNPGAPVYQCTGCCFSRAYPTPLQSKRAMLVPKNIISEATCCVAKEG 93
```

AC   Q90286;
DT   01-NOV-1996 (TREMBLREL, 01, CREATED)
DT   01-NOV-1996 (TREMBLREL, 01, LAST SEQUENCE UPDATE)
DT   01-NOV-1996 (TREMBLREL, 01, LAST ANNOTATION UPDATE)

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RX   MEDLINE; 94197892.
RA   GEN K., MARUYAMA O., KATO T., TOMIZAWA K., WAKABAYASHI K., KATO Y.;
RL   J. MOL. ENDOCRINOL. 11:265-273(1993).
DR   EMBL; S69274; G5462260;.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_2; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_1; 1.
SQ   SEQUENCE   114 AA;  12519 MW;  473D3C83 CRC32;

Query Match             22.4%;  Score 446;  DB 12;  Length 114;
Best Local Similarity   71.3%;  Pred. No. 6.95e-83;
Matches   62;  Conservative   6;  Mismatches 15;  Indels   4;  Gaps   2;

Qy    170 GCPECTLQENPFFSQPGAPILQCMGGCCFSRAYPTPLRSKQTMLVPKNITHSEATCCVAKEG 87
          ||:|| |     |||  ||   ||||||||||||||||||||| |||||||||||||||
Db     32 GCEECTLKPNTIF--PN--IIQCTGCCFSRAYPTPLRSKOTMLVPKNITHSEATCCVAKEG 87

Db     88 ERVTTKDGFPVTNHTECHCSTCYYHKS 114
          :||| ||| || || | |||||||||||
Qy    230 NRVTVMGGFKVENHTGCHCSTCYYHKS 256


RESULT 7
ID   Q91119      PRELIMINARY;   PRT;   117 AA.
AC   Q91119;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (GONADOTROPIN ALPHA
DE   CHAIN) (GTH-ALPHA).
OS   MORONE SAXATILIS (STRIPED BASS)
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OC   OSTEICHTHYES; ACTINOPTERYGII; PERCIFORMES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PITUITARY GLAND;
RX   MEDLINE; 96020549.
RA   HASSIN S., ELIZUR A., ZOHAR Y.;
RL   J. MOL. ENDOCRINOL. 15:23-35(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PITUITARY GLAND;
RA   HASSIN S.;
RL   SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC   -!- FUNCTION: INVOLVED IN GAMETOGENSIS AND STEROIDOGENSIS (BY
CC       SIMILARITY).
CC   -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN (BY SIMILARITY).
DR   EMBL; L35071; G2322657;.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL        1     23
FT   CHAIN        24    117       GLYCOPROTEIN HORMONES ALPHA CHAIN.
FT   DISULFID     34     57       BY SIMILARITY.
FT   DISULFID     37     86       BY SIMILARITY.
FT   DISULFID     54    107       BY SIMILARITY.
FT   DISULFID     58    109       BY SIMILARITY.
FT   DISULFID     85    112       BY SIMILARITY.
FT   DISULFID     78    112       BY SIMILARITY.
FT   CARBOHYD     78              POTENTIAL.
FT   CARBOHYD    103              POTENTIAL.
SQ   SEQUENCE   117 AA;  13066 MW;  CAFB9D0C CRC32;

Query Match             21.7%;  Score 433;  DB 12;  Length 117;
Best Local Similarity   65.5%;  Pred. No. 1.34e-79;
Matches   57;  Conservative 14;  Mismatches 12;  Indels   4;  Gaps   4;

Qy    170 GCPECTLQENPFFSOPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAK-S 228
          ||:||||  ||| ||   ||| ||| |||||||||||||||:|| ||||| || |||| |
Db     33 GCEECTLRKNSVSR-DRPVYQCMGCCFSRAYPTPLKAMKTMTIPKNITSEATCCVAKHS 91

Db     92 YE-TEV-AGIKVRNHTDCHCSTCYFHK 116
          |:| ||   ||||||| |||||||:||
Qy    229 YNRVTVMGGFKVENHTGCHCSTCYYHK 255


RESULT 8
ID   Q62589      PRELIMINARY;   PRT;   55 AA.
AC   Q62589;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   ALPHA SUBUNIT OF GLYCOPROTEIN HORMONES (FRAGMENT).
OS   PHODOPUS SUNGORUS (STRIPED HAIRY-FOOTED HAMSTER) (DJUNGARIAN HAMSTER).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PITUITARY;
RX   MEDLINE; 96198779.
RA   BOCKMANN J., BOCKERS T.M., VENNEMANN B., NIKLOWITZ P., MÜLLER J.,
RA   WITTKOWSKI W., SABEL B., KREUTZ M.R.;
RL   ENDOCRINOLOGY 137:1804-1813(1996).
DR   EMBL; X90776; E195654;.
DR   NON_TER        1
SQ   SEQUENCE   55 AA;  6047 MW;  E5AAE0F8 CRC32;

Query Match             16.7%;  Score 333;  DB 10;  Length 55;
Best Local Similarity   76.4%;  Pred. No. 1.06e-54;
Matches   42;  Conservative   6;  Mismatches   7;  Indels   0;  Gaps   0;

Qy    202 PTPLRSKKTMLVQKNVTSESTCCVAKSYNRVTVMGGFKVENHTGCHCSTCYYHKS 256
          |||| ||||||| |||||||||||:  |||| |||||||||||| |||||||||||
Db      1 PTPARSKKTMLVPKNITSEATCCVAKAFTRATVMGNARVENHTECHCSTCYYHKS 55


RESULT 9
ID   000276      PRELIMINARY;   PRT;   253 AA.
AC   000276;
DT   01-JUL-1997 (TREMBLREL. 04, CREATED)
DT   01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 2.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   SCREATON G., XU X.N., OLSEN A., COWPER A., TAN R., MCMICHAEL A.,
RA   BELL J.;
RL   SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U94503; G2071953;.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
SQ   SEQUENCE   253 AA;  26934 MW;  A21C863E CRC32;

Query Match             13.7%;  Score 273;  DB 2;  Length 253;
Best Local Similarity   32.4%;  Pred. No. 3.29e-40;
Matches   60;  Conservative 34;  Mismatches 74;  Indels  17;  Gaps  13;

Qy      3 TSLLLAFGLLCLPWLQEGSADSVCP-QGKYIHPQNNSICCTKCHKGTYLYNDCPGPQDT 61
          :|||   | ||    |:     :|   |::|| : | :||| | |||  || :| || |
Db     69 TCLVCPQDTFLAWENHHNSECARCQACDEQAASQVALENCSAVADTRCGCRPGWFVECQVS 128

Db    129 QCVSSSPFYCQPCLDCGALRHHTRLLC--SRRDTDCGTCLPGFYEHGDGCVSCPTSTLGSC 187
          :  :||      |   | :| || |    ||  || | | |||   ||||| |  :  | |
Qy     62 DCRECESGSFTASENHLR-HCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYW-S 119

Db    188 PERCA 192
          || ||
Qy    172 PE-CT 175

Db    120 ENLFQC-FNCSLCLN-GTVH----LSCQEKQNTVC-TCHAGPFLRENECVSCAGAAPG-C 171
          |||| | ||| ||   |||        ||| ||| | ||| | || ||| || |   | |
Qy    170 GCPECTLQENPFFSOPGAPILQCMGGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSY 256
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RESULT 10
ID 000280

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AC   000280;
DT   01-JUL-1997 (TREMBLREL. 04, CREATED)
DT   01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 9.
OS   HOMO SAPIENS (HUMAN)
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   SCREATON G., XU X.N., OLSEN A., COWPER A., TAN R., MCMICHAEL A.,
RA   BELL J.;
RL   SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U94510; G2071967; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
SQ   SEQUENCE   380 AA;  41192 MW;  17C92A14 CRC32;

     PRELIMINARY;    PRT;    380 AA.

Query Match             13.7%;  Score 273;  DB 2;  Length 380;
Best Local Similarity   32.4%;
Matches   60;  Conservative   34;  Mismatches   74;  Indels   17;  Gaps   13;

Qy   13 AALLIV--LLG-ARAQGGTRSPRCDCAGDF-HKKIGLFCCRGCPAGHYLKAPCTEPCGNS 68
Db    3 TSILLAFGLLCLPWLQEGSADSVCP-QGKYIHPQNNSICCTKCHKGTYLYNDCPGQDT 61

Qy   69 TCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVS 128
Db   69 DCRECESGSFTASENHLR-HCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYW-S 119

Qy  129 QCVSSSPFYCQPCLDCGALHRTHRLLC-SRRDTDCGTCLPGFYEHGDGCVSGCPTSTLGSC 187
Db  120 ENLFQC-FNCSLCLN-GTVH----LSCQEKQNTVC-TCHAGFFLRENECVSCAGAAPG-C 171

Qy  188 PERCA 192
Db  172 PE-CT 175
```

RESULT 11
ID 000275

```
AC   000275;
DT   01-JUL-1997 (TREMBLREL. 04, CREATED)
DT   01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 1B.
OS   HOMO SAPIENS (HUMAN)
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   SCREATON G., XU X.N., OLSEN A., COWPER A., TAN R., MCMICHAEL A.,
RA   BELL J.;
RL   SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U94502; G2071951; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
SQ   SEQUENCE   418 AA;  45456 MW;  3D04954A CRC32;

     PRELIMINARY;    PRT;    418 AA.
```

RESULT 12
ID 014866

```
AC   014866;
DT   01-JAN-1998 (TREMBLREL. 05, CREATED)
DT   01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   SOLUBLE DEATH RECEPTOR 3 BETA.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
GN   DR3.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   WARZOCHA K., RIBEIRO P., RENARD N., CHARLOT C., COIFFIER B.,
RA   SALLES G.;
RL   SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; AF026071; G2570833; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
SQ   SEQUENCE   277 AA;  29111 MW;  06E16SC7 CRC32;

     PRELIMINARY;    PRT;    277 AA.

Query Match             12.9%;  Score 257;  DB 2;  Length 277;
Best Local Similarity   31.5%;
Matches   56;  Conservative   34;  Mismatches   73;  Indels   15;  Gaps   11;

Qy   13 AALLIV--LLG-ARAQGGTRSPRCDCAGDF-HKKIGLFCCRGCPAGHYLKAPCTEPCGNS 68
Db    3 TSILLAFGLLCLPWLQEGSADSVCP-QGKYIHPQNNSICCTKCHKGTYLYNDCPGQDT 61

Qy   69 TCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVS 128
Db   69 DCRECESGSFTASENHLR-HCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYW-S 119

Qy  129 QCVSSSPFYCQPCLDCGALHRTHRLLC-SRRDTDCGTCLPGFYEHGDGCVSGCPTPPPS 185
Db  120 ENLFQC-FNCSLCLN-GTVH----LSCQEKQNTVC-TCHAGFFLRENECVSCAGAAPG 170
```

RESULT 13
ID 014865

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AC   014865;
DT   01-JAN-1998 (TREMBLREL. 05, CREATED)
DT   01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   DEATH RECEPTOR 3 BETA.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
GN   DR3.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   WARZOCHA K., RIBEIRO P., RENARD N., CHARLOT C., COIFFIER B.,
RA   SALLES G.;
RL   SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; AF026070; G2570831; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
SQ   SEQUENCE   426 AA;  45950 MW;  87E00821 CRC32;

     PRELIMINARY;    PRT;    426 AA.

Query Match             12.9%;  Score 257;  DB 2;  Length 426;
Best Local Similarity   31.5%;
Matches   56;  Conservative   34;  Mismatches   73;  Indels   15;  Gaps   11;

Qy   13 AALLIV--LLG-ARAQGGTRSPRCDCAGDF-HKKIGLFCCRGCPAGHYLKAPCTEPCGNS 68
Db    3 TSILLAFGLLCLPWLQEGSADSVCP-QGKYIHPQNNSICCTKCHKGTYLYNDCPGQDT 61

Qy   69 TCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVS 128
Db   69 DCRECESGSFTASENHLR-HCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYW-S 119

Qy  120 ENLFQC-FNCSLCLN-GTVH----LSCQEKQNTVC-TCHAGFFLRENECVSCAGAAPG 170
```

```
Db   13  AALLLV--LLG-ARAQGGTRSPRCDCAGDF-HKKIGLFCCRGCPAGHYLKAPCTEPCGNS  68
             | ||| ||  | |:||  |||:|| :        ::
Qy    3  TSILLAFGLLCLPWLQEGSADSVCP-QGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDT  61

Db   69  TCLVCPQDFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCCGCKPGWFVECQVS  128
            :: |:| | |||  |:|  ||  |:  ||||  :|  |
Qy   62  DCRECESGSFTASENHLR-HCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYW-S  119

Db  129  QCVSSSPFYCQPCLDCGALHRHTRLLC-SRRDTDCGTCLPGFYEHGDGCVSCPPPPPS  185
           |||:     |  :|: | |  ::  ||:| |  :|||  |  :| |||  :::
Qy  120  ENLFQC-FNCSLCLN-GTVH----LSCQEKQNTVC-TCHAGFFLRENECVSCAGAAPG  170
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RESULT 14
ID Q85407   PRELIMINARY;   PRT;   348 AA.

AC Q85407;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE HOMOLOG OF VACCINIA VIRUS CDS B28R.
GN G2R.
OS VARIOLA VIRUS.
OC VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPOXVIRINAE;
OC ORTHOPOXVIRUSES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BANGLADESH-1975;
RX MEDLINE; 94088747.
RA MASSUNG R.F., ESPOSITO J.J., LIU L.I., QI J., UTTERBACK T.R.,
RA KNIGHT J.C., AUBIN L., YURAN T.E., PARSONS J.M., LOPAREV V.N.;
RL NATURE 366:748-751(1993).
DR EMBL; L22579; G439102; -.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
SQ SEQUENCE 348 AA; 38075 MW; 2A911AF6 CRC32;

Query Match   10.7%; Score 214; DB 11; Length 348;
Best Local Similarity   38.5%; Pred. No. 1.76e-26;
  Matches   30; Conservative   14; Mismatches 32; Indels   2; Gaps   2;

```
Db   39  HNLCCLSCPPGTYASRLCDSKT-NTQCTPCGSGTFTSRNNHLPACLSCNG-RCNSNQVET  96
            ::|:|| |||  :|:|| ||||||  |||:| |||:|||:     |  |||
Qy   37  NSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEI  96

Db   97  RSCNTTHNRICECSPGYY  114
           ||  ||  ::|| | |:|
Qy   97  SSCTVDRDTVCGCRKNQY  114
```

```
Db   40  HNLCCLSCPPGTYASRLCDSKT-NTQCTPCGSGTFTSRNNHLPACLSCNG-RCNSNQVET  97
            ::|:|| |||  :|:|| ||||||  |||:| |||:|||:     |  |||
Qy   37  NSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEI  96

Db   98  RSCNTTHNRICECSPGYY  115
           ||  ||  ::|| | |:|
Qy   97  SSCTVDRDTVCGCRKNQY  114
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Search completed: Wed May 6 08:49:44 1998
Job time : 78 secs.

RESULT 15
ID Q89918   PRELIMINARY;   PRT;   349 AA.

AC Q89918;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE SOMALIA-1977 RIGHT NEAR-TERMINAL REGION.
OS VARIOLA VIRUS.
OC VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPOXVIRINAE;
OC ORTHOPOXVIRUSES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SOMALIA-1977;
RA MASSUNG R.F., LOPAREV V.N., KNIGHT J.C., CHIZHIKOV V.E., PARSONS J.M.,
RA TOTMENIN A.V., SHCHELKUNOV S.N., ESPOSITO J.J.;
RL SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR EMBL; U18341; G885855; -.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
SQ SEQUENCE 349 AA; 38272 MW; 0FDCC784 CRC32;

Query Match   10.7%; Score 214; DB 11; Length 349;
Best Local Similarity   38.5%; Pred. No. 1.76e-26;
  Matches   30; Conservative   14; Mismatches 32; Indels   2; Gaps   2;

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**************************************************************************
 _   _ ___  ___  ___  __ _ _  _
| \ / | _ \/ __|| _ \/ _| || |
|  V  |  _/\__ \|   /| (_|| __ |
|_| |_|_|  |___/|_|_\ \__||_||_|   (TM)
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MPsrch_nn   n.a. -   n.a. database search, using Smith-Waterman algorithm

Run on: Wed May 6 12:57:57 1998; MasPar time 1227.99 Seconds
                 1496.959 Million cell updates/sec

Title: >US-08-804-166-3
Description: (1-1202) from US08804166.seq
Perfect Score: 1202
N.A. Sequence: 1 CTCGAGAТGGCTACAGGTAA.........CCCGGATCCTCCCACAATAA 1202
N.A. Comp: GAGCTCTACCGATGTCCATT.........GGGGCTAGGAGGGTGTTATT

Scoring table: TABLE default
                 Gap 6

Nmatch   STD :   Dbase 0; Query 0
Searched: 436399 seqs, 764661465 bases x 2
Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database: embl53
                 1:em_in 2:em_or 3:em_om 4:em_ov 5:em_pl 6:em_htg
                 7:em_hum1 8:em_hum2 9:em_ba 10:em_ro 11:em_un 12:em_vi
                 13:em_pat

Database: genbank105
                 14:gb_ro 15:gb_om 16:gb_ov 17:gb_in 18:gb_pl 19:gb_ba
                 20:gb_st 21:gb_vl 22:gb_ph 23:gb_sy 24:gb_un 25:gb_pat
                 26:gb_htg 27:gb_prl 28:gb_pr2

Statistics: Mean 11.143; Variance 5.206; scale 2.140

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	424	35.3	483	25	A29099	Synthetic DNA for TNF-	0.00e+00
2	424	35.3	510	25	A21525	oligonucleotide probe.	0.00e+00
3	424	35.3	600	25	A20257	Synthetic nucleotide s	0.00e+00
4	424	35.3	1331	25	A29103	H.sapiens mRNA for TNF	0.00e+00
5	424	35.3	1368	25	A29098	Synthetic DNA for TNF-	0.00e+00
6	424	35.3	2050	27	HUMTNFRP	Human tumor necrosis f	0.00e+00
7	424	35.3	2062	25	I43805	Sequence 24 from paten	0.00e+00
8	424	35.3	2062	25	A21522	TNF alpha gene.	0.00e+00
9	424	35.3	2087	27	HUMTNFR	Human tumor necrosis f	0.00e+00
10	424	35.3	2111	25	HUMTNFRB	Homo sapiens tumor nec	0.00e+00
11	424	35.3	2111	25	A26412	cDNA for (55KD TNF-BP)	0.00e+00
12	424	35.3	2112	27	HUMTNFRC	Human tumor necrosis f	0.00e+00
13	424	35.3	2161	27	HSTNFR1A	H.sapiens TNF-R mRNA f	0.00e+00
14	424	35.3	2175	25	A43873	Sequence 1 from Patent	0.00e+00
15	424	35.3	2175	25	I64751	Sequence 1 from patent	0.00e+00
16	424	35.3	2176	25	A19907	Synthetic nucleotide s	0.00e+00
17	424	35.3	6889	25	I26928	Sequence 2 from patent	0.00e+00
18	424	34.9	600	25	I43808	Sequence 47 from paten	0.00e+00
19	424	34.7	2061	25	A20255	55kD receptor gene for	0.00e+00
20	414	34.4	539	27	HUMCGB	Human chorionic gonado	0.63e-237
21	504	31.7	504	25	I43813	Sequence 56 from paten	0.63e-237
22	381	31.7	381	25	A20713	Synthetic nucleotide s	0.00e+00
23	379	31.5	501	25	I43786	Sequence 1 from patent	0.00e+00
24	372	30.9	500	25	A20254	Synthetic nucleotide s	0.00e+00
25	372	30.9	372	25	A20253	Sequence 1 from patent	1.14e-294
26	370	30.8	372	25	I43787	Sequence 3 from patent	1.14e-294
27	642	27.5	642	27	BABBGCA	Baboon beta-chorionic	1.27e-258
28	330	27.5	1665	27	HUMGHCSA	Human growth hormone (	1.27e-258
29	330	25.6	1665	27	HSGG02	Human chorionic gonado	7.42e-239
30	306	25.5	468	27	HUMCGBBA3	Human chorionic gonado	4.63e-237
31	306	25.5	475	27	HUMCGBEL03	Human chorionic gonado	4.63e-237
32	306	25.5	1665	25	HSCG01	Human chorionic gonado	4.63e-237
33	303	25.2	1826	25	I02855	Sequence 1 from Patent	2.27e-234
34	302	25.1	581	25	FCU72244	Felis catus tumour nec	1.79e-233
35	302	25.1	1964	27	HUMGH	Human growth hormone	1.79e-233
36	302	25.1	1964	27	HSGROW2	Human growth hormone (	1.79e-233
37	302	25.1	2771	25	I41411	Human chorionic gonado	1.79e-233
38	300	25.0	474	25	I43809	Sequence 49 from paten	1.11e-231
39	300	25.0	474	25	A20259	Synthetic nucleotide s	1.11e-231
40	301	25.0	2657	27	HUMGHN	Human growth hormone g	1.41e-232
41	301	25.0	4283	25	I63120	Sequence 3 from patent	1.41e-232
42	293	24.4	2004	15	SSU19994	Sus scrofa p55 TNF rec	2.08e-225
43	283	23.5	426	25	I08477	Sequence 18 from Paten	1.86e-216
44	255	21.2	426	25	A20263	Synthetic nucleotide s	1.84e-191
45	255	21.2	477	25	I43811	Sequence 53 from paten	1.84e-191

ALIGNMENTS

RESULT 1

LOCUS	A29099	483 bp	DNA	PAT	03-JUL-1995

DEFINITION   Synthetic DNA for TNF-binding polypeptide from patent EP0393438.
ACCESSION   A29099
NID   g1248693
KEYWORDS   unidentified.
SOURCE   unidentified.
  ORGANISM   unidentified
             unclassified.
REFERENCE   1 (bases 1 to 483)
  AUTHORS   Hauptmann,R., Himmler,A., Maurer-Fogy,I. and Stratowa,C.
  TITLE   TNF-receptor, TNF-binding protein and DNA coding therefor
  JOURNAL   Patent: EP 0393438-A 49 24-OCT-1990;
             BOEHRINGER INGELHEIM INTERNATIONAL G.M.B.H
FEATURES   Location/Qualifiers
     source   1..483
                     /organism="unidentified"
                     /db_xref="taxon:32644"
     source   1..483
                     /organism="artificial sequence"
                     /db_xref="taxon:29278"
BASE COUNT   130 a   124 c   123 g   106 t
ORIGIN

Query Match   35.3%; Score 424; DB 25; Length 483;
Best Local Similarity   99.8%;
Matches   425; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

```
Qy    1 GATAGTGTGTGTGTCCCCAAGGAAAAATATATCCACCCTCAAAATAATTCAITTCGTGTACC   60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 GATAGTGTGTGTGTCCCCAAGGAAAAATATATCCACCCTCAAAATAATTCAITTCGTGTACC   60

Qy  345 GATAGTGTGTGTGTCCCCAGGAAAATATATCCACCCTCAAATAATTCAITTCGTGTACC      404
Db   61 AAGTGCCACAAAGGAAACCTACTTGTTACAATGACTGTCCAGGCGCCCAGGAGATACGGAC   120

Qy  405 AAGTGCCACAAAGGAAACCTACTTGTTACAATGACTGTCCAGGCGCCCAGGATACGGAC     464
Db  121 TGCAGGGGAGTGTGAGAGCGGCGGCGCTCCTTCACCGGCTTCAGAGAAAACCACCTCAGACACTGCCTC 180
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Qy  465 TGCAGGGAGTGTGAGAGCGGCGGCTCTTCACCGGCTTCAGAAAAACCACTCAGACACTGCCTC 524
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Db  121 TGCAGGGAGTGTGAGAGCGGCGGCTCTTCACCGGCTTCAGAAAAACCACTCAGACACTGCCTC 180
Qy  525 AGCTGCTCCAAAATGCCGAAAGGAGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584
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Db  181 AGCTGCTCCAAAATGCCGAAAGGAGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 240
Qy  585 CGGGACACCCGTGTGTGGCCTCCAGGAAGAACCAGTACCGGCCATTATTGGAGTGAAAACCTT 644
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Db  241 CGGGACACCCGTGTGTGGCCTCCAGGAAGAACCAGTACCGGCCATTATTGGAGTGAAAACCTT 300
Qy  645 TTCCAGTGCTTCAATTGCAGCCTCTCAATTGGGACCGTGCACCTCTCCCTGCCAGGAG 704
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 TTCCAGTGCTTCAATTGCAGCCTCTCAATTGGGACCGTGCACCTCTCCCTGCCAGGAG 360
Qy  705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764
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Db  361 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 420
Qy  765 TCCTGT 770
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Db  421 TCCTGT 426
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RESULT   2

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LOCUS       A21525       510 bp    DNA              PAT       26-JUL-1994
DEFINITION  oligonucleotide probe.
ACCESSION   A21525
NID         g583574
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 510)
  AUTHORS
  JOURNAL   Patent: GB 2246569-A 4 05-FEB-1992;
FEATURES             Location/Qualifiers
     source          1..510
                     /organism="Artificial sequences"
BASE COUNT      136 a    132 c    133 g    109 t
ORIGIN
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Query Match   35.3%; Score 424; DB 25; Length 510;
Best Local Similarity 99.8%; Pred. No. 0.00e+00;
Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db   34 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 93
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Qy  345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404
Db   94 AAGTGCCACAAAAGGAACCTACTTGTACAAATGACTGTCCAGGCCGCCGGGGGCAGGATACGGAC 153
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Qy  405 AAGTGCCACAAAAGGAACCTACTTGTACAAATGACTGTCCAGGCCGCCGGGGGCAGGATACGGAC 464
Db  154 TGCAGGGAGTGTGAGAGCGGCGGCTCCTTCACCGGCTTCAGAAAAACCACTCAGACACTGCCTC 213
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Qy  465 TGCAGGGAGTGTGAGAGCGGCGGCTCTTCACCGGCTTCAGAAAAACCACTCAGACACTGCCTC 524
Db  214 AGCTGCTCCAAAATGCCGAAAGGAGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 273
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Qy  525 AGCTGCTCCAAAATGCCGAAAGGAGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584
Db  274 CGGGACACCCGTGTGTGGCCTCCAGGAAGAACCAGTACCGGCCATTATTGGAGTGAAAACCTT 333
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Qy  585 CGGGACACCCGTGTGTGGCCTCCAGGAAGAACCAGTACCGGCCATTATTGGAGTGAAAACCTT 644
Db  334 TTCCAGTGCTTCAATTGCAGCCTCTCAATTGGGACCGTGCACCTCTCCCTGCCAGGAG 393
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  645 TTCCAGTGCTTCAATTGCAGCCTCTCAATTGGGACCGTGCACCTCTCCCTGCCAGGAG 704
Db  394 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 453
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Qy  705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764
Db  454 TCCTGT 459
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Qy  765 TCCTGT 770
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RESULT   3

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LOCUS       A20257       600 bp    DNA              PAT       20-SEP-1995
DEFINITION  Synthetic nucleotide sequence of plasmid p-TNFred.
ACCESSION   A20257
NID         g1247896
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 600)
  AUTHORS
  TITLE     MODIFIED HUMAN TNFALPHA (TUMOR NECROSIS FACTOR ALPHA) RECEPTOR
  JOURNAL   Patent: WO 9207076-A 25 30-APR-1992;
FEATURES             Location/Qualifiers
     source          1..600
                     /organism="unidentified"
                     /db_xref="taxon:32644"
     source          1..600
                     /organism="artificial sequence"
                     /db_xref="taxon:29278"
BASE COUNT      148 a    157 c    162 g    133 t
ORIGIN
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Query Match   35.3%; Score 424; DB 25; Length 600;
Best Local Similarity 99.8%; Pred. No. 0.00e+00;
Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db  121 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 180
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Qy  345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404
Db  181 AAGTGCCACAAAAGGAACCTACTTGTACAAATGACTGTCCAGGCCGCCGGGGGCAGGATACGGAC 240
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Qy  405 AAGTGCCACAAAAGGAACCTACTTGTACAAATGACTGTCCAGGCCGCCGGGGGCAGGATACGGAC 464
Db  241 TGCAGGGAGTGTGAGAGCGGCGGCTCCTTCACCGGCTTCAGAAAAACCACTCAGACACTGCCTC 300
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Qy  465 TGCAGGGAGTGTGAGAGCGGCGGCTCTTCACCGGCTTCAGAAAAACCACTCAGACACTGCCTC 524
Db  301 AGCTGCTCCAAAATGCCGAAAGGAGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 360
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Qy  525 AGCTGCTCCAAAATGCCGAAAGGAGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584
Db  361 CGGGACACCCGTGTGTGGCCTCCAGGAAGAACCAGTACCGGCCATTATTGGAGTGAAAACCTT 420
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Qy  585 CGGGACACCCGTGTGTGGCCTCCAGGAAGAACCAGTACCGGCCATTATTGGAGTGAAAACCTT 644
Db  421 TTCCAGTGCTTCAATTGCAGCCTCTCAATTGGGACCGTGCACCTCTCCCTGCCAGGAG 480
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Qy  645 TTCCAGTGCTTCAATTGCAGCCTCTCAATTGGGACCGTGCACCTCTCCCTGCCAGGAG 704
Db  481 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 540
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Qy  705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764
Db  541 TCCTGT 546
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Qy  765 TCCTGT 770
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RESULT   4

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LOCUS       A29103      1331 bp    DNA              PAT       03-JUL-1995
DEFINITION  H.sapiens mRNA for TNF-binding polypeptide from patent EP0933438.
ACCESSION   A29103
```

```
NID         g1247517
SOURCE      human.
KEYWORDS    Homo sapiens
ORGANISM    Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1331)
AUTHORS     Hauptmann,R., Himmler,A., Maurer-Fogy,I. and Stratowa,C.
TITLE       TNF-receptor, TNF-binding protein and DNA coding therefor
JOURNAL     Patent: EP 0393438-A 53 24-OCT-1990;
            BOEHRINGER INGELHEIM INTERNATIONAL G.M.B.H
FEATURES    Location/Qualifiers
     source      1..1331
                 /organism="Homo sapiens"
                 /db_xref="taxon:9606"
BASE COUNT  298 a   407 c   343 g   283 t
ORIGIN
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RESULT 5

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LOCUS       A29098   1368 bp   DNA   PAT   03-JUL-1995
DEFINITION  Synthetic DNA for TNF-receptor from patent EP0393438.
ACCESSION   A29098
NID         g1248892
KEYWORDS    .
SOURCE      unidentified.
ORGANISM    unidentified
            unclassified.
REFERENCE   1 (bases 1 to 1368)
AUTHORS     Hauptmann,R., Himmler,A., Maurer-Fogy,I. and Stratowa,C.
TITLE       TNF-receptor, TNF-binding protein and DNA coding therefor
JOURNAL     Patent: EP 0393438-A 48 24-OCT-1990
            BOEHRINGER INGELHEIM INTERNATIONAL G.M.B.H
FEATURES    Location/Qualifiers
     source      1..1368
                 /organism="unidentified"
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Query Match       35.3%;  Score 424;  DB 25;  Length 1331;
Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
Matches  425;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy  333 GATAGTGTGTGGTCCCCAAGGAAAAAATATATCCACCCTCAAAATAATATTCGATTTGCTGTACC 392
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Db  345 GATAGTGTGTGTCCCCAAGGAAAAAATATATCCACCCTCAAAATAATATTCGATTTGCTGTACC 404

Qy  393 AAGTGCCACAAAAGGAAACCTACTTGTACAATGACACTGTCCAGGCGGCCCGGGGCAGGATACGGAC 452
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  405 AAGTGCCACAAAAGGAAACCTACTTGTACAATGACACTGTCCAGGCGGCCCGGGGCAGGATACGGAC 464

Qy  453 TGCAGGGAGTGTGTGAGAGCGGCGGCTCTTCACCGCTCAGAAAAACCACCTCACACTGCCCTC 512
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Db  465 TGCAGGGAGTGTGAGAGCGGCGGCTCTTCACCGCTCAGAAAAACCACCTCACACTGCCCTC 524

Qy  513 AGCTGCTCCAAATGCCGAAAAGGAAAATGGGTCAGGTGGGAGATCTCTTCTTGCACAGTGGAC 572
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Db  525 AGCTGCTCCAAATGCCGAAAAGGAAAATGGGTCAGGTGGGAGATCTCTTCTTGCACAGTGGAC 584

Qy  573 CGGGACACCGTGTGTGGCTGCAGGAAGAAACACAGTACCGGCATTATTGGAGTGAAAACCTT 632
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  585 CGGGACACCGTGTGTGGCTGCAGGAAGAAACACAGTACCGGCATTATTGGAGTGAAAACCTT 644

Qy  633 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAACCTCTCCTGCCAGGAG 692
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Db  645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAACCTCTCCTGCCAGGAG 704

Qy  693 AAACAGAACACCGTGTGCACCTGCAGGTTCTTTCTAAGAGAAAAGAGAGTGTGTC 752
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Db  705 AAACAGAACACCGTGTGCACCTGCAGGTTCTTTCTAAGAGAAAAGAGAGTGTGTC 764

Qy  753 TCCTGT 758
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Db  765 TCCTGT 770
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BASE COUNT   293 a   424 c   375 g   276 t
ORIGIN

Query Match       35.3%;  Score 424;  DB 25;  Length 1368;
Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
Matches  425;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy  121 GATAGTGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATATTCGATTTGCTGTACC 180
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Db  345 GATAGTGTGTGTCCCCAAGGAAAAAATATATCCACCCTCAAAATAATATTCGATTTGCTGTACC 404

Qy  181 AAGTGCCACAAAAGGAAACCTACTTGTACAATGACACTGTCCAGGCGGCCCGGGGCAGGATACGGAC 240
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Db  405 AAGTGCCACAAAAGGAAACCTACTTGTACAATGACACTGTCCAGGCGGCCCGGGGCAGGATACGGAC 464

Qy  241 TGCAGGGAGTGTGAGAGCGGCGGCTCTTCACCGCTCAGAAAAACCACCTCACACTGCCCTC 300
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Db  465 TGCAGGGAGTGTGAGAGCGGCGGCTCTTCACCGCTCAGAAAAACCACCTCACACTGCCCTC 524

Qy  301 AGCTGCTCCAAATGCCGAAAAGGAAATGGGTCAGGTGGGAGATCTCTTCTTGCACAGTGGAC 360
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Db  525 AGCTGCTCCAAATGCCGAAAAGGAAATGGGTCAGGTGGGAGATCTCTTCTTGCACAGTGGAC 584

Qy  361 CGGGACACCGTGTGTGGCTGCAGGAAGAAACAGTACCGGCATTATTGGAGTGAAAACCTT 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  585 CGGGACACCGTGTGTGGCTGCAGGAAGAAACAGTACCGGCATTATTGGAGTGAAAACCTT 644

Qy  421 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGGTGCACCTGCCAGGAG 480
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Db  645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGGTGCACCTGCCAGGAG 704

Qy  481 AAACAGAACACCGTGTGCACCTGCAGGTTCTTTCTTGAAGAGAAAAGAGAGTGTGTC 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  705 AAACAGAACACCGTGTGCACCTGCAGGTTCTTTCTTGAAGAGAAAAGAGAGTGTGTC 764

Qy  541 TCCTGT 546
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Db  765 TCCTGT 770
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RESULT 6

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LOCUS       HUMTNFRP   2050 bp   mRNA   PRI   11-OCT-1991
DEFINITION  Human tumor necrosis factor receptor (TNF) mRNA, complete cds.
ACCESSION   M60275 M37764
NID         g339759
KEYWORDS    TNF receptor; transmembrane receptor; tumor necrosis factor
            receptor.
SOURCE      Human placenta, cDNA to mRNA.
ORGANISM    Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 2050)
AUTHORS     Gray,P.W., Barrett,K.J., Chantry,D., Turner,M. and Feldman,M.
TITLE       Cloning of human tumor necrosis factor (TNF) receptor cDNA and
            expression of recombinant soluble TNF-binding protein
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384 (1990)
MEDLINE     91017509
COMMENT     Draft entry and computer-readable sequence for [Proc. Natl. Acad.
            Sci. U.S.A. (1990) In press] kindly submitted
            by P.W.Gray, 13-AUG-1990.
FEATURES    Location/Qualifiers
     source      1..2050
                 /organism="Homo sapiens"
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                 /tissue_type="placenta"
     sig_peptide 155..274
                 /gene="TNF receptor"
     CDS         155..1516
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Left column (RESULT 7)

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RESULT 7
LOCUS        I43805              2062 bp        DNA              PAT    10-JUL-1997
DEFINITION   Sequence 24 from patent US 5631145.
ACCESSION    I43805
NID          g2468903
KEYWORDS
SOURCE       Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE    1 (bases 1 to 2062)
  AUTHORS    Feldmann,M., Gray,P.W., Turner,M.J.C. and Brennan,F.M.
  TITLE      TNF.alpha. receptor-derived binding protein
  JOURNAL    Patent: US 5631145-A 24 27-MAY-1997;
FEATURES             Location/Qualifiers
  source             1..2062
                     /organism="unknown"
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ORIGIN
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BASE COUNT    429 a     611 c     566 g     444 t

gene          155..274
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              KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVI
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              PGFTPTLGFSPVPSSTFTSSSTYTPGDCPNFAAPRREVAPPYQGADPILATALASDPI
              PNPLQKWEDSAHKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQN
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              LLR"
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Top-right block (RESULT, Query Match)

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Query Match      35.3%;     Score 424;    DB 27;    Length 2050;
Best Local Similarity   99.8%;     Pred. No. 0.00e+00;
Matches    425;   Conservative     0;   Mismatches   1;   Indels   0;   Gaps   0;
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Qy   275  GATAGTGTGTGTCCCCAAGGAAAAAATATATCCACCCTCAAAATAATAATTCATTTGCTGTGTACC  334
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Db   275  GATAGTGTGTGTCCCCAAGGAAAAAATATATCCACCCTCAAAATAATAATTCATTTGCTGTGTACC  334

Qy   335  AAGTGCCACAAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGGGGGCCGAGGATACGGAC  394
Db   335  AAGTGCCACAAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGGGGGCCGAGGATACGGAC  394

Qy   395  TGCAGGGAGTGTGAGAGCGGCGGCTCCTTCACGGCCTCAGAAAACCACCTCAGACACTGCCTC  454
Db   395  TGCAGGGAGTGTGAGAGCGGCGGCTCCTTCACGGCCTCAGAAAACCACCTCAGACACTGCCTC  454

Qy   455  AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC  514
Db   455  AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC  514

Qy   515  CGGGACACCGTGTGTGGGCTGCAGGAAGAACCAGTACCGGCCATTATTGGAGTGAAAACCTT  574
Db   515  CGGGACACCGTGTGTGGGCTGCAGGAAGAACCAGTACCGGCCATTATTGGAGTGAAAACCTT  574

Qy   575  TTCCAGTGCTTCAATTGCAGCCTCTGCCTCTCCTGCAGGAG  634
Db   575  TTCCAGTGCTTCAATTGCAGCCTCTGCCTCTCCTGCAGGAG  634

Qy   635  AAACAGAACACCCGTGCACCTGCACCTGTTCTTTCTTAAGGAGAAAACGAGTGTGTC  694
Db   635  AAACAGAACACCCGTGCACCTGCACCTGTTCTTTCTTAAGGAGAAAACGAGTGTGTC  694

Qy   705  AAACAGAACACCCGTGCACCTGCACCTGTTCTTTCTTAAGAGAAAAACGAGTGTGTC  764
Db   705  AAACAGAACACCCGTGCACCTGCACCTGTTCTTTCTTAAGAGAAAAACGAGTGTGTC  764

Qy   765  TCCTGT  770
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Db   765  TCCTGT  770
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Right column (RESULT 8)

ORIGIN
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BASE COUNT    429 a     617 c     573 g     443 t
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Query Match      35.3%;     Score 424;    DB 25;    Length 2062;
Best Local Similarity   99.8%;     Pred. No. 0.00e+00;
Matches    425;   Conservative     0;   Mismatches   1;   Indels   0;   Gaps   0;
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Qy   275  GATAGTGTGTGTCCCCAAGGAAAAAATATATCCACCCTCAAAATAATAATTCATTTGCTGTGTACC  334
Db   275  GATAGTGTGTGTCCCCAAGGAAAAAATATATCCACCCTCAAAATAATAATTCATTTGCTGTGTACC  334

Qy   335  AAGTGCCACAAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGGGGGCCGAGGATACGGAC  394
Db   335  AAGTGCCACAAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGGGGGCCGAGGATACGGAC  394

Qy   395  TGCAGGGAGTGTGAGAGCGGCGGCTCCTTCACGGCCTCAGAAAACCACCTCAGACACTGCCTC  454
Db   395  TGCAGGGAGTGTGAGAGCGGCGGCTCCTTCACGGCCTCAGAAAACCACCTCAGACACTGCCTC  454

Qy   455  AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC  514
Db   455  AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC  514

Qy   515  CGGGACACCGTGTGTGGGCTGCAGGAAGAACCAGTACCGGCCATTATTGGAGTGAAAACCTT  574
Db   515  CGGGACACCGTGTGTGGGCTGCAGGAAGAACCAGTACCGGCCATTATTGGAGTGAAAACCTT  574

Qy   575  TTCCAGTGCTTCAATTGCAGCCTCTGCCTCTCCTGCAGGAG  634
Db   575  TTCCAGTGCTTCAATTGCAGCCTCTGCCTCTCCTGCAGGAG  634

Qy   635  AAACAGAACACCCGTGCACCTGCACCTGTTCTTTCTTAAGGAGAAAACGAGTGTGTC  694
Db   635  AAACAGAACACCCGTGCACCTGCACCTGTTCTTTCTTAAGGAGAAAACGAGTGTGTC  694

Qy   705  AAACAGAACACCCGTGCACCTGCACCTGTTCTTTCTTAAGAGAAAAACGAGTGTGTC  764
Db   705  AAACAGAACACCCGTGCACCTGCACCTGTTCTTTCTTAAGAGAAAAACGAGTGTGTC  764

Qy   765  TCCTGT  770
Db   765  TCCTGT  770
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RESULT 8
LOCUS        A21522              2062 bp        RNA              PAT    26-JUL-1994
DEFINITION   TNF alpha gene.
ACCESSION    A21522
NID          g579599
KEYWORDS
SOURCE       human.
  ORGANISM   Homo sapiens
             Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
             Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 2062)
  AUTHORS
  JOURNAL    Patent: GB 2246569-A 1 05-FEB-1992;
FEATURES             Location/Qualifiers
  source             1..2062
                     /organism="Homo sapiens"
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BASE COUNT    429 a    617 c    573 g    443 t
ORIGIN

Query Match      35.3%;   Score 424;   DB 25;   Length 2062;
Best Local Similarity  99.8%;   Pred. No. 0.00e+00;
Matches  425;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy   275  GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTGATTTGCTGTACC  334
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Db   345  GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTGATTTGCTGTACC  404

Qy   335  AAGTGCCACAAAAGGAAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC  394
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Db   405  AAGTGCCACAAAAGGAAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC  464

Qy   395  TGCAGGGAGGAGTGTGAGAGCGGGCGGCTCTTCACCCCTTCAGAGAAAACCACTGCCTC  454
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Db   465  TGCAGGGAGGAGTGTGAGAGCGGGCGGCTCTTCACCCCTTCAGAGAAAACCACTGCCTC  524

Qy   455  AGCTGCTCCAAATGCCGAAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC  514
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Db   525  AGCTGCTCCAAATGCCGAAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC  584

Qy   515  CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGTGGAGTGAAAACCTT  574
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Db   585  CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGTGGAGTGAAAACCTT  644

Qy   575  TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTTCACCTCTCCTGCCAGGAG  634
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Db   645  TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTTCACCTCTCCTGCCAGGAG  704

Qy   635  AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTTAAGAGAAAAAGGAGTGTGTC  694
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Db   705  AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTTAAGAGAAAAAGGAGTGTGTC  764

Qy   695  TCCTGT  700
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Db   765  TCCTGT  770
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RESULT  9
LOCUS       HUMTNFR         2087 bp    mRNA            PRI       10-NOV-1993
DEFINITION  Human tumor necrosis factor receptor mRNA, complete cds.
ACCESSION   M33294
NID         g339744
KEYWORDS    cell surface receptor; tumor necrosis factor receptor.
SOURCE      Human placenta, cDNA to mRNA.
ORGANISM    Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2087)
AUTHORS     Schall,T.J., Lewis,M., Koller,K.J., Lee,A.L., Rice,G.C., Wong,G.H.,
            Gatanaga,T., Granger,G.A., Lentz,R., Raab,H., Kohr,W.J. and
            Goeddel,D.V.
TITLE       Molecular cloning and expression of a receptor for human tumor
            necrosis factor
JOURNAL     Cell 61, 361-370 (1990)
MEDLINE     90235285
COMMENT     Draft entry and computer-readable sequence for [1] kindly submitted
            by T.Schall, 26-MAR-1990.
FEATURES             Location/Qualifiers
     source          1..2087
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     CDS             182..1549
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BASE COUNT    433 a    624 c    581 g    449 t
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Query Match      35.3%;   Score 424;   DB 27;   Length 2087;
Best Local Similarity  99.8%;   Pred. No. 0.00e+00;
Matches  425;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

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Db   345  GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC  404

Qy   362  AAGTGCCACAAAAGGAAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC  421
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Db   405  AAGTGCCACAAAAGGAAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC  464

Qy   422  TGCAGGGAGGAGTGTGAGAGCGGGCTCCTCACCCGCTTCAGAAAAACCACCTCAGACACTGCCTC  481
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Db   465  TGCAGGGAGGAGTGTGAGAGCGGGCGGCTCCTCACCCGCTTCAGAAAAACCACCTCAGACACTGCCTC  524

Qy   482  AGCTGCTCCAAATGCCGAAAAGGAAATGGGTCAGGTGGAGGATCTCTTCTTGCACAGTGGAC  541
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Db   525  AGCTGCTCCAAATGCCGAAAAGGAAATGGGTCAGGTGGAGGATCTCTTCTTGCACAGTGGAC  584

Qy   542  CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGTGGAGTGAAAACCTT  601
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Db   585  CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGTGGAGTGAAAACCTT  644

Qy   602  TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTTCACCTCTCCTGCCAGGAG  661
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Db   645  TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTTCACCTCTCCTGCCAGGAG  704

Qy   662  AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTTAAGAGAAAAACGAGTGTGTC  721
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Db   705  AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTTAAGAGAAAAACGAGTGTGTC  764

Qy   722  TCCTGT  727
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Db   765  TCCTGT  770
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RESULT  10
LOCUS       HUMTNFRB        2111 bp    mRNA            PRI       14-NOV-1990
DEFINITION  Homo sapiens tumor necrosis factor receptor mRNA, complete cds.
ACCESSION   M58286 M33480
NID         g339753
KEYWORDS    tumor necrosis factor receptor.
SOURCE      Human cell line HL60, cDNA to mRNA.
ORGANISM    Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2111)
AUTHORS     Loetscher,H., Pan,Y.-C.E., Lahm,H.-W., Gentz,R., Brockhaus,M.,
            Tabuchi,H. and Lesslauer,W.
TITLE       Molecular cloning and expression of the human 55 kd tumor necrosis
            factor receptor
JOURNAL     Cell 61, 351-359 (1990)
MEDLINE     90235284
FEATURES             Location/Qualifiers
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Left column

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BASE COUNT   445 a   629 c   587 g   450 t
ORIGIN

Query Match   35.3%; Score 424; DB 27; Length 2111;
Best Local Similarity   99.8%; Pred. No. 0.00e+00;
Matches   425; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

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Db  345 GATAGTGTGTGTCCCCAAGGAAAAATAATATATCCACCCTCAAAATAATTAATTCGATTTGCTGTACC 404

Qy  367 AAGTGCCACAAAGGAAACCTACTTGTACAAATGACTGTCCAGGCCCGGGGACCCGGGGACCAGGGGAC 426
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Db  405 AAGTGCCACAAAGGAAACCTACTTGTACAAATGACTGTCCAGGCCCGGGGACCCGGGGACCAGGGGAC 464

Qy  427 TGCAGGGAGTGTGAGAGCGGCCTCCTCTTCACCGCTTCAGAAAAACCACCTCAGACACTGCCTC 486
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Db  465 TGCAGGGAGTGTGAGAGCGGCCTCCTCTTCACCGCTTCAGAAAAACCACCTCAGACACTGCCTC 524

Qy  487 AGCTGCTCCAAAATGCCGAAAGGAAAATGGGTCAGTGGAGATCTCTTCTTGCACAGTGGAC 546
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Db  525 AGCTGCTCCAAAATGCCGAAAGGAAAATGGGTCAGTGGAGATCTCTTCTTGCACAGTGGAC 584

Qy  547 CGGGACACCGTGTGTGGGCTGCAGGAAGAACCAGTACCGCCGCCATTATTGGGAGTGAAAACCTT 606
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Qy  607 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCCTCCTGCCAGGAG 666
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Db  645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCCTCCTGCCAGGAG 704

Qy  667 AAACAGAAACACCGTGTGCACCTGCCATGCGCAGGTTTTCTTTCTTAAGAGAAAAACGAGTGTGTC 726
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Db  705 AAACAGAAACACCGTGTGCACCTGCCATGCGCAGGTTTTCTTTCTTAAGAGAAAAACGAGTGTGTC 764

Qy  727 TCCTGT 732
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RESULT   11
LOCUS   A26412   2111 bp   DNA   PAT   26-APR-1995
DEFINITION   cDNA for (55kD TNF-BP) tumor necrosis factor binding protein from
     patent EP0417563.
ACCESSION   A26412
NID   g904968
KEYWORDS   .
SOURCE   unidentified.
     ORGANISM   unidentified
     unclassified.
REFERENCE   1 (bases 1 to 2111)
AUTHORS   Brockhaus,M., Dembic,Z., Gentz,R., Lesslauer,W., Loetscher,H. and
     Schlaeger,E.J.

Right column

FEATURES   Location/Qualifiers
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     /product="55 kD TNF-BP"
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     FGLCLLSLLFIGLMYRYQRWKSKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPT
     PGFTPTLGFSPVPSSTFTSSSTYTPGDCPNFAAPRREYAPPYQGADPILATALASDPI
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BASE COUNT   445 a   629 c   587 g   450 t
ORIGIN

Query Match   35.3%; Score 424; DB 25; Length 2111;
Best Local Similarity   99.8%; Pred. No. 0.00e+00;
Matches   425; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

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Db  307 GATAGTGTGTGTCCCCAAGGAAAAATAATATATCCACCCTCAAAATAATTAATTCGATTTGCTGTACC 366
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Qy  345 GATAGTGTGTGTCCCCAAGGAAAAATAATATATCCACCCTCAAAATAATTAATTCGATTTGCTGTACC 404

Db  367 AAGTGCCACAAAGGAAACCTACTTGTACAAATGACTGTCCAGGCCCGGGGACCCGGGGACCAGGGGAC 426
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Qy  405 AAGTGCCACAAAGGAAACCTACTTGTACAAATGACTGTCCAGGCCCGGGGACCCGGGGACCAGGGGAC 464

Db  427 TGCAGGGAGTGTGAGAGCGGCCTCCTCTTCACCGCTTCAGAAAAACCACCTCAGACACTGCCTC 486
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Qy  465 TGCAGGGAGTGTGAGAGCGGCCTCCTCTTCACCGCTTCAGAAAAACCACCTCAGACACTGCCTC 524

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Qy  525 AGCTGCTCCAAAATGCCGAAAGGAAAATGGGTCAGTGGAGATCTCTTCTTGCACAGTGGAC 584

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Qy  585 CGGGACACCGTGTGTGGGCTGCAGGAAGAACCAGTACCGCCGCCATTATTGGGAGTGAAAACCTT 644

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Qy  645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCCTCCTGCCAGGAG 704

Db  667 AAACAGAAACACCGTGTGCACCTGCCATGCGCAGGTTTTCTTTCTTAAGAGAAAAACGAGTGTGTC 726
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Qy  705 AAACAGAAACACCGTGTGCACCTGCCATGCGCAGGTTTTCTTTCTTAAGAGAAAAACGAGTGTGTC 764

Db  727 TCCTGT 732
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Qy  765 TCCTGT 770
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RESULT   12
LOCUS   HUMTNFRC   2112 bp   mRNA   PRI   30-SEP-1991
DEFINITION   Human tumor necrosis factor receptor (TNF receptor) mRNA, complete
     cds.
ACCESSION   M63121 M75861
NID   g339755
KEYWORDS   tumor necrosis factor receptor.
SOURCE   Human cDNA to mRNA.
     ORGANISM   Homo sapiens
     Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
     Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 2112)

AUTHORS   Himmler,A., Maurer-Fogy,I., Kroenke,M., Scheurich,P.,
           Pfizenmaier,K., Lantz,M., Olson,I., Hauptmann,R., Stratowa,C. and
           Adolf,G.R.
TITLE   Molecular cloning and expression of human and rat tumor necrosis
           factor receptor chain (p60) and its soluble derivative, tumor
           necrosis factor-binding protein
JOURNAL   DNA Cell Biol. 9, 705-715 (1990)
MEDLINE   91090841
FEATURES   Location/Qualifiers
    source   1..2112
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                    /db_xref="taxon:9606"
    sig_peptide   207..293
                    /gene="TNF receptor"
    CDS   207..1574
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                    /codon_start=1
                    /product="tumor necrosis factor receptor"
                    /db_xref="PID:g339756"
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BASE COUNT   435 a   632 c   589 g   456 t
ORIGIN

Query Match   35.3%; Score 424; DB 27; Length 2112;
Best Local Similarity   99.8%; Pred. No. 0.00e+00;
Matches 425; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

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Qy   387 AAGTGCCACAAAAGGAACCTACTTGTACAAATGACTGTCCAGGCCCGGGCAGGATACGGAC 446
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Db   405 AAGTGCCACAAAAGGAACCTACTTGTACAAATGACTGTCCAGGCCCGGGCAGGATACGGAC 464

Db   447 TGCAGGGAGTGTGAGAGCGGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 506
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Qy   465 TGCAGGGAGTGTGAGAGCGGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db   507 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 566
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Qy   525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db   567 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCACCATTATTGGAGTGAAAACCTT 626
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Qy   645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACGGTGCACCTCCTGCCAGGAG 704

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Qy   705 AAACAGAACACCGTGTGCACCTGCCATGCAGGATTCTTTCTRAAGAGAAAACGAGTGTC 764

Db   747 TCCTGT 752
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Qy   765 TCCTGT 770

RESULT   13
LOCUS   HSTNFR1A   2161 bp   RNA   PRI   18-JAN-1993
DEFINITION H.saplens TNF-R mRNA for tumor necrosis factor receptor type 1.
ACCESSION X55313
NID   g37223
KEYWORDS   TNF-R gene; tumor necrosis factor receptor 1.
SOURCE   human.
ORGANISM   Homo sapiens
           Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
           Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2161)
AUTHORS   Nophar,Y., Kemper,O., Brakebusch,C., Engelmann,H., Zwang,R.,
           Aderka,D., Holtmann,H. and Wallach,D.
TITLE   Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA
           for the type I TNF-R, cloned using amino acid sequence data of its
           soluble form, encodes both the cell surface and a soluble form of
           the receptor
JOURNAL   EMBO J. 9 (10), 3269-3278 (1990)
MEDLINE   91006021
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BASE COUNT   459 a   642 c   604 g   456 t
ORIGIN

Query Match   35.3%; Score 424; DB 27; Length 2161;
Best Local Similarity   99.8%; Pred. No. 0.00e+00;
Matches 425; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   376 GATAGTGTGTGTCCCCAAGGAAAAATATATCACACCCTCAAAAATAATTCGATTTGCTGTACC 435
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   345 GATAGTGTGTGTCCCCAAGGAAAAATATATCACACCCTCAAAAATAATTCGATTTGCTGTACC 404

Qy   436 AAGTGCCACAAAAGGAACCTACTTGTACAAATGACTGTCCAGGCCCGGGCAGGATACGGAC 495
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Db   405 AAGTGCCACAAAAGGAACCTACTTGTACAAATGACTGTCCAGGCCCGGGCAGGATACGGAC 464

Db   465 TGCAGGGAGTGTGAGAGCGGCGGCTCCTTTTCACCGCTTCACCGGAAAACCACCTCAGACACTGCCTC 524

RESULT 14

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LOCUS       A43873       2175 bp   DNA             PAT       06-MAR-1997
DEFINITION  Sequence 1 from Patent EP0657536.
ACCESSION   A43873
NID         g2299022
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 2175)
  AUTHORS   Wallach,D., Brakebusch,C., Varfolomeev,E. and Batkin,M.
  TITLE     Proteases capable of shedding the soluble TNF-receptor and TNF-R
            derived peptides and antibodies against the proteases inhibiting
            the shedding
  JOURNAL   Patent: EP 0657536-A 1 14-JUN-1995;
            YEDA RES & DEV (IL)
COMMENT     Other publication 2A 9407962 951121
            Other publication JP 7194376 950801
            Other publication AU 7574294 950504
            Other publication CA 2133872 950413.
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     CDS             256..1623
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ORIGIN

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Qy  525  AGCTGCTCCAAAATGCCGAAAGGAAAATGGGTGGGGTGGAGATCTCTTCTTCTTGCACAGTGGAC  584
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Db  616  CGGGACACCGTGTGTGGGCTGCGCAGGAAGAACCAGTACCGGCCGCATTATTGGTGAAAACCTT  675

Qy  585  CGGGACACCGTGTGTGGGCTGCGCAGGAAGAACCAGTACCGGCCGCATTATTGGTGAAAACCTT  644
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Qy  765  TCCTGT  770
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Best Local Similarity 99.8%; Pred. No. 0.00e+00;
Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db  436  AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCGCCCGGGGCGAGGATACGGAC  495
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RESULT 15

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ACCESSION   I64751
NID         g2481645
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2175)
  AUTHORS   Wallach,D., Brakebusch,C., Varfolomeev,E. and Batkin,M.
  TITLE     Molecules influencing the shedding of the TNF receptor, their
            preparation and their use
  JOURNAL   Patent: US 5665859-A 1 09-SEP-1997;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
BASE COUNT     474 a    641 c    604 g    456 t
ORIGIN

Qy  765  TCCTGT  770
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Db  796  TCCTGT  801

Qy  405  AAGTGCCACAAAGGAAGAACCTACTTGTACAATGACTGTCCAGGCGCCCGGGGCGAGGATACGGAC  464
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Qy  525  AGCTGCTCCAAAATGCCGAAAGGAAAATGGGTGGGGTGGAGATCTCTTCTTCTTGCACAGTGGAC  584
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Db  676  TTCCAGTGCTTCAATTGCAGCCTGTGCCTGAACGGTACCGTGCACCTCTCCTGCCAGGAG  735
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Query Match 35.3%; Score 424; DB 25; Length 2175;
Best Local Similarity 99.8%; Pred. No. 0.00e+00;
Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy  405  AAGTGCCACAAAGGAAGAACCTACTTGTACAATGACTGTCCAGGCGCCCGGGGCGAGGATACGGAC  464

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Qy   705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTTCTAAGAGAGAAAAACGAGTGTGTC 764

Db   796 TCCTGT 801
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Qy   765 TCCTGT 770
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            M P S R C H  (TM)

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MPsrch_nn   n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed May 6 13:37:52 1998;   MasPar time 155.56 Seconds
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Perfect Score: 1202
N.A. Sequence:
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Scoring table: TABLE default
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Nmatch STD : Dbase 0; Query 0

Searched: 159651 seqs, 57698962 bases x 2

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Statistics: Mean 9.195; Variance 5.326; scale 1.727

                            SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	424	35.3	608	4	Q24441	Encodes truncated TNF	1.67e-282
2	424	35.3	606	4	Q06282	Plasmid Tumour Necros	1.67e-282
3	424	35.3	1334	8	Q49932	Lambda-derived TNF-R	1.67e-282
4	424	35.3	1368	8	Q24440	Encodes TNF-alpha 55k	1.67e-282
5	424	35.3	2062	3	020973	Encodes TNF-alpha	1.67e-282
6	424	35.3	2088	2	Q10883	TNF-alpha binding pro	1.67e-282
7	424	35.3	2111	2	Q10955	30kD TNF inhibitor pr	1.67e-282
8	424	35.3	2141	1	Q06285	Encodes human 55kD TN	1.67e-282
9	424	35.3	2175	1	090513	Human Tumour Necrosis	1.67e-282
10	424	35.3	6889	18	H15931	p55 TNF-R gene.	1.67e-282
11	422	35.1	2170	9	050870	DHFR/intron (WTrasSD)	1.67e-281
12	422	35.1	2176	2	012215	p55 Tumour necrosis f	1.91e-281
13	414	34.4	579	2	014800	Type I TNF receptor.	4.91e-281
14	409	34.0	836	17	T03212	Human chorionic gonad	3.68e-275
15	409	34.0	836	17	T03243	Single chain gonador	1.73e-271
16	405	31.7	575	17	T03240	Human CG beta-subunit	1.49e-268
17	381	31.1	504	4	Q24445	Encodes truncated TNF	5.96e-251
18	315	26.2	743	17	T03219	Single chain gonadotr	1.09e-202
19	302	25.1	2771	31	T76770	Rat Fabpl gut-specifi	3.27e-193
20	300	25.0	474	4	Q24442	Encodes truncated TNF	9.37e-192
21	301	25.0	2160	33	T62826	Human growth hormone	1.75e-192
22	294	24.5	336	6	Q41459	Human growth hormone	2.19e-187
23	283	23.5	426	2	N60524	Sequence encoding hum	2.20e-179
24	276	23.0	743	17	T03231	Single chain gonadotr	2.69e-174
25	276	23.0	752	17	T03233	Single chain gonadotr	2.69e-174
26	276	23.0	743	17	T03229	Single chain gonadotr	2.69e-174
27	274	22.8	752	17	T03227	Single chain gonadotr	2.08e-173
28	261	21.7	477	4	Q24444	Encodes truncated TNF	4.65e-159
29	255	21.2	2173	1	006284	Encodes truncated TNF	4.31e-138
30	226	18.8	525	1	O03851	Bovine beta LH subun1	7.56e-126
31	209	17.4	525	1	O03844	Porcine beta LH subun	7.56e-126
32	209	17.4	1027	1	O10878	Encodes truncated TNF	3.19e-97
33	206	17.1	2660	4	N30032	Sequence encoding ami	1.15e-69
34	184	15.3	496	2	N60523	Sequence encoding of	1.53e-49
35	179	14.9	611	2	O03848	Equine beta LH subun1	6.37e-108
36	169	14.1	462	4	Q24443	Encodes truncated TNF	2.38e-104
37	130	10.8	1027	2	O10876	Partial sequence of c	1.15e-69
38	101	8.4	114	2	N60522	Sequence encoding of	1.53e-49
39	99	8.2	138	13	080819	LH-beta -5 to 41 frag	3.59e-48
40	84	7.0	1047	2	Q10572	Human Natriuretic Pep	5.61e-38
41	77	6.4	1047	2	Q10571	Human Natriuretic Pep	2.75e-33
42	72	6.0	114	6	O34669	DNA encoding hCG beta	5.75e-30
43	71	5.9	651	2	N71239	Sequence encoding hum	2.63e-29
44	71	5.9	700	2	N60678	Sequence encoding pre	2.63e-29
45	71	5.9	3557	2	N60801	Human pro-growth horm	2.63e-29

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                            ALIGNMENTS

RESULT
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ID   Q24441 standard; DNA; 608 BP.
AC   Q24441;
DT   05-NOV-1992 (first entry)
DE   Encodes truncated TNF-alpha 55kD receptor (197 amino acids).
KW   tumour necrosis factor alpha; extracellular binding domain;
KW   treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
KW   malaria; viral meningitis; graft versus host disease;
KW   autoimmune disease; rheumatoid arthritis.
OS   Homo sapiens.
OS   WO9207076-A
PN   30-APR-1992;
PF   18-OCT-1991; G01826.
PD   18-OCT-1990; GB-022648.
PF   (CHAR-) CHARING CROSS SUNLEY RES CENT.
PA   Brennan FM, Feldmann M, Gray PW, Turner MJC;
PI   WPI; 92-167156/20.
PR   P-PSDB; R24080.
DR   P-PSDB; R24080.
PT   New polypeptide capable of binding human TNF alpha - comprises
PT   first three cysteine-rich subdomains of TNF alpha receptor for
PT   treating autoimmune disease, septic shock, HIV etc.
PS   Example; Fig 7; 43pp; English.
CC   This sequence encodes the designed TNF-alpha 55kD receptor
CC   derivative, as present in pTNFRecd. This was produced as described in
CC   Q24441. This derivative lacks the 81 carboxyl terminal residues of
CC   the cytoplasmic domain. The derivative could be used in the
CC   regulation of TNF-alpha mediated responses by binding and
CC   sequestering human TNF-alpha e.g. in the treatment of pulmonary
CC   diseases, septic shock, HIV infection, malaria, viral meningitis,
CC   graft versus host disease and autoimmune diseases, esp. rheumatoid
CC   arthritis.
CC   See also Q24440-51, R24000, R24080-84, R27585, Q29236-8
SQ   Sequence 608 BP; 148 A; 159 C; 165 G; 136 T;

Query Match   35.3%;   Score 424; DB 4; Length 608;
Best Local Similarity 99.8%;
Matches 425;   Conservative   0;   Mismatches   1;   Indels   0;   Gaps   0;

Db 129 gatagtgtgtcccaaggaaatatatccacctcaaaatatcgattgtctacc 188
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Qy    345  GATAGTGTGTGTCCCCAAGGAAAAATATATCCACCCTCAAAAATAATTCGATTTGCTGTACC
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    189  aagtgccacaaaggaacctacttgtacaatgactgtccaggccccgggggcaggatacggac  248

Qy    405  AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCCGGGGGCAGGATACGGAC  464
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    249  tgcaggagtgtgagagcggctcctcaggccgttcaggaaaacaacctcagacactgccctc  308

Qy    465  TGCAGGAGTGTGAGAGCGGCTCCTCAGGCCGTTCAGGAAAACAACCTCAGACACTGCCCTC  524
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    309  agctgctccaaatgccgaaagtgggtcaggtgggagatctctgttcttcttcgcacagtggac  368

Qy    525  AGCTGCTCCAAATGCCGAAAGTGGGTCAGGTGGGAGATCTCTGTTCTTCTTCGCACAGTGGAC  584
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    369  cgggacaccgtgtgggctgcaggaagaaccagtaccggcgcattattggagtgaaaacctt  428

Qy    585  CGGGACACCGTGTGGGCTGCAGGAAGAACCAGTACCGGCGCATTATTGGAGTGAAAACCTT  644
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    429  ttccagtgttcaattgcagcctctgcctctctcctcctgccaggag  488

Qy    645  TTCCAGTGTTCAATTGCAGCCTCTGCCTCTCTCCTCCTGCCAGGAG  704
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Db    489  aaacagaacaccgtgtcacctgccatgcaggtttcttcttaagagaaaacgagtgtgtc  548

Qy    705  AAACAGAACACCGTGTCACCTGCCATGCAGGTTTCTTCTTAAGAGAAAACGAGTGTGTC  764
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Db    549  tcctgt  554

Qy    765  TCCTGT  770
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Db    765  TCCTGT  770
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RESULT  2
ID    Q06282  standard; DNA; 1334 BP.
AC    Q06282;
DT    29-JAN-1991  (first entry)
DE    Plasmid Tumour Necrosis Factor-Binding Protein 15 cDNA insert.
KW    Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
OS    Homo sapiens; ss.
PN    pTNF-BP15;
FH    Key            Location/Qualifiers
FT    CDS            213..1325
FT    /*tag= a
FT    /product=TNF-BP
PN    EP-393438-A.
DR    WPI; 90-321987/43.
DR    P-PSDB; R07449.
PI    Hauptmann R, Himmler A, Maurer-Fogy I, Stratowa C;
PA    (BOEH ) BOEHRINGER INGELHEIMINT.
PR    21-JUN-1989; DE-920282.
PR    21-APR-1989; DE-913101.
PF    06-APR-1990; 106624.
PD    24-OCT-1990.
PS    Disclosure: Fig 1(1-3); 51pp; German.
PT    tumour treatment and to understand mechanismsm to TNF action
PT    DNA encoding TNF binding protein and TNF- receptor - used in
CC    pTNF-BP15 is one of 30 positives clones in a screened cDNA library
CC    from induced fibrosarcoma cells. A TNF-BP had been
CC    isolated from the urine of patients with uremia and probes/primers
CC    were constructed from the determined amino acid sequence.
CC    To produce a vector expressing a soluble form of TNF-binding
CC    protein, this plasmid was cut with XmnI, amplified by PCR and the
CC    amplified DNA cut with BamHI and EcoRI.
CC    The resulting 0.75 kb DNA fragment was inserted into pT7/T3 alpha-19
CC    (BRL), cut with the same enzymes to recover pTNF-BP. This was cut
CC    with BamHI and EcoRI, and the recovered fragment inserted into
CC    pAD-CMVI (Q06203) to give the required plasmid pADTNF-BP.
CC    See also Q06282-Q06285.
SQ    Sequence 1334 BP; 299 A; 409 C; 342 G; 284 T;

Query Match    35.3%;  Score 424;  DB 1;  Length 1334;
Best Local Similarity  99.8%;  Pred. No. 1.67e-282;
Matches   425;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;
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Db    333  gatagtgtgtgtccccaaggaaaaatatatccaccctcaaaaataattcgatttgctgtacc  392
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Qy    345  GATAGTGTGTGTCCCCAAGGAAAAATATATCCACCCTCAAAAATAATTCGATTTGCTGTACC  404

Db    393  aagtgccacaaaggaacctacttgtacaatgactgtccaggccccgggggcaggatacggac  452
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Qy    405  AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCCGGGGGCAGGATACGGAC  464

Db    453  tgcaggagtgtgagagcggctcctcaggccgttcaggaaaacaacctcagacactgccctc  512
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    465  TGCAGGAGTGTGAGAGCGGCTCCTCAGGCCGTTCAGGAAAACAACCTCAGACACTGCCCTC  524

Db    513  agctgctccaaatgccgaaagtgggtcaggtgggagatctctgttcttcttcgcacagtggac  572
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    525  AGCTGCTCCAAATGCCGAAAGTGGGTCAGGTGGGAGATCTCTGTTCTTCTTCGCACAGTGGAC  584

Db    573  cgggacaccgtgtgggctgcaggaagaaccagtaccggcgcattattggagtgaaaacctt  632
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    585  CGGGACACCGTGTGGGCTGCAGGAAGAACCAGTACCGGCGCATTATTGGAGTGAAAACCTT  644

Db    633  ttccagtgttcaattgcagcctctgcctctctcctcctgccaggag  692
           ||||||||||||||||||||||||||||||||||||||||||||||
Qy    645  TTCCAGTGTTCAATTGCAGCCTCTGCCTCTCTCCTCCTGCCAGGAG  704

Db    693  aaacagaacaccgtgtcacctgccatgcaggtttcttcttaagagaaaacgagtgtgtc  752
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    705  AAACAGAACACCGTGTCACCTGCCATGCAGGTTTCTTCTTAAGAGAAAACGAGTGTGTC  764

Db    753  tcctgt  758
           ||||||
Qy    765  TCCTGT  770
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RESULT  3
ID    Q49932  standard; cDNA to mRNA; 1368 BP.
AC    Q49932;
DT    29-APR-1994  (first entry)
DE    Lambda-derived TNF-R cDNA.
KW    Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;
KW    IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;
KW    rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;
KW    pulmonary fibrosis; silicosis; allograft; xenograft; rejection;
KW    graft verses host disease; sepsis; inflammation; allergy;
KW    autoimmune dysfunction; ss.
OS    Homo sapiens;
OS    Lambda-gt10-7-ctnfbp.
FH    Key            Location/Qualifiers
FT    CDS            1..1366
FT    /*tag= a
FT    /product= hTNF-R
FT    sig_peptide    1..120
FT    /*tag= b
FT    mat_peptide    121..1363
FT    /*tag= c
PN    WO9319777-A.
DR    WPI; 93-335592/42.
DR    P-PSDB; R42059.
PI    Smith CA;
PA    (IMMV ) IMMUNEX CORP.
PR    30-MAR-1992; US-860710.
PF    26-MAR-1993; U02938.
PD    14-OCT-1993.
PS    Disclosure; Page 57-59; 85pp; English.
PT    New fusion protein tumour necrosis factor and human interleukin-1
PT    receptor - useful in therapy, diagnosis and assays of e.g.
PT    rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.
CC    The sequences given in Q49931-32 encode human tumour necrosis factor
CC    receptor (TNF-R) and the sequences in Q49933-34 encode human
CC    interleukin-1 receptor (IL-1R). These sequences were used in the
CC    production of a fusion protein which conformed to one of the
CC    formulae:
CC    TNF-R-linker-TNF-R-linker-IL-1R
```

Left column

```
CC   Il-1r-linker-TNF-R-linker-TNF-R or
CC   TNF-R-linker-TNF-R.
CC   The linker may comprise 5-100 amino acids selected from Gly, Asp,
CC   Ser, Thr and Ala. These linkers separate the individual moieties
CC   by such a distance that each component of the fusion protein is
CC   capable of folding into the secondary or tertiary structure required
CC   for its biological activity. These fusion proteins may be used in
CC   therapy, diagnosis and assays for conditions mediated by TNF or IL-1,
CC   particularly in conditions in which both TNF and IL-1 play a causitive
CC   role. They may be used to treat cachexia, rheumatoid arthritis,
CC   diabetes, multiple sclerosis, cerebral malaria, allograft
CC   and xenograft rejection in graft verses
CC   host disease, sepsis, septic shock, inflammation, allergies and
CC   autoimmune dysfunctions.
SQ   Sequence 1368 BP;  292 A;  424 C;  376 G;  276 T;

Query Match       35.38%;  Score 424;  DB 8;  Length 1368;
Best Local Similarity   99.8%;
Matches   425;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Db  121 gatagtgtgtcccccaaggagaaaatatatccaccctcaaaataattcgattcgtgtacc 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  345 GATAGTGTGTCCCCAAGGAGAAAATATATCCACCCTCAAAATAATTCGATTCGTGTACC 404

Db  181 aagtgcccacaaaggagaacctacttgtacacatgactgtccaggccaccggggatacggac 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGCAGGATACGGAC 464

Db  241 tgcaggagtgtgagagcggctccttcaccgcttcaagaaaaccacctcagaacactgcctc 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  465 ... 524

Db  301 agctgctccaaatgccgaaagtgaaatgggtcaggtcggagatctctcttcttcagcacgtggac 360
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  465 TGCAGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCACTGCCCTC 524

Db  361 cgggacacccgtgtggctgcaggaagaaccacgtaccggcatattgagtgaaaacctt 420
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  525 AGCTGCTCCAAAATGCCGAAAGGGTCAGGTGGAGATCTCTCTTCTTGCACAGTGGAC 584

Db  421 ttccaagtgcttcaattgcagcctctgcagaggaagaaccagtaccggcaattatgtgag 480
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Qy  585 CGGGACACCGTGTGGCTGGCTGCAGGAAGAACCAGCATTATTGGAGTGAAAAACCTT 644

Db  481 aaacggaacaccgtgtgtgtgcaatgcaggtttctttcttctctaagagaagaacgagttgtgtc 540
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Qy  645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCTCGCCTCAATGGGACGTGCACAGTGTACC 704

Db  541 tcctgt 546
        ||||||
Qy  705 AAACAGAACACCGTGTGCCACTCGCCATGCAGGTTTCTTTCTTAAGAGAAAAGCGAGTGTGTC 764

Db  765 tcctgt 770
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Qy  765 TCCTGT 770
```

```
RESULT 4

ID   Q24440 standard; DNA; 2062 BP.
AC   Q24440;
DT   05-NOV-1992 (first entry)
DE   Encodes TNF-alpha 55kD receptor.
KW   tumour necrosis factor alpha; extracellular binding domain;
KW   treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
KW   malaria; viral meningitis; graft versus host disease;
KW   autoimmune disease; rheumatoid arthritis.
OS   Homo sapiens.
FH   Key               Location/Qualifiers
FT   CDS               156.1517
FT   /product= human TNF-alpha
FT   mat_peptide       1265.1267
FT   /tag= a
FT   /product= human TNF-alpha
FT   mat_peptide       1265.1267
FT   /tag= b
FT   /note= "3"
FT   mat_peptide       1265.1267
FT   /tag= c
FT   /codon= seq="TGG", aa:Thr
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Right column

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FT   mat_peptide       1258.1260
FT   /tag= d
FT   /codon= Seq="AAG", aa:Leu
FT   mat_peptide       1433.1435
FT   /tag= e
FT   /codon= Seq="GAC", aa:Asn
FT   sig_peptide       156.274
FT   /tag= f

PN   WO9207076-A.
PD   30-APR-1992.
PF   18-OCT-1991; G01826.
PF   18-OCT-1990; GB-022648.
PA   (CHAR-) CHARING CROSS SUNLEY RES CENT.
PI   Brennan FM, Feldmann M, Gray PW, Turner MJC;
DR   WPI; 92-167156/20.
DR   P-PSDB; R24000.
PS   Claim 4; Fig 1; 43pp; English.
PT   New polypeptide capable of binding human TNF alpha - comprises
PT   first three cysteine-rich subdomains of TNF alpha receptor for
PT   treating autoimmune disease, septic shock, HIV etc.
CC   This sequence encodes human TNF-alpha 55kD receptor. A placenta cDNA
CC   library in gt10 was screened with probe Q29236. Ten hybridising clones
CC   were plaque purified and cDNA size determined by PAGE against an
CC   Eco RI digested phage DNA. The inserts of two cDNA clones were then
CC   sequenced. The coding region of the majority of the human TNF-alpha
CC   55kD receptor was isolated as an EcoRI fragment encoding 374 amino
CC   acids, and cloned into a mammalian cell expression vector, resulting
CC   in prTNFR. A derivative of the TNF-alpha receptor was produced by
CC   engineering a termination codon just prior to the transmembrane
CC   domain. PCR with primers Q29237,8 generated a 300bp
CC   restriction fragment which was cloned into prTNFR, giving pTNFRecd.
CC   DNA sequencing confirmed this contained the designed DNA sequence.
CC   The TNF-alpha receptor expression plasmids were then transfected
CC   into monkey COS-7 cells.
CC   See also Q24440-51, R24000, R24080-84, R27585, Q29236-8
SQ   Sequence 2062 BP;  429 A;  618 C;  572 G;  443 T;

Query Match       35.38%;  Score 424;  DB 4;  Length 2062;
Best Local Similarity   99.8%;
Matches   425;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Db  275 gatagtgtgtcccccaaggagaaaatatatccaccctcaaaataattcgattggtgtacc 334
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Qy  345 GATAGTGTGTCCCCAAGGAGAAAATATATCCACCCTCAAAATAATTCGATTGGTGTACC 404

Db  335 aagtgcccacaaaggagaacctacttgtacaatgactgtccaggccaccggggatacggac 394
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGCAGGATACGGAC 464

Db  395 tgcaggagtgtgagagcggctccttcaccgcttctctcctcaatgggacgtgcacagtgctc 454
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  465 TGCAGGGAGTGTGAGAGCGGCGCCTCTTCACCGCTTCAGAAAACCACCACTGCCCTC 524

Db  455 agctgctccaaatgccgaaagtgaaatggtcaggtggagatctctcttcttgcacagtggac 514
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  525 AGCTGCTCCAAAATGCCGAAAGGGTCAGGTGGAGATCTCTCTTCTTGCACAGTGGAC 584

Db  515 cgggacaccgtgtggctgcaggaagaaccagcattattggagtgaaaaacctt 574
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  585 CGGGACACCGTGTGGCTGGCTGCAGGAAGAACCAGCATTATTGGAGTGAAAAACCTT 644

Db  575 ttccaagtgcttcaattgcagcctctgcctctcgcctcaatgggacgtgcacagtgtacc 634
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCTCGCCTCAATGGGACGTGCACAGTGTACC 704

Db  635 aaacagaacaccgtgtgccactcgccatgcaggtttctttcttaagagaaaagcgagtgtgtc 694
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  705 AAACAGAACACCGTGTGCCACTCGCCATGCAGGTTTCTTTCTTAAGAGAAAAGCGAGTGTGTC 764

Db  695 tcctgt 700
        ||||||
Qy  765 TCCTGT 770
```

RESULT 5

ID   Q20973 standard; DNA; 2062 BP.
AC   Q20973;
DT   11-MAY-1992 (first entry)
DE   TNF-alpha binding protein gene.
KW   Tumour necrosis factor alpha; autoimmune diseases; cachectin; ss;
OS   Homo sapiens.
FH   Key   Location/Qualifiers
FH
FT   CDS   155..1522
FT   /*tag=   a
FT   sig_peptide   155..274
FT   /*tag=   b
FT   mat_peptide   275..1522
FT   /*tag=   c
FT   misc_feature   473..532
FT   /*tag=   d
FT   misc_feature   242..751
FT   /*tag=   e
FT   /note=   "encodes the extracellular domain of human
FT   TNF alpha receptor"
PN   GB2246569-A.
PD   05-FEB-1992.
PF   15-JUN-1990; 013410.
PR   15-JUN-1990; GB-013410.
PA   (CHAR-) CHARING CROSS SUNLE.
PI   Feldman M, Gray P, Turner M, Brennan F;
PW   WPI; 92-043613/06.
PN   P-PSDB; R20787.
PT   New tumour necrosis factor alpha binding protein and polypeptide
PT   - useful in treating cachexia, sepsis and auto immune diseases
PT   e.g. rheumatoid arthritis
PS   Disclosure; Fig 1; 25pp; English.
CC   The sequence is that of DNA encoding tumour necrosis factor alpha
CC   binding protein which was obtd. from a human placental cDNA library
CC   in lambda gt11 using a probe (Q20974). The DNA also encodes the
CC   extracellular domain of human TNF alpha receptor and as such it is
CC   useful for treating diseases where TNF alpha is involved as a
CC   causative agent, e.g. cachexia, sepsis and autoimmune diseases,
CC   specifically rheumatoid arthritis. See also Q20974.
SQ   Sequence 2062 BP; 429 A; 616 C; 573 G; 444 T;

Query Match   35.3%; Score 424; DB 3; Length 2062;
Best Local Similarity 99.8%;
Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy    275 gatagtgtgtgtcccccaaggaaaatatatccacccctcaaaataattgatttgctgtacc 334
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    345 gatagtgtgtgtcccccaaggaaaatatatccacccctcaaaataattgatttgctgtacc 404

Qy    335 aagtgcacaaaggaacctactacttgtacaatgactgtcctcaggtgcccgggggcaggat 394
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    405 aagtgcacaaaggaacctactacttgtacaatgactgtcctcaggtgcccgggggcaggat 464

Qy    395 tgcaggggagtgtgagcggcgtcctcaccgcttcagaaaaccacctcagacactgcctc 454
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    465 tgcaggggagtgtgagcggcgtcctcaccgcttcagaaaaccacctcagacactgcctc 524

Qy    455 agctgtctcccaaatgccgaaaggaaatgggtcaggtggagagatctcttcttcttgcacagtggac 514
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    525 agctgtctcccaaatgccgaaaggaaatgggtcaggtggagagatctcttcttcttgcacagtggac 584

Qy    515 cgggacaccgtgtgtggggctgcaggagaaccagtaccggccatattattgggagtgaaaacctt 574
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    585 cgggacaccgtgtgtggggctgcaggagaaccagtaccggccatattattgggagtgaaaacctt 644

Qy    575 ttccagtgcttcaattgcaggcctctgcctcacctctcctgtgccaggag 634
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    635 ttccagtgcttcaattgcaggcctctgcctcacctctcctgtgccaggag 694

Qy    635 aaacagaacacgtgtcacctgccatgcaggtttcttcttctaagagaaaacgagtgtgtc 694
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    705 aaacagaacacgtgtcacctgccatgcaggtttcttcttctaagagaaaacgagtgtgtc 764

Qy    705 AAACAGAACACGTGTCACCTGCCATGCAGGTTTCTTCTTCTAAGAGAAAACGAGTGTGTC 764
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    695 tcctgt 700
          ||||||
Qy    765 TCCTGT 770
          ||||||
Db    709 tcctgt 714
          ||||||
```

RESULT 6

ID   Q10883 standard; cDNA; 2088 BP.
AC   Q10883;
DT   13-MAY-1991 (first entry)
DE   30kD TNF inhibitor precursor gene in lambda-gt10-7ctnfbp.
KW   Tumour necrosis factor; inhibitor; ss;
OS   Homo sapiens.
FH   Key   Location/Qualifiers
FH
FT   CDS   171..1536
FT   /*tag=   a
PN   AU9058976-A.
PD   24-JAN-1991.
PF   16-JUL-1990; 058976.
PR   16-JUL-1990; US-381080.
PR   18-JUL-1989; US-381080.
PR   11-DEC-1989; US-450329.
PR   07-FEB-1990; US-479661.
PA   (SYNE-) SYNERGEN INC.
PW   WPI; 91-073847/11.
PN   P-PSDB; R10986.
PT   Tumour necrosis factor inhibitor - for suppression of TNF-alpha
PT   and -beta, useful as therapeutic agent.
PS   Disclosure; Fig 21; 142pp; English.
CC   The sequence encodes the entire 30 kD TNF inhibitor. The clone from
CC   which the sequence was obtd. was isolated from a cDNA library
CC   prepd. from RNA form U937 cells treated with PMA/PHA. The whole
CC   gene can be inserted into expression vectors for prepn. of TNF
CC   inhibitor for use in the treatment of inflammatory and degenerative
CC   diseases.
CC   See also Q10878, Q10884 and Q10907.
SQ   Sequence 2088 BP; 439 A; 626 C; 578 G; 445 T;

Query Match   35.3%; Score 424; DB 2; Length 2088;
Best Local Similarity 99.8%;
Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy    289 gatagtgtgtgtcccccaaggaaaatatatccacccctcaaaataattcgatttgctgtacc 348
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    345 gatagtgtgtgtcccccaaggaaaatatatccacccctcaaaataattcgatttgctgtacc 404

Qy    349 aagtgcacaaaggaacctactacttgtacaatgactgtcctcaggtgcccgggggcaggat 408
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    405 aagtccacaaaggaacctactacttgtacaatgactgtcctcaggtgcccgggggcaggat 464

Qy    409 tgcaggggagtgtgagcggcgtcctcaccgcttcagaaaaccacctcagacactgcctc 468
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    465 tgcaggggagtgtgagcggcgtcctcaccgcttcagaaaaccacctcagacactgcctc 524

Qy    469 agctgtctcccaaatgccgaaaggaaatgggtcaggtggagatctcttcttcttgcacagtggac 528
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    525 agctgtctcccaaatgccgaaaggaaatgggtcaggtggagatctcttcttcttgcacagtggac 584

Qy    529 cgggacaccgtgtgtggggctgcaggagaaccagtaccggccatattattgggagtgaaaacctt 588
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    585 CGGGACACCGTGTGTGGGGCTGCAGGAGAACCAGTACCGGCCATTATTGGGAGTGAAAACCTT 644

Qy    589 ttccagtgcttcaattgcaggcctctgcctcacctctcctgtgccaggag 648
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    645 TTCCAGTGCTTCAATTGCAGGCCTCTGCCTCACCTCTCCTGTGCCAGGAG 704

Qy    649 aaacagaacacgtgtcacctgccatgcaggtttcttcttctaagagaaaacgagtgtgtc 708
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    705 AAACAGAACACGTGTCACCTGCCATGCAGGTTTCTTCTTCTAAGAGAAAACGAGTGTGTC 764

Qy    709 tcctgt 714
          ||||||
Db    705 tcctgt 700
          ||||||
Qy    765 TCCTGT 770
          ||||||
```

Qy   765 TCCTGT 770

RESULT   7
ID   Q10955 standard; cDNA; 2111 BP.
AC   Q10955;
DT   24-MAY-1991 (first entry)
DE   Encodes human 55kD TNF-binding protein.
KW   Tumour Necrosis Factor; binding proteins; septic shock;
KW   autoimmune glomerulonephritis; lymphokine; cytokine.
FH   Key   Location/Qualifiers
FT   sig_peptide   187..273
FT   /*tag= a
FT   mat_peptide   274..1551
FT   /*tag= b
PN   EP-417563-A.
PD   20-MAR-1991.
PN   31-AUG-1990; 116707.
PF   12-SEP-1989; CH-003319.
PR   08-MAR-1990; CH-000746.
PR   20-APR-1990; CH-001347.
PA   (HOFF) HOFFMANN-LA ROCHE AG.
PI   Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;
PI   Schlaeger EJ;
WPI   91-081851/12.
P-PSDB; R11082.
PT   Insoluble tumour necrosis factor binding proteins - and DNA
PT   encoding them, useful in pharmaceutical prods. and for antibody
PT   prodn.
PS   Claim 4; Fig 1; 26pp; German.
CC   Partial amino acid Sequences were determined for the 55 and 75kD
CC   TNF-BPs (see R11072-R11081) and oligonucleotide primers were
CC   synthesised based on these partial sequences. The primers were used
CC   to produce a cDNA fragment for use as aprobe to screen a human
CC   placental cDNA bank constructed in lambda gt11. Positive clones were
CC   identified and sequenced. DNA constructs comprising the TNF-BP coding
CC   sequence may also contain a fragment encoding a human Ig domain.
CC   Recombinant constructs are used to transform cells to confer
CC   improved TNF-binding properties.
CC   See also Q10956.
SQ   Sequence   2111 BP;   445 A;   628 C;   588 G;   450 T;

Query Match   35.38%;   Score 424;   DB 2;   Length 2111;
Best Local Similarity   99.8%;   Pred. No. 1.67e-282;
Matches   425;   Conservative   0;   Mismatches   1;   Indels   0;   Gaps   0;

Db   307 gatagtgtgtgtcccccaaggagaaatatatccacccctcaaaataattcgattgctgtacc 366
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Qy   345 GATAGTGTGTGTCCCCCAAGGAGAAATATATCCACCCCTCAAAATAATTCGATTGCTGTACC 404

Db   367 aagtgccacaaaggagaacctacttgtacaatgactgtccaggcccgggcaggatacggac 426
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Qy   405 AAGTGCCACAAAGGAGAACCTACTTGTACAATGACTGTCCAGGCCCGGGCAGGATACGGAC 464

Db   427 tgcagggagtgtgagagcggctcctcaccgcttcagaagaccactgcctc 486
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   465 TGCAGGGAGTGTGAGAGCGGCTCTTCACCGCTTCAGAAGACCACTGCCTC 524

Db   487 agctgctcccaaaatgccgaaaggaaatgggtcagytggagatctctcttcttgcacagtggac 546
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   525 AGCTGCTCCCAAAATGCCGAAAAGGGTCGAGGTGAGAGATCTCTTCTTGCACAGTGGAC 584

Db   547 cgggacaccgtgtgtcggtcaggacgaaccacgtaccggcattattggagtgaaaacctt 606
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   585 CGGGACACCGTGTGTCGGTCAGGACGAACCACGTACCGGCATTATTGGAGTGAAAACCTT 644

Db   607 ttccagtgcttcaaattgcagcctctgcctccactctctcctgccaggag 666
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   645 TTCCAGTGCTTCAAATTGCAGCCTCTGCCTCCACTCTCTCCTGCCAGGAG 704

Db   667 aaacagaacaccgtgtgcacctgccatgcaggtttcttcttctaagagagaaaacgagtgtgtc 726
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTCTTCTAAGAGAGAAAACGAGTGTGTC 764

Qy   705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTCTTCTAAGAGAGAAAACGAGTGTGTC 764

Db   727 tcctgt 732
          ||||||
Qy   765 TCCTGT 770

RESULT   8
ID   Q06285 standard; DNA; 2141 BP.
AC   Q06285;
DT   29-JAN-1991 (first entry)
DE   Human Tumour Necrosis Factor-Receptor cDNA insert.
KW   Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
KW   lambdaTNF-R2; raTNF-R8; ss.
OS   Homo sapiens.
FH   Key   Location/Qualifiers
FT   CDS   213..1577
FT   /*tag= a
PN   (BOEH) BOEHRINGER INGELHEIMNT.
PA   Hauptmann R; Himmler A, Maurer-Fogy I, Stratowa C;
WPI   90-321987/43.
P-PSDB; R07451.
PT   DNA encoding TNF binding protein and TNF- receptor - used in
PT   tumour treatment and to understand mechanismm to TNF action
PS   Disclosure; Fig 91(1-2); 51pp; German.
CC   raTNF-R8 (Q06284) was used to screen the HS913T cDNA library.
CC   LambdaTNF-R2 encodes the complete human TNF-R2 and was used to
CC   construct a plasmid (pADTNF-R) expressing the product the same way
CC   as PADTNF-BP (see Q06282).
CC   See also Q06282-Q06285.
SQ   Sequence   2141 BP;   455 A;   633 C;   593 G;   460 T;

Query Match   35.38%;   Score 424;   DB 1;   Length 2141;
Best Local Similarity   99.8%;   Pred. No. 1.67e-282;
Matches   425;   Conservative   0;   Mismatches   1;   Indels   0;   Gaps   0;

Db   333 gatagtgtgtgtcccccaaggagaaatatatccacccctcaaaataattcgattgctgtacc 392
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   345 GATAGTGTGTGTCCCCCAAGGAGAAATATATCCACCCCTCAAAATAATTCGATTGCTGTACC 404

Db   393 aagtgccacaaaggagaacctacttgtacaatgactgtccaggcccgggcaggatacggac 452
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   405 AAGTGCCACAAAGGAGAACCTACTTGTACAATGACTGTCCAGGCCCGGGCAGGATACGGAC 464

Db   453 tgcagggagtgtgagagcggctcctcaccgcttcagaagaccactgcctc 512
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   465 TGCAGGGAGTGTGAGAGCGGCTCTTCACCGCTTCAGAAGACCACTGCCTC 524

Db   513 agctgctcccaaatgccgaaagaaatgggtcaggtggagatctctcttcttgcacagtggac 572
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Qy   525 AGCTGCTCCCAAAATGCCGAAAAGGGTCGAGGTGAGAGATCTCTTCTTGCACAGTGGAC 584

Db   573 cgggacaccgtgtgtggggtcaggaagaaccacggccattattggagtgaaaacctt 632
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   585 CGGGACACCGTGTGTCGGTCAGGACGAACCACGTACCGGCATTATTGGAGTGAAAACCTT 644

Db   633 ttccagtgcttcaaattgcagcctctgcctctgcctccactctctcctgccaggag 692
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   645 TTCCAGTGCTTCAAATTGCAGCCTCTGCCTCCACTCTCTCCTGCCAGGAG 704

Db   693 aaacagaacaccgtgtgcacctgccatgcaggtttcttctttctaagagagaaaacgagtgtgtc 752
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTCTTCTAAGAGAGAAAACGAGTGTGTC 764

Db   753 tcctgt 758
          ||||||
Qy   765 TCCTGT 770

RESULT 9

ID   Q90513 standard; DNA; 2175 BP.
AC   Q90513;
DT   19-JAN-1996 (first entry)
DE   p55 TNF-R gene.
KW   p55; tumour necrosis factor receptor; TNF-R; human; murine; chimera;
KW   epidermal growth factor receptor; EGF-R; protease; inhibitor;
KW   phorbol myristate acetate; PMA; ss.
OS   Homo sapiens.
FH   Key   Location/Qualifiers
FT   CDS   256..1623
FT   /*tag= a
FT   /product= p55 TNF-R
FT   misc_signal   2143..2149
FT   /*tag= b
FT   /note= "possible poly-A signal"
PN   AU94757A2-A.
PD   04-MAY-1995.
PF   11-OCT-1994; 075742.
PR   12-OCT-1993; IL-107268.
PA   (YEDA) YEDA RES & DEV CO LTD.
PI   Batkin M, Brakebusch C, Varfolomeev E, Wallach D;
PS   Disclosure; Fig 1; 40pp; English.
PT   This sequence represents human p55 tumour necrosis factor
PT   (TNF) receptor - from cell-bound TNF- receptor, useful for
PT   antagonising deleterious effects of TNF.
CC   New protease capable of cleaving soluble tumour necrosis factor
CC   Expression of this receptor is regulated by shedding of the
CC   receptor fragment. The p55 TNF-R can be shed in response to different
CC   inducing agents, e.g. phorbol myristate acetate (PMA), depending on cell
CC   type. The only region of the receptor whose structure affects the
CC   shedding response is the spacer region (see R75012) in the extracellular
CC   domain. This region is located close to a site of cleavage of TNF.
CC   molecule, and links the Cys rich module to the transmembrane domain. The
CC   spacer region of the encoded protein was used to create the chimeras
CC   between human p55 TNF-R and murine epidermal growth factor receptor
CC   (EGF-R) that are represented by R75007-11. This spacer region was
CC   subjected to deletion mutations (R75013-25) and substitutions
CC   (R75026-47). Of the spacer region, the most important residues are
CC   Asn 172, Val 173, Lys 174 and Gly 175, with Val 173 being the most
CC   important of these. The shedding of the receptor is independent of the
CC   side chain identity of these residues, with the exception of a limited
CC   dependence on the identity of Val 173. Mutations which alter the
CC   conformation of the protein adversely effect the shedding process. The
CC   mutations shown in R75013-47 were introduced in order to create the
CC   inhibitor of a protease that is capable of cleaving the soluble TNF-R
CC   from the cell bound TNF-R. Fragments of these inhibitors can be seen in
CC   R75017-9, R75025, R75033-5 and R75042-3. These protease inhibitors can
CC   be used for enhancing TNF function.
SQ   Sequence 2175 BP;   474 A;   642 C;   603 G;   456 T;

Query Match   35.3%; Score 424; DB 15; Length 2175;
Best Local Similarity 99.8%;
Matches   425; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   376 gatagtgtgtgtcccaaaggaaatatatccaccctccaaataattcgatttgctgtacc   435
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   345 GATAGTGTGTGTCCCAAGGAAAAATAATACCACCCTCAAATAATTCGATTTGCTGTACC   404

Qy   436 aagtgccacaaaggaacctacttgtacaatgacttcaggggcaggcggatacggac   495
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTTCAGGCCCGGGCAGGATACGGAC   464

Qy   496 tgcaggggagtgtgagagcggcctcttcacccgcttcagaaaaccacctcagaccactgccctc   555
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   465 TGCAGGGAGTGTGAGAGCGGCCTCTTCACCCGCTTCAGAAAACCACCTCAGACACTGCCCTC   524

Db   556 agctgctccaaatgccgaaaagtgggtcagtgtggagatctcttcttgcacagtggac   615
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   556 agctgctccaaatgccgaaaagtgggtcagtgtggagatctcttcttgcacagtggac   615

Qy   616 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcagttattggagtgaaaacctt   675
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   585 CGGGACACCGTGTGTGGGCTGCCGGAAGAACCAGTACCGGCCATTATTGGGAGTGAAAACCTT   644

Qy   676 ttccagtgcttcaattgcagccctgtgctgcctctcgccaatggggccggatgggccaggag   735
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   645 TTCCAGTGCTTCAATTGCAGCCCTGTGCTGCCTCTCGCCAATGGGACCGGATGGGCCAGGAG   704

Qy   736 aaacagacaaccgtgtgtcacctgccatgcaggttttcctttctaagagagaaacgagtgtgtc   795
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   705 AAACAGACAACCGTGTGCCACCTGCCATGCAGGTTTTCTTTCTAAGAGAGAAAACGAGTGTC   764

Qy   796 tcctgt   801
            ||||||
Db   705 TCCTGT   770

RESULT 10

ID   T15931 standard; DNA; 6889 BP.
AC   T15931;
DT   20-JUN-1996 (first entry)
DE   DHFR/intron (WTrasSD)-TnFr-IgG dicistronic vector.
KW   Recombinant host cell; dihydrofolate reductase; selectable marker;
KW   DHFR; ras splice donor; dicistronic vector; gene expression;
KW   Immunoadhesin; TnFr-IgG; tumour necrosis factor; ds.
OS   Synthetic.
PN   WO9604391-A1.
PD   15-FEB-1996.
PF   28-JUL-1995; U09576.
PR   05-AUG-1994; US-286740.
PA   (GETH) GENENTECH INC.
PI   Crowley CW;
PS   Example 2; Page 36-42; 137pp; English.
PT   Improved process for the selection of recombinant host cells
PT   expressing high level of a desired product - uses eukaryotic host
PT   cells contg. a DNA construct comprising a selectable gene
CC   A distronic vector (T15930) comprises a regulatory region
CC   derived from the cytomegalovirus immediate-early gene, a
CC   selectable dihydrofolate reductase gene positioned within an
CC   intron having a 5' wild-type ras splice donor site, a downstream
CC   sequence coding for an immunoadhesin, TnFr-IgG, capable of binding
CC   tumour necrosis factor, and a poly-A sequence. Transfection of CHO
CC   DHFR- cells and subsequent methotrexate amplification and growth of
CC   the cells in nutrient-rich medium gave TnFr-IgG in yields of 9.5
CC   ug/ml (15-fold higher compared to conventional vector amplified
CC   pools).
SQ   Sequence 6889 BP;   1729 A;   1826 C;   1681 G;   1653 T;

Query Match   35.3%; Score 424; DB 18; Length 6889;
Best Local Similarity 99.8%;
Matches   425; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Db   1725 gatagtgtgtggctgcaggaagaaccagtaccggcgattgtttgctgtacc   1784
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   345 GATAGTGTGTGTCCCAAGGAAAAATAATACCACCCTCAAATAATTCGATTTGCTGTACC   404

Db   1785 aagtgccacaaaggaacctacttgtacaatgacttcaggggcaggcggatacggac   1844
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTTCAGGCCCGGGCAGGATACGGAC   464

Db   1845 tgcaggggagtgtgagagcggcctcttcacccgcttcagaaaaccacctcagacactgccctc   1904
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   465 TGCAGGGAGTGTGAGAGCGGCCTCTTCACCCGCTTCAGAAAACCACCTCAGACACTGCCCTC   524

Db   1905 agctgctccaaatgccgaaaagtgggtcagtgtggagatctcttcttgcacagtggac   1964
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   525 AGCTGCTCCAAATGCCGAAAAGTGGGTCAGTGTGGAGATCTCTTCTTGCACAGTGGAC   584

Db   1965 cgggacaccgtgtggctgcaggaagaaccagtaccggcattattgggagtgaaaacctt   2024
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Left column (RESULT 11)

```
Qy    585 CGGGACACCGTGTGGGCTCCAGGAAGAACCAGTACCGGCGATTATTGGAGTGAAAAACCTT 644
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2025 ttccagtgtgctcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 2084

Qy    645 TTCCAGTGTGCTTCAATTGCAGCCTCTGCCTCAAATGGGACCGTGCACCTCTCCTGCCAGGAG 704
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2085 aaacagaacaccgtgtgcacctgcaccatgcaggttctttcttttctaagagaagaacgagtgtgtc 2144

Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTTTCTAAGAGAAAACGAGTGTGTC 764
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2145 tcctgt 2150

Qy    765 TCCTGT 770
          ||||||
Db    765 TCCTGT 770
```

RESULT 11

ID   Q50870 standard; DNA; 2170 BP.
AC   Q50870;
DT   13-MAY-1994 (first entry)
DE   p55 Tumour necrosis factor receptor coding sequence.
KW   TNF; tumour necrosis factor; receptor; disease; autoimmunity;
KW   rheumatoid arthritis; graft rejection; graft vs. host; septic shock;
KW   effector protein; ss.
OS   Homo sapiens.
FH   Key   Location/Qualifiers
FH
FT   CDS   256..1623
FT   /*tag= a
FT   /product= p55 Tumour necrosis factor receptor.
PN   EP-568925-A.
PD   10-NOV-1993.
PF   29-APR-1993; 106981.
PR   03-MAY-1992; IL-101769.
PA   (YEDA) YEDA RES & DEV CO LTD.
PI   Brakebusch C, Wallach D;
DR   WPI; 93-353057/45.
DR   P-PSDB; R42197.
PT   Modulating activity of tumour necrosis factor receptor - using
PT   peptide(s), antibodies, etc. which interact with critical regions
PT   of receptor or effector protein, for controlling auto-immune
PT   disease, septic shock, etc.
PS   Claim 2; Figure 1; 17pp; English.
CC   Modification of the tumour necrosis factor receptor by mutation or
CC   deletion modulates signal transduction and/or cleavage effected by
CC   the receptor. This modulation of activity can also be achieved
CC   using effector proteins which interact with the TNF receptor.
CC   Molecules which interact with the TNF receptor or the effector
CC   proteins can be used to treat or prevent diseases associated with
CC   TNF activity e.g. autoimmune disease; rheumatoid arthritis; graft
CC   rejection; graft vs. host disease or septic shock. They can also
CC   be used to treat overdoses of exogenous TNF.
SQ   Sequence 2170 BP; 474 A; 657 C; 584 G; 455 T;

```
Query Match     35.1%;  Score 422;  DB 9;  Length 2170;
Best Local Similarity   99.5%;            Pred. No. 4.91e-281;
Matches  424;  Conservative  0;  Mismatches  2;  Indels  0;  Gaps  0;

Qy    376 gatagtgtgtctcccaaggaaaatatatccacccctcaaaataattcgattgctgtacc 435
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    345 GATAGTGTGTGTCCCAAGGAAAATAATATATCCACCCTCAAAATAATTCGATTTGCGTACC 404

Qy    436 aagtgccacaaggaacctactgtgtacaatgactgtccaggccgggggcaggataccggac 495
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCGCCGGGGATACGGAC 464

Qy    496 tgcaggggagtgtgagagcgggtcctcacgcgttcagaaaaccaactcagacaactgcctc 555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    465 TGCAGGGAGTGTGAGAGCGGGTCTTCACGCGTTCAGAAAAACCAACTCAGACACTGCCTC 524

Qy    556 agctgctccaaatgccgaaagaaatgggtcaggtggagatctctcttcttgcacagtggac 615
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    525 AGCTGCTCCAAATGCCGAAAGAAATGGGTCAGGTGGAGATCTCTCTTCTTGCACAGTGGAC 584

Qy    616 cgggacaccgtgtggctgcaggaagaaccagtaccggcgattattggagtgaaaacctt 675
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    616 ...
```

Right column (RESULT 12)

```
Qy    585 CGGGACACCGTGTGGGCTGGCTGGCAGGAAGAACCAGTACCGGCGATTATTGGAGTGAAAAACCTT 644
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    585 CGGGACACCGTGTGGGCTGGCTGGCAGGAAGAACCAGTACCGGCGATTATTGGAGTGAAAAACCTT 644

Qy    645 TTCCAGTGTGCTTCAATTGCAGCCTCTGCCTCAAATGGGACCGTGCACCTCTCCTGCCAGGAG 704
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    676 ttccagtgtgctcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 735

Qy    705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTTTCTAAGAGAAAACGAGTGTGTC 764
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    736 aaacagaacaccgtgtgcacctgccatgcaggtttctttcttttctaagagaagaacgagtgtgtc 795

Qy    765 TCCTGT 770
          ||||||
Db    796 tcctgt 801
```

RESULT 12

ID   Q12215 standard; DNA; 2176 BP.
AC   Q12215;
DT   12-SEP-1991 (first entry)
DE   Type I TNF receptor.
KW   Tumour Necrosis Factor; TNF; binding protein; TBP-I; ss.
OS   Homo sapiens.
FH   Key   Location/Qualifiers
FH
FT   CDS   256..1620
FT   /*tag= a
FT   /note= "in-frame termination codon"
FT   terminator   244..246
FT   /*tag= a
FT   misc_feature   376..414
FT   /*tag= e
FT   /note= "TBP-I derived sequence"
FT   sig_peptide   256..318
FT   /*tag= b
FT   mat_peptide   319..1620
FT   /*tag= c
FT   misc_RNA   319..864
FT   /*tag= d
FT   /label= soluble_domain
FT   misc_feature   256..318
FT   /*tag= f
FT   /note= "may be 2 codons shorter or a few codons
FT   longer"
FT   misc_feature   583..627
FT   /*tag= f
FT   /note= "TBP-I derived sequence"
FT   misc_feature   850..858
FT   /*tag= g
FT   /note= "TBP-I derived sequence"
FT   misc_RNA   889..957
FT   /*tag= h
FT   /note= "TBP-I derived sequence"
FT   repeat_unit   385..504
FT   /*tag= i
FT   /label= transmembrane_domain
FT   repeat_unit   505..633
FT   /*tag= j
FT   /number= 1
FT   repeat_unit   634..756
FT   /*tag= k
FT   /number= 2
FT   repeat_unit   757..858
FT   /*tag= l
FT   /number= 3
FT   /number= 4
FT   polyA_signal   2145..2150
FT   /*tag= m
PN   EP-433900-A.
PD   26-JUN-1991.
PF   13-DEC-1990; 124133.
PR   13-DEC-1989; IL-092697.
PR   12-JUL-1990; IL-095064.
PA   (YEDA) YEDA RES & DEV CO LTD.
PI   Wallach D, Nophar Y, Kemper O, Engelmann H, Brakebusch C;
PI   Aderka D;

DR   WPI; 91-186774/26.
DR   P-PSDB; R12550.

PT   Recombinant tumour necrosis factor binding protein I - prepd. by
PT   transfecting eukaryotic cells with vector contg. deoxyribonucleic
PT   acid encoding human type I TNF receptor or soluble deriv.
PT   Disclosure; Fig 1(D); 30pp; English.
CC   The Tumour Necrosis Factor Binding Protein I is the soluble form of
CC   type I TNF-receptor and constitutes a fragment of the cell surface
CC   form of this receptor, corresp. to its extracellular domain.
CC   There is no characteristic poly(A) addition signal near the 3' end
CC   of the cDNA. The sequence ACTAAA (tag m) may serve as an
CC   alternative to this signal, but with low efficiency.
CC   See also Q12212-15.
SQ   Sequence 2176 BP;

Query Match   35.1%; Score 422; DB 2; Length 2176;
Best Local Similarity 99.5%; Pred. No. 4.91e-281;
Matches 424; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db   376 gatagtgtgtgtcccccaggagaaaatatatccaccctccaaaataattcgatttgcagtacc   435
           |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Qy   345 GATAGTGTGTGTCCCCCAGGAGAAAATATATCCACCCTCCAAAATAATTCGATTTGCGTACC   404

Db   436 aagtgcacaaaggagaacctactctgtacaacatgactgtctcaggcccggggcgatacggac   495
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   405 AAGTGCCACAAAGGAGAACCTACTTGTACAAGACTGTCCAGGCCCGGGGCGAGGATACGGAC   464

Db   496 tgcaggggaagtgcagacggcggctccttcaccgcttcaagagaaacccctcagacactgcctc   555
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   405 TGCAGGGGAGTGTGAGAGCGGCGGCTCTTCACCGCTTCAGAGAAAACCACCTCAGACACTGCCTC   524

Db   556 agctgctccaaatgccgaaagaaaatggttcaggtggagatctcttcttcttgcacagtggac   615
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   525 AGCTGCTCCAAATGCCGAAAGAAAATGGGTCAGGTGGAGATCTCTTCTTCTTGCACAGTGGAC   584

Db   616 cgggacaccgtgtgtggctgtcaggagaacccagtaccggccggaccttgaagtgaaaaacctt   675
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   585 CGGGACACCGTGTGTGGCTGTCAGGAGAACCCAGTACCGGCCGCATTATTTGGAGTGAAAACCTT   644

Db   676 ttccagtgcttcaattgcagcctctgcctccctgccaggag   735
           ||||||||||||||||||||||||||||||||||||||||
Qy   645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCCCTGCCCGTGACC   704

Db   736 aaacagaacaccgtgtgcacctgccaggttctcttcttctaagaagaaaacgagtgtgttgtc   795
           |||||||||||||||||||||||||||||||||||||||||||||||||
Qy   705 AAACAGAACACCGTGTGCACCTGCCAGGTTTCTTCTTCTAAGAGAAAAACGAGAGTGTGTC   764

Db   796 tcctgt   801
           ||||||
Qy   765 TCCTGT   770

FT   /*note= "c -> g"

RESULT   13
ID   Q14800 standard; DNA; 579 BP.
AC   Q14800;
DT   11-FEB-1992 (first entry)
DE   Human chorionic gonadotropin beta subunit analogue.
KW   Glycoprotein hormone; hCGB/; fertility; vaccine; immuno-castration;
OS   Homo sapiens.
FH   Key   Location/Qualifiers
FT   CDS   26..523
FT   /*tag=   a
FT   mat_peptide   86..520
FT   /*tag=   b
FT   sig_peptide   26..85
FT   /*tag=   c
FT   polyA_site   524..579
FT   /*tag=   d
FT   mutation   229
FT   /*tag=   e
FT   /*note= "c -> g"   232
FT   mutation

FT   /*tag=   f
FT   /*note= "c -> g"

PT   New glyco-protein hormone analogues - for inducing fertility as
PT   immuno-castration agents, for suppressing reproductive system
PT   development and as immuno-contragestive vaccines.
PS   Example 3; Fig 4a; 94pp; English.
CC   The sequence is an analogue of hCG beta subunit cDNA contg. two
CC   silent mutations which eliminate restriction sites. It was prepd.
CC   from the plasmid pKMB-hCG-beta, a construct contg. the hCG beta
CC   subunit isolated from human placenta (Fiddes and Goodman) in
CC   plasmid pKMB, a derivative of pUC18 designed to facilitate cloning
CC   of glycoprotein hormones. The sequence was used as the starting
CC   construct for many mutants. (See R15061-R15125 and R15161-R15198).
SQ   Sequence 579 BP;

Query Match   34.4%; Score 414; DB 3; Length 579;
Best Local Similarity 99.3%; Pred. No. 3.68e-275;
Matches 417; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db   104 ccaggtgcgcccaccatcaatgcaacccctgggctgtggagaaggagggggcccgtgtgc   163
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   783 CCACGGTGCGCGCCCATCAATGCCAACCCGGCTGTGGAGAAGGAGGGGCTGCGCCCGTGTGC   842

Db   164 atcaccgtcaacacaccaccatcctgtgccgggtactgccccacca   223
           |||||||||||||||||||||||||||||||||||||||||||||
Qy   843 ATCACCGTGAACACACCACCATCCTGTGCCGGGTACTGCCCCACCA   902

Db   224 ggggtgctccccggcccctgccgaggtggtgtgcaactacccggagtgtgttcggcttcggagtcc   283
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   903 GGGGTGCTCCCCGGCCCCTGCCGGGTGGTGCAACTACCGCGGAGTGTGGCTTCGAGTCC   962

Db   284 atcaggctcccctgggcgccgcggcagcaccaactgactgcgtgggtgttctcctactcc   343
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   963 ATCCGGCTCCCCTGGGCTCCGCGGCAGCAGCCACCACTGACTGCGTGGGTGTTCTCCTACTCC   1022

Db   344 agctgtcatgtgcactctgccgcgccagcaccaactgactgcgtgggggtcccaagggaccac   403
           |||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1023 AGCTGTCAATGTGCACTCTGCCCGCGCGCAGCACCACTGACTGCGTGCGGGGGTCCCAAGGACCAC   1082

Db   404 ccccttgacctgtgatgacccccggcgcttccaggactcctctttcctcaaaggccccctccccccc   463
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1083 CCCCTTGACCTGTGATGAGACCCCGGCGCTTCCAGGACTCCTCTCTTCCCCTCAAAAGGCCCCCTCCCCCC   1142

Db   464 agcctccaagcccccatccccggactccccgggggcccccgacaccccggatctctcccacaataa   523
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1143 AGCCTTCCAAGCCCCATCCCGGACTCCCCGGGGGCCCCCGGACACCCCGGATCTCCACAATAA   1202

RESULT   14
ID   T03212 standard; cDNA; 836 BP.
AC   T03212;
DT   26-APR-1996 (first entry)
DE   Single chain gonadotropin analogue 1 coding sequence.
DE   Single chain gonadotropin; human chorionic gonadotropin; hCG;
KW   alpha: beta; subunit; analogue; glycoprotein hormone; fertility;
KW   inhibit; stimulate; increase; lutropin; luteinising hormone; LH;
KW   follicle stimulating hormone; FSH; vaccine; contraceptive; ds.
OS   Synthetic.
FH   Key   Location/Qualifiers
FT   CDS   33..830
FT   /*tag=   a
FT   /transl_except= pos:240..242, aa:Arg
FT   sig_peptide   33..92
FT   /*tag=   b
FT   mat_peptide   93..827

Left entry

```
FT   /*tag-  c
FT   /label-  Analogue.1
FT   /note-  "nucleotides 93..527 encode amino acids
FT          1-145 of hCG beta-subunit; nucleotides
FT          528..551 encode a (Gly-Ser)4 linker and
FT          nucleotides 552..827 encode amino acids
FT          1-92 of gonadotropin alpha-subunit"
FT   misc_feature  1..26
FT   /*tag-  d
FT   /label-  sticky_end
FT   /note-  "single-strand overhang. The complementary
FT          strand also has a single-strand overhang at
FT          its 5'-end; the sequence of the overhang is
FT          5'-TCCGGATTAGCTTGAGATGGATCC-3'"
DR   WO952340-A1.
PN   24-AUG-1995.
PD   17-FEB-1995; U02067.
PR   18-FEB-1994; US-199382.
PA   (SENS-) SENSI-TEST.
PS   Moyle WR;
     WPI; 95-302553/39.
DR   P-PSDB; R86247.
```

Methods for altering fertility in mammals, esp. humans - e.g.
stimulating fertility by reducing the activity and/or levels of
circulating glyco:protein hormones having lutropin activity
Example 12; Fig 6; 102pp; English.
Analogue 1 (human CG-beta(1-145)-linker-human CG-alpha(1-92)) is a
specific example of a single chain gonadotropin having a chorionic
gonadotropin (CG) beta-subunit at the N-terminus, and a CG alpha-
subunit at the C-terminus, joined by a linker of 1-16 amino acids.
The analogue has luteinising hormone (lutropin) activity and is
useful for inducing ovulation and increasing male fertility.
The sequences coding for analogue 1 were cloned from a human
placental cDNA library using strand overlap extension PCR.
Sequence   836 BP;   166 A;   282 C;   222 G;   166 T;

```
Query Match            413;  Score 409;  DB 17;  Length 836;
Best Local Similarity  99.0%;        Pred. No. 1.73e-271;
Matches  413;  Conservative  0;  Mismatches  4;  Indels  0;  Gaps  0;

Db   111 ccacggtgccgcccccatcaatgcaccacctggctgtggaggaaggaggagctgcccgtgtc 170
         ||||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||||
Qy   783 CCACGGTGCCGCCCCCATCAANGCCACCTGGCTGTGGAGAAGGAGGAGCTGCCCGTGTGC 842

Db   171 atcaccgtcaacacaccacatctgtgccggctactgcccaccaatgaccgccgttgctgcag 230
         |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Qy   843 ATCACCGTCAACACCACCATCTGTGCCGGCTACTGCCCACCAATGACCGCCGTTGCTGCAG 902

Db   231 ggggtcctgccggccctgcctcaggtggtgtgcaactaccgcgatgtgcgcttcgagtcc 290
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   903 GGGGTCCTGCCGGCCCTGCCTCAGGTGGTGTGCAACTACCGCGATGTGCGCTTCGAGTCC 962

Db   291 atccggccctggtcgccgccgggcggtgaaccccgtgtctcctacgccgtggcctctc 350
         ||||||||| |||||||||||||||||||||||||||| |||||||||||||| |||||
Qy   963 ATCCGGCCGTCCCTGGCCTGGGCGGGCGGTGAACCCCGTGGTCTCCTACGCCGTGGCTCTC 1022

Db   351 agctgtcaatgcactctgcccgcccgcaccacactgactctgcgggggtccaaggaccac 410
         |||||||| ||||||||| ||||||||||||||||||||||||||||||| |||||||||
Qy  1023 AGCTGTCAAATGTGCACTCTGCGCGCCGCGAGCACCACACTGACTCTGCGGGGGTTCCAAGGACCAC 1082

Db   411 ccctgtgacctgatgaccccgcttccaggaactcttcttcctcaaggcccctcccccc 470
         |||| ||||||||||||||||||||||||| ||||||||||||||| |||||||||||
Qy  1083 CCCTTGACCTGATGACCCCGCTTCCAGGACTCCTTCTTCCTCAAAGGCCCCTCCCCCC 1142

Db   471 agcctccaagcccaaccgactccgggggccctcggggacaccctcctcccccaa 527
         |||||| ||||||| ||||||||||||||||| ||||| |||||| |||| ||
Qy  1143 AGCCTTCCAAGCCCACCCCATCCCGACTCCTCGGGACTCCACACCCCTCCCACAA 1199
```

Right entry

```
DE   Single chain gonadotropin analogue 1a coding sequence.
KW   Single chain gonadotropin; human chorionic gonadotropin; hCG;
KW   alpha; beta; subunit; analogue; glycoprotein hormone; fertility;
KW   inhibit; stimulate; increase; lutropin; luteinising hormone; LH;
KW   follicle stimulating hormone; FSH; vaccine; contraceptive; ds.
OS   Synthetic.
FH   Key            Location/Qualifiers
FT   CDS            33..830
FT   /*tag-  a
FT   /transl_except-  pos:240..242, aa:Arg
FT   sig_peptide    33..92
FT   /*tag-  b
FT   mat_peptide    93..827
FT   /*tag-  c
FT   /label-  Analogue.1a
FT   /note-  "nucleotides 93..527 encode amino acids
FT          1-145 of hCG beta-subunit; nucleotides
FT          528..551 encode a (Gly-Ser)4 linker and
FT          nucleotides 552..827 encode amino acids
FT          1-92 of gonadotropin alpha-subunit lacking
FT          the glycosylation sites at amino acid
FT          positions 52 and 78"
FT   misc_difference  705..707
FT   /*tag-  d
FT   /note-  "wild-type Asn 52 codon has been changed to a
FT          Gln codon to remove a glycosylation site"
FT   misc_difference  783..785
FT   /*tag-  e
FT   /note-  "wild-type Asn 78 codon has been changed to a
FT          Gln codon to remove a glycosylation site"
FT   misc_feature   1..26
FT   /*tag-  f
FT   /label-  sticky_end
FT   /note-  "single-strand overhang. The complementary
FT          strand also has a single-strand overhang at
FT          its 5'-end; the sequence of the overhang is
FT          5'-TCCGGATTAGCTTGAGATGGATCC-3'"
DR   WO952340-A1.
PN   24-AUG-1995.
PD   17-FEB-1995; U02067.
PR   18-FEB-1994; US-199382.
PA   (SENS-) SENSI-TEST.
PI   Moyle WR;
     WPI; 95-302553/39.
DR   P-PSDB; R86259.
```

Methods for altering fertility in mammals, esp. humans - e.g.
stimulating fertility by reducing the activity and/or levels of
circulating glyco:protein hormones having lutropin activity
Example 23; Fig 18; 102pp; English.
Analogue 1a (human CG-beta(1-145)-linker-human CG-alpha(1-92)[N53Q,
N78Q]) is a specific example of a single chain gonadotropin having
a chorionic gonadotropin (CG) beta-subunit at the N-terminus and a
CG alpha-subunit at the C-terminus, joined by a linker of 1-16 amino
acids. The analogue 1a was derived from analogue 1 by removing the
two glycosylation sites from the alpha-subunit. The analogue has
anti-luteinising hormone (lutropin) activity and can be used for
facilitating ovulation, terminating pregnancy and reducing androgen
secretion. The present sequence codes for analogue 1a.
Sequence   836 BP;   166 A;   282 C;   222 G;   166 T;

```
Query Match            413;  Score 409;  DB 17;  Length 836;
Best Local Similarity  99.0%;        Pred. No. 1.73e-271;
Matches  413;  Conservative  0;  Mismatches  4;  Indels  0;  Gaps  0;

Db   111 ccacggtgccgcccccatcaatgcaccacctggctgtggaggaaggaggagctgcccgtgtc 170
         ||||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||||
Qy   783 CCACGGTGCCGCCCCCATCAANGCCACCTGGCTGTGGAGAAGGAGGAGCTGCCCGTGTGC 842

Db   171 atcaccgtcaacacaccacatctgtgccggctactgcccaccaatgaccgccgttgctgcag 230
         |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Qy   843 ATCACCGTCAACACCACCATCTGTGCCGGCTACTGCCCACCAATGACCGCCGTTGCTGCAG 902

Db   231 ggggtcctgccggccctgcctcaggtggtgtgcaactaccgcgatgtgcgcttcgagtcc 290
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   903 GGGGTCCTGCCGGCCCTGCCTCAGGTGGTGTGCAACTACCGCGATGTGCGCTTCGAGTCC 962
```

Bottom left

```
RESULT   15
ID    T03243 standard; cDNA; 836 BP.
AC    T03243;
DT    08-MAY-1996 (first entry)
```

```
Qy    903 GGGGTCCTTCCCCCCCCCCCTGCCTCAGGTGGTGTGCAACTACCGGCGATGTGCGGCTTCGAGTCC 962
          |||||||| ||| ||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    291 atccggctccctggctgccccgcgcgggcgtgaaccccgtggtctcctacggcgtggctctc 350
          ||||||||||||||||||||||||||||| ||||||||||||||||||| ||||||||||
Qy    963 ATCCGGGCTCCCTGGCTGCCCCGCGGGGGTGAACCCGTGGTCTCCTACGCTGTGGCTCTC 1022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    351 agctgtcaatgtgcactctgcgcgcgcaggcacacactgactgcgggggtcccaaggacac 410
          ||||||||| ||||||||||||| |||||||||| ||||||||||||||||||||||||| ||||
Qy   1023 AGCTGTCAAATGTGCACTCTGCCGCGCGCAGCACCACTGACTGCGGGGGTCCCAAGGACCAC 1082
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    411 ccccttgacctgtgatgaccccgcttccaggactcctcttcctcaaaggcccctccccc 470
          |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Qy   1083 CCCTTGACCTGTGATGACCCCGCTTCCAGGACTCCTCTTCCTCAAAAGGCCCCTCCCCCC 1142
          |||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db    471 agccttccaagcccatcccgactcccggggcccctcggacaccccgaatcctccccaa 527
          ||||||||||||||||||||||||||||||||||||||||||||||||| ||| |||
Qy   1143 AGCCTTCCAAGCCCATCCCGACTCCCGGGGCCCTCGGACACCCCGAATCCTCCCACAA 1199
```

```
*****************************************************************
*                                                               *
*    M P S R C H                                         (TM)   *
*                                                               *
*****************************************************************
```
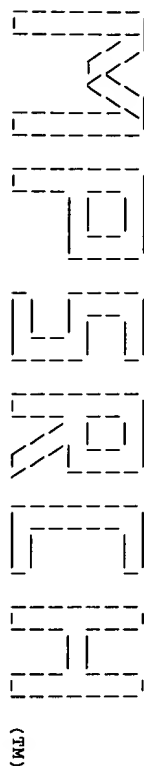
Release 3.0.5AA John F. Collins, Biocomputing Research Unit.
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Distribution rights by Oxford Molecular Ltd

MPsrch_nn   n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed May 6 13:18:57 1998; MasPar time 1103.82 Seconds
                                        1323.848 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-3
Description: (1-1202) from US08804166.seq
Perfect Score: 1202
N.A. Sequence: Comp: 1 CTCGAGATGGCTCACAGGTAA...............CCCGAGCTCCTCCACAATAA 1202
                        GAGCTCTACCGAGTGTCCATT.............GGGGCTAGAGAGGTGTTATT

Scoring table: TABLE default
               Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 1610801 seqs, 607859669 bases x 2

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database: embl-est
             1:em_est1 2:em_est2 3:em_est3 4:em_est4 5:em_est5
             6:em_est6 7:em_est8 8:em_gss 9:em_est13
Database: genbank-est
             10:gb_est1 11:gb_est2 12:gb_est3 13:gb_est4 14:gb_est5
             15:gb_est6 16:gb_est7 17:gb_est8 18:gb_est9 19:gb_est10
             20:gb_est11 21:gb_sts 22:gb_gss 23:gb_est12 24:gb_est13
             25:gb_est14 26:gb_est15 27:gb_est16 28:gb_est17
             29:gb_est18 30:gb_est19 31:gb_est20

Statistics: Mean 11.212; Variance 2.135; scale 5.252

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

## SUMMARIES

| Result NO. | Score | % Query Match | Length | DB | ID | Description | Pred. No. |
|---|---|---|---|---|---|---|---|
| 1 | 391 | 32.5 | 601 | 13 | N32759 | yw91b05.s1 Homo sapien | 0.00e+00 |
| 2 | 384 | 31.9 | 537 | 13 | N30276 | yw69d04.s1 Homo sapien | 0.00e+00 |
| 3 | 382 | 31.9 | 593 | 13 | N29730 | yw78h03.s1 Homo sapien | 0.00e+00 |
| 4 | 381 | 31.7 | 564 | 13 | N32604 | yw95d03.s1 Homo sapien | 0.00e+00 |
| 5 | 379 | 31.5 | 442 | 13 | N32233 | yw81f08.s1 Homo sapien | 0.00e+00 |
| 6 | 379 | 31.5 | 473 | 13 | N27302 | yw71f12.s1 Homo sapien | 0.00e+00 |
| 7 | 379 | 31.5 | 548 | 13 | N30036 | yw80b11.s1 Homo sapien | 0.00e+00 |
| 8 | 377 | 31.4 | 566 | 13 | N30831 | yw70b04.s1 Homo sapien | 0.00e+00 |
| 9 | 373 | 31.0 | 563 | 13 | N31955 | yw89a07.s1 Homo sapien | 0.00e+00 |
| 10 | 371 | 30.9 | 473 | 25 | AA400910 | zt7lh09.s1 Soares test | 0.00e+00 |
| 11 | 372 | 30.9 | 479 | 13 | N30684 | yw77h04.s1 Homo sapien | 0.00e+00 |
| 12 | 365 | 30.4 | 446 | 13 | N31616 | yw84a02.s1 Homo sapien | 0.00e+00 |
| 13 | 363 | 30.2 | 526 | 28 | AA644163 | af62d08.s1 Soares NhHM | 0.00e+00 |
| 14 | 354 | 29.5 | 400 | 25 | AA232905 | zr46c04.s1 Soares NhHM | 0.00e+00 |
| 15 | 350 | 29.1 | 531 | 16 | W71989 | zd66b03.s1 Soares feta | 0.00e+00 |
| 16 | 345 | 28.7 | 419 | 16 | H95374 | yw60b03.s1 Soares plac | 0.00e+00 |
| 17 | 331 | 27.5 | 403 | 13 | N26397 | yw76g11.s1 Soares test | 0.00e+00 |
| 18 | 325 | 27.0 | 441 | 13 | N30741 | yw74b04.s1 Homo sapien | 0.00e+00 |
| 19 | 322 | 26.8 | 422 | 11 | R23214 | yh28a03.s1 Homo sapien | 0.00e+00 |
| 20 | 319 | 26.5 | 515 | 13 | N30608 | yw72c07.s1 Homo sapien | 0.00e+00 |
| 21 | 317 | 26.4 | 404 | 13 | N30833 | yw70b08.s1 Homo sapien | 0.00e+00 |
| 22 | 311 | 25.9 | 386 | 13 | N30822 | yw65h07.s1 Homo sapien | 0.00e+00 |
| 23 | 309 | 25.7 | 367 | 11 | R68815 | yj143c05.s1 Homo sapien | 0.00e+00 |
| 24 | 301 | 25.0 | 329 | 12 | H12587 | yj12g11.s1 Homo sapien | 0.00e+00 |
| 25 | 299 | 24.9 | 367 | 16 | H94446 | yw55f02.s1 Soares plac | 0.00e+00 |
| 26 | 298 | 24.8 | 380 | 13 | H87464 | yw99f05.s1 Homo sapien | 0.00e+00 |
| 27 | 294 | 24.5 | 526 | 25 | AA393716 | yw16e05.s1 Homo sapien | 0.00e+00 |
| 28 | 290 | 24.1 | 427 | 16 | AA393716 | zt7lh09.r1 Soares test | 0.00e+00 |
| 29 | 289 | 24.0 | 427 | 13 | N27111 | yw5sg08.s1 Homo sapien | 0.00e+00 |
| 30 | 288 | 23.9 | 319 | 13 | H87631 | yw75h12.s1 Homo sapien | 0.00e+00 |
| 31 | 283 | 23.5 | 329 | 11 | H87156 | yw1fe12.s1 Homo sapien | 0.00e+00 |
| 32 | 278 | 23.1 | 311 | 10 | T47334 | yw15b04.s1 Homo sapien | 0.00e+00 |
| 33 | 276 | 23.0 | 284 | 13 | H93656 | yb10e11.s1 Homo sapien | 0.00e+00 |
| 34 | 269 | 22.4 | 303 | 13 | H86993 | yw55a11.s1 Homo sapien | 0.00e+00 |
| 35 | 267 | 22.2 | 291 | 10 | T90191 | yw15b10.s1 Homo sapien | 0.00e+00 |
| 36 | 257 | 21.4 | 266 | 13 | H93668 | yd38g09.s1 Homo sapien | 0.00e+00 |
| 37 | 249 | 20.7 | 251 | 19 | AA330413 | yw55c12.s1 Homo sapien | 0.00e+00 |
| 38 | 241 | 20.0 | 519 | 23 | C18044 | ES134462 Embryo, 6 wee | 0.00e+00 |
| 39 | 238 | 19.8 | 278 | 10 | T49170 | Human placenta cDNA 5' | 0.00e+00 |
| 40 | 237 | 19.7 | 348 | 16 | H95381 | yb09g02.r1 Homo sapien | 0.00e+00 |
| 41 | 233 | 19.4 | 348 | 16 | H95381 | yw60d07.s1 Soares plac | 0.00e+00 |
| 42 | 228 | 19.0 | 341 | 16 | T29543 | ES83815 Homo sapiens | 0.00e+00 |
| 43 | 222 | 18.5 | 244 | 16 | H94107 | ES83815 Homo sapiens | 0.00e+00 |
| 44 | 217 | 18.1 | 255 | 11 | R63352 | yw58h09.s1 Soares plac | 0.00e+00 |
| 45 | 214 | 17.8 | 275 | 10 | T47316 | yb10c02.r1 Homo sapien | 0.00e+00 |

## ALIGNMENTS

```
RESULT         1
LOCUS          N32759         601 bp     mRNA              EST       10-JAN-1996
DEFINITION     yw91b05.s1 Homo sapiens cDNA clone 259569 3' similar to gb:J00117
               CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
ACCESSION      N32759
NID            g1153158
KEYWORDS       EST.
SOURCE         human clone=259569 primer=rml3 -40 forward library=Soares placenta
               8to9weeks 2NbHP8to9W vector=pT7/T3D (Pharmacia) with a modified
               polylinker host=DH10B (ampicillin resistant) Rsite1=Not I
               Rsite2=Eco RI two placenta: one from 8 weeks and another from 9
               weeks post conception. 1st strand cDNA was primed with a Not I -
               oligo(dT) primer
               [5'-TGTTACCAATCTGAAGTGGGAGGACGGCGCGGGATTTTTTTTTTTTTTTTTT-3'],
               double-stranded cDNA was size selected, ligated to Eco RI adapters
               (Pharmacia), digested with Not I and cloned into the Not I and Eco
               RI sites of a modified pT7T3 vector (Pharmacia). Library
               constructed by Bento Soares and M. Fatima Bonaldo.
ORGANISM       Homo sapiens
               Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
               Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
               Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
               Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 601)
AUTHORS        Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
               Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
               Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
               Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
               Wilson,R.
TITLE          The WashU-Merck EST Project
JOURNAL        Unpublished (1995)
COMMENT        Contact: Wilson RK
               WashU-Merck EST Project
               Washington University School of Medicine
               4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
```

REFERENCE   1 (bases 1 to 537)
  ORGANISM   Homo sapiens
              Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
              Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
              Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
              Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
  DEFINITION yw69d04.s1 Homo sapiens cDNA clone 257479 3' similar to gb:J00117
              CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
  ACCESSION   N30276
  NID   g1148796
  KEYWORDS   EST.
  SOURCE   human clone=257479 primer=m13 -40 forward library=Soares placenta
              8to9weeks 2NbHP8to9W vector=pT7T3D (Pharmacia) with a modified
              polylinker host=DH10B (ampicillin resistant) Rsite1=Not I
              Rsite2=Eco RI two placente: one from 8 weeks and another from 9
              weeks post conception. 1st strand cDNA was primed with a Not I -
              oligo(dT) primer
              [5'-TGTTACCAATCTGAAGTGGGACGGCGCGCCGGATTTTTTTTTTTTTTTTTT-3'],
              double-stranded cDNA was size selected, ligated to Eco RI adapters
              (Pharmacia), digested with Not I and cloned into the Not I and Eco
              RI sites of a modified pT7T3 vector (Pharmacia). Library
              constructed by Bento Soares and M. Fatima Bonaldo.

LOCUS   N30276   537 bp   mRNA   EST   05-JAN-1996

RESULT 2

Cp 842   GCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGCATTGATTGGGGCGGGCACCGTGG 783
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 376   GCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGCATTGATTGGGGCGGGCACCGTGA 435

Cp 902   CTGCCAGCACGCGGGTCATGGTGGGGCAGTAGCCGGCACGGTAGCCCGGGATGGTGAT 843
          |||||||||||||||||||||||||||||||||||||||||||||||
Db 376   GCACACGGGGCAGCC... 435

Db 316   TTGGAGCACGGGGTCATGGTGGGGCAGTAGCCGGCACGGTAGCCGGGGGTGGTGGTGAT 375

Cp 962   GGACTCGAAGCGCACATCGCGGTTCACCGCGCCGCCGGCGAGCCGGATGGCCTTGGAAGGCT 903

Db 256   GGACTCGAAGCGCACATCGCGGTAGTGTTGCACACACCACCTGCCGCCGCCGGGGGCAAGACCCC 315

Cp 1022 GAGAGCCACGGCGTAGGAGAGACCACGGGGTTCACCGCGCCGCACCAAGGGAGCCGCGGAT 963

Db 196   GAGAGCCACGGCGTAGGAGAGACCACGGGGTTCACCGCGCCGCACCAAGGGAGCCGCGGAT 255

Cp 1082 GTGGGTCCTTGGGGACCCCGCAGTCAGTGCTGCTCGCGGGTCGCACATTGACAGCT 1023

Db 137   GTGGGTCCTTGGGACCCC-GCAGTCAGTGCTGCTCGCGGGTCGCACATTGACAGCT 195

Cp 1142 GGGGGGAGGGGCCTTTGAGGAAGAGAGAGTCCTGAAGCGCGGGGGTCATCACAGGTCAAGGG 1083

Db 77   GGGGGGAGGGGCCTTTGAGGAAGAGAGAGTCCTGGAAGCGCGGGGGTCATCACAGGTCAAGGG 136

Cp 1202 TTATTGTGGGAGGATCGGGGGTGTCCGAGGGCCCCGGGGAGTCGGGGATGGGCTTGGAAGGCT 1143

Db 17   TTATTGTGGGAGGATCGGGGGTGTCCGAGGGGCCCGGGAGTCGGGGATGGGCTTGGAAGGCT 76

Matches 408; Conservative 0; Pred. No. 0.00e+00; Mismatches 11; Indels 1; Gaps 1;
Best Local Similarity 97.1%;
Query Match   32.5%; Score 391; DB 13; Length 601;

ORIGIN
BASE COUNT   112 a   154 c   219 g   110 t   6 others

  mRNA   <1. >601
               /clone="259569"
               /organism="Homo sapiens"
  source   1. .601
               Location/Qualifiers
FEATURES

COMMENT   This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.

This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Source: IMAGE Consortium, LLNL
High quality sequence stops: 387
Email: est@watson.wustl.edu
Fax: 314 286 1810
Tel: 314 286 1800

REFERENCE   1 (bases 1 to 537)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
  SOURCE   human clone=258389 primer=m13 -40 forward library=Soares placenta
  KEYWORDS EST.
  NID   g1148250
  ACCESSION N29730
  DEFINITION yw78h03.s1 Homo sapiens cDNA clone 258389 3' similar to gb:J00117
            CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.

LOCUS   N29730   593 bp   mRNA   EST   05-JAN-1996

RESULT 3

Cp 784   GGACCAGC 777
          ||| |||
Db 435   GGCNAAGC 442

Cp 844   ATGCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGCATTGATTGGGGCGGGCACCGT 785
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 375   ATGCACACGGGGCAGCCCTCCTTCTCCACAGTGGTGGGGCGGCACCGAGCCGGTTGGGCAANCGT 434

Cp 903   CC-TGCAGCACGCGGGTCATGGTGGGGCAGTAGCCCGCACAGATGGTGTTGACGGTG 845
          || |||||||||||||||||||||||||||||||||||||||||||||||||
Db 315   CCCTGCAGCACGCGGGTCATGGTGGGGCAGTAGCCCGGCACAGATGGTGTTGACGGTG 374

Cp 963   TGGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGCCGGCAGGGGCAGGAGCC 904
          |||||||||||||||||||||||||||||||||||||||||
Db 255   TGGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGCCGGCAGGGGCAGGAGCC 315

Cp 1022 GAGAGCCACACGCGT-AGGAGACCACGGGGTTCACCGCGCCGCGGGGG-CAGCCAGGGAGCCGGA 964
          |||||||||||| ||| |||||||||||||||||||||||||||||
Db 196   GAGAGCCACGGCGTTAGGAGACCACGGGGTTCACCGCGCCGGCGGGGG-CAGCCAGGGAGCCGGA 254

Cp 1082 GTGGGTCCTTGGGGACCCCGCAGTCAGTGGTGGTGCTGCTCGCGGGTCGCACATTGACAGCT 1023

Db 137   GTGGGTCCTTGGGGACCCCC-GCAGTCAGTGGTGGTGCTGCTCGCGGGTCGCACATTGACAGCT 195

Cp 1142 GGGGGGAGGGGCCTTTGAGGAAGAGAGAGTCCTGGAAGCGCGGGGGTCATCACAGGTCAAGGG 1083

Db 77   GGGGGGAGGGGCCTTTGAGGAAGAGAGAGTCCTGGAAGCGCGGGGGTCATCACAGGTCAAGGG 136

Cp 1202 TTATTGTGGGAGGATCGGGGGTGTCCGAGGGCCCCGGGGAGTCGGGGATGGGCTTGGAAGGCT 1143

Db 17   TTATTGTGGGAGGATCGGGGGTGTCCGAGGGCCCCGGGAGTCGGGGATGGGCTTGGAAGGCT 76

Matches 415; Conservative 0; Pred. No. 0.00e+00; Mismatches 9; Indels 4; Gaps 4;
Best Local Similarity 97.0%;
Query Match   31.9%; Score 384; DB 13; Length 537;

ORIGIN
BASE COUNT   98 a   145 c   201 g   90 t   3 others

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               /clone="257479"
               /organism="Homo sapiens"
  source   1. .537
               Location/Qualifiers
FEATURES

COMMENT   This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Source: IMAGE Consortium, LLNL
            High quality sequence stops: 313
            Email: est@watson.wustl.edu
            Fax: 314 286 1810
            Tel: 314 286 1800
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Contact: Wilson RK
            Washu-Merck EST Project
  JOURNAL   Unpublished (1995)
  TITLE   The Washu-Merck EST Project
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.

8to9weeks 2NDHP8to9W vector-p7713D (Pharmacia) with a modified
polylinker host-DH10B (ampicillin resistant) Rsite1-Not I
Rsite2-Eco RI two placentae: one from 8 weeks and another from 9
weeks post conception. 1st strand cDNA was primed with a Not I -
oligo(dT) primer
[5'-TGTTACCAAATCTGAAGTGGGACGCGGCGCGCCGATTTTTTTTTTTTTTTTT-3'],
double-stranded cDNA was size selected, ligated to Eco RI adapters
(Pharmacia), digested with Not I and cloned into the Not I and Eco
RI sites of a modified p7713 vector (Pharmacia). Library
constructed by Bento Soares and M. Fatima Bonaldo.

ORGANISM   Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

REFERENCE   1 (bases 1 to 593)
AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
TITLE   The WashU-Merck EST Project
JOURNAL   Unpublished (1995)
COMMENT   Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 368
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES   Location/Qualifiers
source   1..593
                     /organism="Homo sapiens"
                     /clone="258389"

BASE COUNT   109 a   151 c   216 g   111 t   6 others
ORIGIN

mRNA   <1..>593

Query Match   31.8%;   Score 382;   DB 13;   Length 593;
Best Local Similarity 96.7%;   Pred. No. 0.00e+00;
Matches 414;   Conservative   0;   Mismatches 10;   Indels 4;   Gaps 4;

Db   18 TTATTGTGGGAGGATCGGGGTGTTCCGAGGGCCCGGGAGTCGGGATGGGCGTTGGAAGGCT   77
           |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Cp   1202 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCGGGAGTCGGGATGGGCGTTGGAAGGCT 1143

Db   78 GGGGGGAGGGGAGGGGCCTTTGAGGAAGAGGAGGAGTCCTTGGAACGCGGGGGGGGGGGGG 137
           ||||||||||||||||||||||||||
Cp   1142 GGGGGGAGGGGGCCTTTGAGGAAGAGGAGGAGTCCTTCATCACACAGGTCAAGG 1083

Db   138 GTGGTCCTTGGGACCCC-GCAGTCAGTGGTGTGTGCCGGCCAGAGTGCACAATTGACAGCT 196
           |||||||||||| ||||||||||||||||||||||||||||||||||
Cp   1082 GTGGTCCTTGGGACCCCGCAGTCAGTGGTGCGTGCCGGGCCAGAGTGCACAATTGACAGCT 1023

Db   197 GAGAGCCACGGCCGTAGGAGAGACCACGGGGGGTTCACGCCCGCGNGG-CAGCCAGGAGCCGGAT 255
           ||||||||| |||||||||||||||||||||| ||||||||||||||
Cp   1022 GAGAGCCACAGGCCTAGGAGACACGGGTTCACGCCCGCGGCGGGCCAGCCAGGAGCCGGAT 963

Db   256 GGACTCGAAGCCCACAATCGCGCGTAGTTCCACACCACCTGAGGCGAGGACCC 315
           |||||||||||||||||||||||||||||||||||||||||||
Cp   962 GGACTCGAAGCCCACAATCGCGTAGTTCCACACCACCTGAGGCGAGGACCC 903

Db   316 CTGCAGCACGCGCGGGGTCATGGTTGGGGAGAGTAGCGGCACAGATGGGTGTGTTGACGGTGA 375
           |||||||||||||||||||||||||||||||||||||
Cp   902 CTGCAGCACGCGCGGGGTCATGGT-GGGGCAGTAGCGGCCGGCACAGATGTGGTGGTTGACGGTGA 844

Db   376 TGCACACGGGCGGGCCTCCTCTCCACAGCCANNGGTTGGCATTGATGGGGGCGGCCACCGT 435
           ||||||||||||||||||||||||||||| ||| ||||||||||||||||||||

Cp   843 TGCACACGGGCGGGCCTCCTCTTCCACAGCCAGGGT-GGCATTGATGGGGCGGCCACCGT 785
           |||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db   436 GGCCAAGC 443
           || ||| |||
Cp   784 GGACCAGC 777

RESULT   4

LOCUS   N32604   564 bp   mRNA   EST   10-JAN-1996
DEFINITION   yw95d03.s1 Homo sapiens cDNA clone 259973 3' similar to gb:J00117
             CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
ACCESSION   N32604
NID   g1153003
KEYWORDS   EST.
SOURCE   human clone=259973 primer=m13 -40 forward library=Soares placenta
             8to9weeks 2NDHP8to9W vector-p7713D (Pharmacia) with a modified
             polylinker host-DH10B (ampicillin resistant) Rsite1-Not I
             Rsite2-Eco RI two placentae: one from 8 weeks and another from 9
             weeks post conception. 1st strand cDNA was primed with a Not I -
             oligo(dT) primer
             [5'-TGTTACCAAATCTGAAGTGGGACGCGGCGCGCCGATTTTTTTTTTTTTTTTT-3'],
             double-stranded cDNA was size selected, ligated to Eco RI adapters
             (Pharmacia), digested with Not I and cloned into the Not I and Eco
             RI sites of a modified p7713 vector (Pharmacia). Library
             constructed by Bento Soares and M. Fatima Bonaldo.

ORGANISM   Homo sapiens
             Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
             Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
             Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
             Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

REFERENCE   1 (bases 1 to 564)
AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
             Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
             Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
             Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
             Wilson,R.
TITLE   The WashU-Merck EST Project
JOURNAL   Unpublished (1995)
COMMENT   Contact: Wilson RK
             WashU-Merck EST Project
             Washington University School of Medicine
             4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
             Tel: 314 286 1800
             Fax: 314 286 1810
             Email: est@watson.wustl.edu
             High quality sequence stops: 364
             Source: IMAGE Consortium, LLNL
             This clone is available royalty-free through LLNL; contact the
             IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES   Location/Qualifiers
source   1..564
                     /organism="Homo sapiens"
                     /clone="259973"

BASE COUNT   103 a   148 c   206 g   99 t   8 others
ORIGIN

mRNA   <1..>564

Query Match   31.7%;   Score 381;   DB 13;   Length 564;
Best Local Similarity 96.5%;   Pred. No. 0.00e+00;
Matches 410;   Conservative   0;   Mismatches 12;   Indels 3;   Gaps 3;

Db   17 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCGGGAGTCGGGATGGGCGTTGGAAGGCT   76
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp   1202 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCGGGAGTCGGGATGGGCGTTGGAAGGCT 1143

Db   77 GGGGGGAGGGGGCCTTTGAGGAAGAGGAGGAGTCCTTGAAAGCGGGGGTCATCACAGGTCAAGGG 136
           |||||||||||||||||||||||||||||||||||||
Cp   1142 GGGGGGAGGGGGCCTTTGAGGAAGAGGAGGAGTCCTTCATCACAGGTCAAGG 1083

Db   137 GTGGTCCTTGGGACCCC-GCAGTCAGTGGTGTGCTCGCGGCGCAGAGTGCACATTGACAGCT 195
           ||||||||||||| |||||||||||||||||||||||||||||||||

RESULT 5

```
LOCUS       N32233      442 bp    mRNA        EST      10-JAN-1996
DEFINITION  yw81f08.s1 Homo sapiens cDNA clone 258663 3' similar to gb:J00117
            CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
ACCESSION   N32233
NID         g1152632
KEYWORDS    EST.
SOURCE      human clone=258663 primer=m13 -40 forward library=Soares placenta
            8to9weeks 2NbHP8to9W vector=pT7T3D (Pharmacia) with a modified
            polylinker host=DH10B (ampicillin resistant) Rsite1=Not I
            Rsite2=Eco RI two placentae: one from 8 weeks and another from 9
            weeks post conception. 1st strand cDNA was primed with a Not I -
            oligo(dT) primer
            [5'-TGTTACCAATCTGAAGTGGAGCGGCCGCGGATTTTTTTTTTTTTTTTT-3'],
            double-stranded cDNA was size selected, ligated to Eco RI adapters
            (Pharmacia), digested with Not I and cloned into the Not I and Eco
            RI sites of a modified pT7T3 vector (Pharmacia). Library
            constructed by Bento Soares and M. Fatima Bonaldo.
ORGANISM    Homo sapiens
            Eukaryotae; Metazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 442)
AUTHORS     Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
TITLE       The WashU-Merck EST Project
JOURNAL     Unpublished (1995)
COMMENT     Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 364
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES             Location/Qualifiers
     source          1..442
                     /organism="Homo sapiens"
                     /clone="258663"
BASE COUNT     85 a    110 c    174 g    68 t      5 others
mRNA
ORIGIN
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Query Match   31.5%;  Score 379;  DB 13;  Length 442;
Best Local Similarity  94.6%;  Pred. No. 0.00e+00;
Matches  402;  Conservative  0;  Mismatches 22;  Indels 1;  Gaps 1;

Cp  1082  GTGGTCCTTGGGACCCCCGCCAGTTCAGGTGGTGCTGCGGCGCGAGAGTGCACATTGACAGCT  1023
          |||||||||||||||||||||||||||||||||||||||||
Db   196  GAGAGCCACGCGGTAGGAGAACCACGGGGTTCACCGCCGCGGCGGGGGGGGAT  255
Cp  1022  GAGAGCCACGCGGTAGGAGAGAGCCACCGGGGTTCACCGCGGCGGGGGGGGAT  963
Db   256  GGACTCGAAGCGCACATCCGCGGGTAGTTGCACACCTGAGGCAGGGCCGCAAGACCCC  315
Cp   962  GGACTCGAAGCGCACATCCGCGGGTAGTTGCACACCTGAGGCAGGGCCGCAAGACCCC  903
Db   316  CTTGCAGCACGCGCGGTCATGGTGGGGCGGCAGTAGC-CGCACAGATGGGTGGTGTTGTTGACGGTGA  374
Cp   902  CT-CCAGCACGCGGGTCATGGGTGGG...  844
Db   375  TGCACACGGGGGCAGCCCCTCCTTCTCCACAGCC...  434
Cp   843  TGCACACGGGGGCAGCCCTCCTTCTCCACAGCCTGGCATTGATGGGGCGGCACCGTG  784
Db   435  GCCNA  439
Cp   783  GACCA  779
```

RESULT 6

```
LOCUS       N27302      473 bp    mRNA        EST      29-DEC-1995
DEFINITION  yw71f12.s1 Homo sapiens cDNA clone 257711 3' similar to gb:J00117
            CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
ACCESSION   N27302
NID         g1141650
KEYWORDS    EST.
SOURCE      human clone=257711 primer=m13 -40 forward library=Soares placenta
            8to9weeks 2NbHP8to9W vector=pT7T3D (Pharmacia) with a modified
            polylinker host=DH10B (ampicillin resistant) Rsite1=Not I
            Rsite2=Eco RI two placentae: one from 8 weeks and another from 9
            weeks post conception. 1st strand cDNA was primed with a Not I -
            oligo(dT) primer
            [5'-TGTTACCAATCTGAAGTGGAGCGGCCGCGGATTTTTTTTTTTTTTTTT-3'],
            double-stranded cDNA was size selected, ligated to Eco RI adapters
            (Pharmacia), digested with Not I and cloned into the Not I and Eco
            RI sites of a modified pT7T3 vector (Pharmacia). Library
            constructed by Bento Soares and M. Fatima Bonaldo.
ORGANISM    Homo sapiens
            Eukaryotae; Metazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 473)
AUTHORS     Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
TITLE       The WashU-Merck EST Project
JOURNAL     Unpublished (1995)
COMMENT     Contact: Wilson RK
```

```
Db    17  TTATTGTGGGAGGAGGATCGGGTGGTGGTTCCGAGGGGTGCCCGAGGGGAGTCGGGGAGGACTGGAAGGCT  76
Cp  1202  TTATTGTGGGAGGAGGATCGGGGGGTGTCCGAGGGGCCCCGGGGGAGTCGGGGGATGGGGACTTGGAAGGCT  1143
Db    77  GGGGGGAGGGGGCCTTTGAGGAAGAGAGTCCTGGAGGGGCCCCCGGGGGAGTCGGGGGATGGGGCTTGGAAGGG  136
Cp  1142  GGGGGGGAGGGGGCCTTTGAGGAAGAGAGTCCTGGAGGGGCCCCCGGGGGAGTCGGGGGATGGGGCTCAAGGG  1083
Db   137  GTGGTCCTTGGGGACCCCCGCCAAGTCAGTTGGTGCTGCGGCACGGGTGCACATTGACAGC  196
Cp  1082  GTGGTCCTTGGGGACCCCCGCAGTCAGT-GGTGCTGCGGCACATTGACAGC  1024
Db   197  TGAGACCACCGGCGTAGGAGACCACGGGGTTCACGCCGCGCNCAAGGACGCCGGA  256
Cp  1023  TGAGACCACCGGCGTAGGAGACCACGGGGTTCACGCCGCGGCGGGGGGCGCACCAGGGAGCCGGA  964
Db   257  TGGGACTCGAAGCGCACATCCGCGGGTAGTTGCACACCACCCACCTGAGGCAGGGCCACGAAGACCAC  316
Cp   963  TGGGACTCGAAGCGCACATCCGCGGGTAGTTGCACACCACCCACCTGAGGCAGGGCCACGAAGACC  904
Db   317  CCTGCAGCACGCGGGTCATGGTGGGGCGGCAGTAACCGGCCACACAGATGGTGGTGTTGTTGACGGTNA  376
Cp   903  CCTGCAGCACGCGGGTCATGGTGGGGCGGCAGTAGCCGGCCACACAGATGGTGGTGTTGTTGACGGTGA  844
Db   377  TGCACACGGGGGCAGCCCCTCCTTCTCCACAGCC...  436
Cp   843  TGCACACGGGGGCAGCCCCTCCTTCTCCACAGCC...  784
Db   437  GCCCA  441
Cp   783  GACCA  779
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RESULT 7

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LOCUS       N30036       548 bp    mRNA             EST    05-JAN-1996
DEFINITION  yw80b11.s1 Homo sapiens cDNA clone 258525 3' similar to gb:J00117
            CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
ACCESSION   N30036
NID         g1148556
KEYWORDS    EST.
SOURCE      human clone=258525 primer=m13 -40 forward library=Soares placenta
            8to9weeks 2NbHP8to9W vector=pT7T3D (Pharmacia) with a modified
            polylinker host=DH10B (ampicillin resistant) Rsite1=Not I
            Rsite2=Eco RI two placentae: one from 8 weeks and another from 9
            weeks post conception. 1st strand cDNA was primed with a Not I -
            oligo(dT) primer
            [5'-TGTTACCAATCTAGAAGTGGGAGCGGCCGCGGGGATTTTTTTTTTTTTTTTT-3'],
            double-stranded cDNA was size selected, ligated to Eco RI adapters
            (Pharmacia), digested with Not I and cloned into the Not I and Eco
            RI sites of a modified pT7T3 vector (Pharmacia). Library
```

```
            constructed by Bento Soares and M. Fatima Bonaldo.
ORGANISM    Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 548)
AUTHORS     Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
TITLE       The WashU-Merck EST Project
JOURNAL     Unpublished (1995)
COMMENT     Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 333
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES             Location/Qualifiers
     source          1..548
                     /organism="Homo sapiens"
                     /clone="258525"
     mRNA            <1..>548
BASE COUNT     99 a   143 c   206 g    93 t   7 others
ORIGIN
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```
Query Match
Best Local Similarity   96.9%;
Matches  410;  Conservative   0;  Score 379;  DB 13;  Length 548;
                                   Pred. No. 0.00e+00;  Mismatches  9;  Indels  4;  Gaps  4;

Db    18 TTATTGTGGGAGGATCGGGGTGTCCGAGGGGCCCCGGAGTCGGGGATTGGGAAGGCT    77
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp  1202 TTATTGTGGGAGGATCGGGGTGTCCGAGGGGCCCCGGAGTCGGGGATTGGGAAGGCT  1143

Db    78 GGGGGAGGGGGGCCTTTGAGGAAGAGAGAGAGTCCTGGAAGAGGGGTCATCACAGGTCAAGG   137
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp  1142 GGGGGAGGGGGGCCTTTGAGGAAGAGAGAGAGTCCTGGAAGAGGGGTCATCACAGGTCAAGG  1083

Db   138 GTGGTCCTTGGGACCCC-GCAGTCAGTGTGCTGCTGCGCGGCGGAGAGTGCACATTGACAGCT   196
         ||||||||||||||||   |||||||||||||||||||||||||||||||||||||||||||
Cp  1082 GTGGTCCTTGGGACCCCGCGCAGTCAGTGTGCTGCTGCGCGGCGGAGAGTGCACATTGACAGCT  1023

Db   197 GAGAGCCACGCGGTAGGAGGACCACGGGGTTCACGCCGCCGCCGGCGGCAAGCCATGGGAGCCGGA   256
         ||||||||||||||||||| |||||||||||||||||||||||||||||||      ||||||||
Cp  1022 GAGAGCCACGCGGTAGGAGACCACGGGGTTCACGCCGCCGCCGGCGGCCGCCA-GGGAGCCGGA   964

Db   257 TGGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGCGGCCGCAAGACCN   316
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp   963 TGGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGCGGCCGCAAGACC   904

Db   317 CCTTGCAAGCACGCGGGTCATGGTGGGGCACTAGCGGGCACAGATGGTGGTTGTTGACGGT   376
         |||  ||| ||||||||||||   ||||||||||||  |||||||||||||||||||||||
Cp   903 CCT-GCA-GCACGCGGGTCA-GCGGGCACTAGCCGGGCACAGATGGTGGTTGTTGACGGT   846

Db   377 GATGNACACGGGGCAGCCCCTCCTTCTCCACAGCCAGTAGCCCAGGGTGGCATTGATGATGGGGCGGCACCG   436
         |||| |||||||||||||  ||||||||||||||||||  |||||||||||||||||||||||||||||
Cp   845 GATGCACACGGGGCAGCCC-TCCTTCTCCACAGCCAGGTGGCATTGATGATGGGGCGGCACCG   786

Db   437 TGG   439
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Cp   785 TGG   783
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RESULT 8

```
LOCUS       N30831       566 bp    mRNA             EST    05-JAN-1996
```

```
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 225
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES             Location/Qualifiers
     source          1..473
                     /organism="Homo sapiens"
                     /clone="257711"
     mRNA            <1..>473
BASE COUNT     87 a   122 c   182 g    76 t   6 others
ORIGIN
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Query Match
Best Local Similarity   95.5%;
Matches  402;  Conservative   0;  Score 379;  DB 13;  Length 473;
                                   Pred. No. 0.00e+00;  Mismatches 17;  Indels  2;  Gaps  2;

Db    18 TTATTGTGGGAGGATCGGGGTGTCCGAGGGGCCCCGGAGTCGGGGATTGGGAAGGCT    77
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp  1202 TTATTGTGGGAGGATCGGGGTGTCCGAGGGGCCCCGGAGTCGGGGATTGGGAAGGCT  1143

Db    78 GGGGGGAGGGGGGCCTTTGAGGAAGAGAGAGAGTCCTGGAAGAGGGGTCATCACAGGTCAAGG   137
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp  1142 GGGGGGAGGGGGGCCTTTGAGGAAGAGAGAGAGTCCTGGAAGAGGGGTCATCACAGGTCAAGG  1083

Db   138 GTGGTCCTTGGGACCCCGCCAGTCAGTGTTGTCTGCGGCGACATTGACAGCT   197
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp  1082 GTGGTCCTTGGGACCCCGCCAGTCAGTGTTGTCTGCGGCGACATTGACAGCT  1023

Db   198 GAGAGCCACGCGGTAGGAGGACCACGGGGTTCACGCCGCCGGG-CAGCCAGGGANCCGGAT   256
         |||||||||||||||||||||||||||||||||||||||||   |||||||||| |||||
Cp  1022 GAGAGCCACAGCGTAGGAGACCACGGGGTTCACGCCGCCGCCGGGGCCAGCCAGCCGGAT  1023

Db   257 GGACTCGAANCGCACATCGCGGGTAGTTGCACACCACCTGAGGCAGGCGGCCAGGACCACC   316
         ||||||||| ||||||||||||||||||||||||||||||||||||||||| ||||||||
Cp   962 GGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGGCAGGCGGCCAGGACCCC   903

Db   317 TTGCAGCACGCGGGTCATGTGGGGCGCAGTANCCGCAGACGTGGTGGTTGGTGTTNACGGTGA   376
         ||||||||||||||||||||||||||||||   ||||||||||||||||| ||| |||||||
Cp   902 CTGCAGCACGCGGGTCATGGTGGGGCGCAGTAGCCGCAGACGTGGTGGTTGTTGACGGTGA   844

Db   377 TGCACACGGGGCGCAGCCNCCTTCTCCACAGCCAGGGTGGCCATTGATGATGGGGCGCACCGTN   436
         ||||||||||||||||||  ||||||||||||||||||||| ||||||||||||||||||||
Cp   843 TGCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGCCATTGATGGGGGCGGCACCGTG   784

Db   437 G   437
         |
Cp   783 G   783
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Record 1

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DEFINITION  yw70b04.s1 Homo sapiens cDNA clone 257551 3' similar to gb:J00117
            CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
ACCESSION   N30831
NID         g1149351
KEYWORDS    EST.
SOURCE      human clone=257551 primer=m13 -40 forward library=Soares placenta
            8to9weeks 2NbHP8to9W vector=pT7T3D (Pharmacia) with a modified
            polylinker host=DH10B (ampicillin resistant) Rsite1=Not I
            Rsite2=Eco RI two placentae: one from 8 weeks and another from 9
            weeks post conception. 1st strand cDNA was primed with a Not I -
            oligo(dT) primer
            [5'-TGTTACCAATCTGAAGTGGGAAGCGCGCCGCGATTTTTTTTTTTTTTTT-3'],
            double-stranded cDNA was size selected, ligated to Eco RI adapters
            (Pharmacia), digested with Not I and cloned into the Not I and Eco
            RI sites of a modified pT7T3 vector (Pharmacia). Library
            constructed by Bento Soares and M. Fatima Bonaldo.
ORGANISM    Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 566)
AUTHORS     Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
TITLE       The WashU-Merck EST Project
JOURNAL     Unpublished (1995)
COMMENT     Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: estewatson.wustl.edu
            High quality sequence stops: 400
            This clone is available royalty-free through LLNL ; contact the
            Source: IMAGE Consortium, LLNL
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES    Location/Qualifiers
    source          1. .566
                    /organism="Homo sapiens"
                    /clone="257551"
    mRNA            <1. .>566
BASE COUNT    103 a    148 c    209 g    100 t    6 others
ORIGIN
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Query Match          31.4%;  Score 377;  DB 13;  Length 566;
Best Local Similarity 96.4%;  Pred. No. 0.00e+00;
Matches  407;  Conservative    0;  Mismatches  12;  Indels    3;  Gaps    3;

Db     316 CCCTGCAGCACCGCGGGGTCATGTGGGGGCGAGTACCGGTCACAGATGGTGGTTGGTGGTG 375
           ||||||||||||||||||| ||||||||||||||| |||||||||||||||||||||||||
Cp     904 CCCTGCAGCACCGCGGGGTTCATGTGGGGGCGAGTTAGCCGGCACAGATGGTGGTTGGTGGTG 845

Db     376 ATGCACACGGGGGCAGCCCTCCTTCTCCACAGCCCAGGTGGTGCCATTGATTGGGGCGGCACCGT 435
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp     844 ATGCACACGGGGGCAGCCCTCCTTCTCCACAGCCCAGGTGGTGCCATTGATTGGGGCGGCACCGT 785

Db     436 GG 437
           ||
Cp     784 GG 783
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Record 2

```
RESULT   9

LOCUS       N31955       563 bp       mRNA       EST       10-JAN-1996
DEFINITION  yw89qa07.s1 Homo sapiens cDNA clone 259380 3' similar to gb:J00117
            CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
ACCESSION   N31955
NID         g1152254
KEYWORDS    EST.
SOURCE      human clone=259380 primer=m13 -40 forward library=Soares placenta
            8to9weeks 2NbHP8to9W vector=pT7T3D (Pharmacia) with a modified
            polylinker host=DH10B (ampicillin resistant) Rsite1=Not I
            Rsite2=Eco RI two placentae: one from 8 weeks and another from 9
            weeks post conception. 1st strand cDNA was primed with a Not I -
            oligo(dT) primer
            [5'-TGTTACCAATCTGAAGTGGGAAGCGCGCCGCGATTTTTTTTTTTTTTTT-3'],
            double-stranded cDNA was size selected, ligated to Eco RI adapters
            (Pharmacia), digested with Not I and cloned into the Not I and Eco
            RI sites of a modified pT7T3 vector (Pharmacia). Library
            constructed by Bento Soares and M. Fatima Bonaldo.
ORGANISM    Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 563)
AUTHORS     Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
TITLE       The WashU-Merck EST Project
JOURNAL     Unpublished (1995)
COMMENT     Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: estewatson.wustl.edu
            High quality sequence stops: 335
            This clone is available royalty-free through LLNL ; contact the
            Source: IMAGE Consortium, LLNL
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES    Location/Qualifiers
    source          1. .563
                    /organism="Homo sapiens"
                    /clone="259380"
    mRNA            <1. .>563
BASE COUNT    101 a    148 c    208 g    103 t    3 others
ORIGIN
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Query Match          31.0%;  Score 373;  DB 13;  Length 563;
Best Local Similarity 97.0%;  Pred. No. 0.00e+00;
Matches  416;  Conservative    0;  Mismatches   7;  Indels    6;  Gaps    6;

Db      17 TTATTGTGGGGGAGGATCGGGGTGTCCGAGGGGGTCCGGAGGGGGGAGTCGGGGATGGGGCTTGGAAGGCT 76
           ||||||||||  |||||||||||||||||||||
Cp    1202 TTATTGTGGAGGATCGGGGGTGTCCGAGGGAGTCGGAGTCGGGAGGGCTTGGAAGGCT 1143
```

Alignment rows (Record 1 ORIGIN):

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Db      17 TTATTGTGGAGGATCGGGGGTGTCCGAGGGAGTCGGAGTCGGGAGGGCTTGGAAGGCT 76
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp    1202 TTATTGTGGAGGATCGGGGGTGTCCGAGGGAGTCGGAGTCGGGAGGGCTTGGAAGGCT 1143

Db      77 GGGGGGGAGGGGGCCTTTGAGGAAGAAGAGAGTCCTCGGAGAGTCGGGGGGTCGGGGGG 136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp    1142 GGGGGGGAGGGGGCCTTTGAGGAAGAAGAGAGTCCTCGGAGAGTCGGGGGGTCGGGGGG 1083

Db     137 GTGGTCCTTGGG--CCCCGCGAGTCAGTGTGTGCTGCGGGGGTGCACATTGACAGCT 195
           ||||||||||||  |||||||||||||||| || |||||||||| ||||||||||||
Cp    1082 GTGGTCCTTGGGACCCCGCGAGTCAGTGGTCGTGCGGCGGGCAGAGTGCACATTGACAGCT 1023

Db     196 GAGAGCCACGCGCTTAGGAGACCACGGGGGTTCACGCGCCGGA 255
           ||||||||||  |||||||||||||||||| ||| ||||||
Cp    1022 GAGAGCCACGCGTAGGAGACCACGGGGGTTCACGCGCCAGCA-GGGAGCCGGA 964

Db     256 TGGACTCGAGACGCAAATCGGGGGGTAGTTGCACACCACCTCGAGGCAGGGGGGCCAGACCC 315
           |||||||||| |||||||||||||| ||||| || || |||||||| |||||| || ||
Cp     963 TGGACTCGAGACGCACCATCGGGG-TAGTTGCACACCACCTCGAGGCAGGGGGGAGGAGACC 905
```

RESULT 10

```
LOCUS       AA400910    473 bp    mRNA             EST        12-AUG-1997
DEFINITION  zt71h09.s1 Soares testis NHT Homo sapiens cDNA clone 727841 3'
            similar to gb:J00117 CHORIOGONADOTROPIN BETA CHAIN PRECURSOR
            (HUMAN);.
ACCESSION   AA400910
NID         g2054783
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
            Homo.
REFERENCE   1  (bases 1 to 473)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
            Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
            White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     Washu-Merck EST Project 1997
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 640  Std Error: 0.00
            Seq primer: -41m13 fwd. ET from Amersham
            High quality sequence stop: 392.
FEATURES             Location/Qualifiers
     source          1..473
                     /organism="Homo sapiens"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from mRNA obtained from Clontech
                     Laboratories, Inc., and primed with a Not I - oligo(dT)
                     primer (5'
                     TGTTACCAATCTGAAGTGGAGGGGCCGCCCCCAATTTTTTTTTTTTTTTTTTT 3').
                     Double-stranded cDNA was ligated to Eco RI adaptors
```

RESULT 11

```
LOCUS       N30684      479 bp    mRNA             EST        05-JAN-1996
DEFINITION  yw77h04.s1 Homo sapiens cDNA clone 258295 3' similar to gb:J00117
            CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
ACCESSION   N30684
NID         g1149204
KEYWORDS    EST.
SOURCE      human clone=258295 primer=m13 -40 forward library=Soares placenta
            8to9weeks 2NbHP8to9W vector=pT7T3D (Pharmacia) with a modified
            polylinker host=DH10B (ampicillin resistant) Rsite1=Not I
            Rsite2=Eco RI two placentae: one from 8 weeks and another from 9
            weeks post conception. 1st strand cDNA was primed with a Not I -
            oligo(dT) primer
            [5'-TGTTACCAATCTGAAGTGGAGGCGGCCGCCGATTTTTTTTTTTTTTTTTT-3'],
            double-stranded cDNA was size selected, ligated to Eco RI adaptors
            (Pharmacia), digested with Not I and cloned into the Not I and Eco
            RI sites of a modified pT7T3 vector (Pharmacia). Library
            constructed by Bento Soares and M. Fatima Bonaldo.
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 479)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
```

RESULT 10 — mRNA / Origin

```
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization to Cot5, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
                     /db_xref="taxon:9606"
                     /clone="727841"
     mRNA            complement(<1..>473)
                     /sex="male"
                     /clone_lib="Soares testis NHT"
                     /lab_host="DH10B"
                     /db_xref="GDB:5924752"

BASE COUNT   84 a   120 c   190 g   78 t   1 others
ORIGIN
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Query Match 30.9%; Score 371; DB 25; Length 473;
Best Local Similarity 97.6%; Pred. No. 0.00e+00;
Matches 405; Conservative 0; Mismatches 5; Indels 5; Gaps 5;

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Qy    20  TTATTGTGGGAGGAGGAATCGGGGTGTGTCAGAGGGCCCCGGGGAGTCGGGGGATGGGCTTGGAAGGCT  79
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1202  TTATTGTGGGAGGAGGAATCGGGGTGTGTCAGAGGGCCCCGGGGAGTCGGGGGATGGGCTTGGAAGGCT  1143

Cp    80  GGGGGGAGGGGGGCCTTTGAGGAAGAGAGGAGGGCCTGAAAGCGGGGGGTGTCATCACAGGTCAAGG    139
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   842  GCACACGGGGGCCAGCCCTCCTTCTCCACAGCCACCAGGGGTGGGCATTGAGGGGGCGGGCAC  788
```

Cp 1142 GTGGTTCCTTGGGGACCCC-GCAGTCAGTGGTTGCTCGGGGGGCCGGCAGAGTGCACATTTGACAGCT 1023
Cp 842 GCACACGGGGGCCAGCCCTCCTTCTCCACAGCCACCAGGGGTGGGCATTGAGGGGGCGGGCAC 788

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Db   77  GGGGGGAGGGGGGCCTTTGAGGAAGAGAGGAGAGTCCTTGGAAGCGGGGGGGGTCATCACAGGTCAAGG  136
Cp 1142  GGGGGGAGGGGGGCCTTTGAGGAAGAGAGGAGAGTCCTTGGAAGCGGGGGGGGTCATCACAGGTCAAGG  1083

Db  137  GTGGTTCCTTGGGACCCC-GCAGTCAGTGTTGGTGCTGCGGGCAGAGTGCACATTGACAGC  195
Cp 1082  GTGGTTCCTTGGGACCCC-GCAGTCAGTGTTGGTGCTGCGGGCAGAGTGCACATTGACAGC  1024

Db  196  TGAGAGCGCACGGCCGTTAGGAGACCACCAGGGGTTCACGACGGCCAAGCCACAGGGAGACGCCG  255
Cp 1023  TGAGAGCCACCACGGGT-AGGAGACCACGGGGTTCACGCGGGCACCCA-GGGAGCCG  966

Db  256  GATGGGACTCGAAGCGCACATCGGGGTAGTTGCACACCTGAGGCAGGGCAGGGGGGCCAAG-AC  314
Cp  965  GATGGGACTCGAAGCGCACATCGGGGTAGTTGCACACCTGAGGCAGGGCAGGGGGGCCAAG-AC  906

Db  315  CCC-TGCAGCACCGGGTCATGGTGGGGGCCACAGCATGTGTGTGTTGACCGT  373
Cp  905  CCCCTGCAGCACCGGGTCATGGTGGGGGCCACAGCATGTGTGTGTTGACCGT  846

Db  374  GATGCACACGGGGCACGCCCTCCTTCTCCACAGCCACCAGGGTGGGCATTGAGGGGCGGGCCACCG  433
Cp  845  GATGCACACGGGGCCAGCCCTCCTTCTCCACAGCCACCAGGGTGGGCATTGAGGGGCGGGCCACCG  786

Db  434  TGGCCAAGC  442
Cp  785  TGGACCAGC  777
```

Record 1

```
COMMENT     Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 333
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
```

```
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P., and
            Wilson,R.
```

```
ORGANISM    Homo sapiens
            Eukaryotae; Metazoa;

FEATURES             Location/Qualifiers
    source           1..479
                     /organism="Homo sapiens"
                     /clone="258295"

BASE COUNT      86 a      122 c      184 g       79 t        8 others
ORIGIN
    mRNA        <1. >479

Query Match     30.9%;   Score 372;   DB 13;   Length 479;
Best Local Similarity   95.5%;   Pred. No. 0.00e+00;
Matches  401;  Conservative  0;  Mismatches  16;  Indels  3;  Gaps  3;
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Db    17  TTATTGTGGGAGGATCGGGGTGTCCGGAGGGCGGGGGTGTCGGGGANTGGGGGGCTTGGAAGGCT    76
          ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Cp  1202  TTATTGTGGGAGGATCGGGGTGTCCGGAGGGCGGGGGTGTCGGGGANTGGGGGGCTTGGAAGGCT  1143

Db    77  GGGGGGAGGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGGTCATCACAGGTCAAGGG    136
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp  1142  GGGGGGAGGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGGTCATCACAGGTCAAGGG   1083

Db   137  GTGGGTCCTTGGGACCCC-GCAGTCAGTGGTGCTCGGGTGCGCGGGCAGAGTGCACATTGACAGCT   195
          ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Cp  1082  GTGGGTCCTTGGGACCCCCGCAGTCAGTGGTGCTCGGGTGCGCGGGCAGAGTGCACATTGACAGCT  1023

Db   196  GAGAGCCAGGCNTAGGAGACCACGGGGTTCACGCGGCACCCAGGGAGCCGGAT   255
          ||||||||||| |||||||||||||||||||||||||||||||||||||||||
Cp  1022  GAGAGCCACAGGGTAGGAGACCACGGGGTTCACGCGGCACCCAGGGAGCCGGAT  963

Db   256  GGACTCGAACGCACATCCGGCGGTAGTTGCACACCACCTGAGGCAGGCGGCGC-AGACCCC   314
          |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Cp   962  GGACTCGAACGCACATCCGGCGGTAGTTGCACACCACCTGAGGCAGGCGGCGCCAGACCCC  903

Db   315  TTGCAGCACGCGCGGGTCATGTGGTGGGCAGTAGCCGGCCACAGATGGTGTGGGTGGGTGGTTNACGGTGAT   374
Cp   902  CTGCAGCACGCGGGGTCATGGGGCGGCAGTAGCCGGCCACAGATGGTGTGGGTGGGTGGTTGACGGTGAT    843

Db   375  GCACACGCGGGGCAGCCCTCCTTCTCCACAGCCA-GGGTGGCCATTGATGGGGGGGCGGCACNTTG   434
          ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Cp   842  GCACACGGGGCAGCCCTCCTTCTCCACAGCCA-GGGTGGCCATTGATGGGGGGGCGGCACCGTG    784
```

Record 2

```
COMMENT     Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 329
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
```

```
REFERENCE
AUTHORS     Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P., and
            Wilson,R.
```

```
ORGANISM    Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 446)

FEATURES             Location/Qualifiers
    source           1..446
                     /organism="Homo sapiens"
                     /clone="258890"

BASE COUNT      82 a      108 c      170 g       71 t       15 others
ORIGIN
    mRNA        <1. >446

Query Match     30.4%;   Score 365;   DB 13;   Length 446;
Best Local Similarity   94.1%;   Pred. No. 0.00e+00;
Matches  396;  Conservative  0;  Mismatches  21;  Indels  4;  Gaps  4;
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Db    17  TTANTGTGGGANGATNGGGGGTTTNCANGGCCCCGGGANTNNNNATGGACTTGGNAGGCT    76
Cp  1202  TTATTGTGGGAGGATCGGGGTGTCCGGAGGGCGGGGGTGTCGGGGAGTCGGGATGGGGGCTTGGAAGGCT  1143

Db    77  GGGGGGAGGGGGCCTTTNAGGAAGAGGAGTCCTGGAAGCGGGGGGTCATCACAGGTCAAGGG    136
Cp  1142  GGGGGGAGGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGGTCATCACAGGTCAAGGG   1083

Db   137  GTGGGTCCTTGGGACCCC--GCAGTCAGTGGTGCTGCGGGTGCGCGGGCAGAGTGCACATTNACAGCT   195
Cp  1082  GTGGGTCCTTGGGACCCCCGCAGTCAGTGGTGCTCGGGTGCGCGGGCAGAGTGCACATTGACAGCT   1023

Db   196  GAGAGCCACGCGGTAGGAGACCACGGGGTTCACGCGGCACCCAGGGAGCCGGAT   255
Cp  1022  GAGAGCCACAGGGTAGGAGACCACGGGGTTCACGCGGCACCCAGGGAGCCGGAT   963

Db   256  GGACTCGGAAGGCACATCGGGCGGTAGTTGCACCACCACCTGAGGCCGGCGCGG-CACCCAGGGAGCCGGAT   314
Cp   962  GGACTCGAAGGCACATCCGGCGGTAGTTGCACACCACCTGAGGCCGGCGCG-CACCCAGGGAGCCGGAT    903

Db   315  GTGGTCCTTGGGACCCC--GCAGTCAGTGGTGCTGCGGGGCAGAGTGCAGAGTGCACATTNACAGCT   374
Cp   902  GTGGGTCCTTGGGACCCCCGCAGTCAGTGGTGCTCGGGTGCGCGGGCAGAGTGCACATTGACAGCT   843

Db   375  GCACACGCGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCCATTGATGGGGNGGGCGGCACCGTG   434
Cp   842  GCACACGGGGCAGCCCTCCTTCTCCACAGCCATT-GATGGGGCGGCCGCACCGTG    784

Db   434  G    434
             |
Cp   783  G    783
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```
RESULT  13

LOCUS        AA644163        526 bp       mRNA         EST        27-OCT-1997
DEFINITION   af62d08.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 1046607 3'
             similar to gb:J00117 CHORIOGONADOTROPIN BETA CHAIN PRECURSOR
             (HUMAN);.
ACCESSION    AA644163
NID          g2569381
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
             Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
             Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 526)
AUTHORS      Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
             Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
             Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
             Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
TITLE        WashU-NCI human EST Project
JOURNAL      Unpublished (1997)
COMMENT      High quality sequence stop: 335.
             Contact: Wilson RK
             Washington University School of Medicine
             4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
             Tel: 314 286 1800
             Fax: 314 286 1810
             Email: est@watson.wustl.edu
             This clone is available royalty-free through LLNL ; contact the
             IMAGE Consortium (info@image.llnl.gov) for further information.
             Seq primer: -40m13 fwd. ET from Amersham
FEATURES             Location/Qualifiers
     source          1..526
                     /organism="Homo sapiens"
                     /note="Organ: mixed (see below); Vector: pT7T3D-Pac
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; Equal amounts of plasmid DNA from three
                     normalized libraries (melanocyte 2NbHM, pregnant uterus
                     NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
                     were made in vitro. Following HAP purification, this DNA
                     was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from pools of
                     5,000 clones made from the same 3 libraries. The pools
                     consisted of I.M.A.G.E. clones 260232-265223,
                     340488-345479, and 484488-489479."
                     /db_xref="taxon:9606"
                     /clone="1046607"
                     /clone_lib="Soares NhHMPu S1"
                     /tissue_type="Pooled human melanocyte, fetal heart, and
                     pregnant uterus"
                     /lab_host="DH10B"
BASE COUNT     100 a    140 c    201 g     85 t
ORIGIN

Query Match     30.2%;  Score 363;  DB 28;  Length 526;
Best Local Similarity   96.7%;  Pred. No. 0.00e+00;
Matches   407;  Conservative   0;  Mismatches   8;  Indels   6;  Gaps   6;

Db       16  TTAATGTGTGGGAGGAATCGGGGTGTCCGAGGGCCCGGGAGTGGGGATGGACTGGAAGGCT   75
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp     1202  TTAATGTGTGGGAGGATCGGGGTGTCCGGAGGGCCCCGGGAGTGGGGATGGACTGGAAGGCT  1143

Db       76  GGCAGGAGGGGGCCCTTTAAGGAAGAAGGAGAGTCCTGGAGAGAGCGGGGGTCATCACAGGG  135
             || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp     1142  GGGGGAGGGGGGCCCTTTGAGGAAGGAGAGTCCTGGAAGCGGGGGGTCATCACAGGTCAAGGG  1083

Db      136  GTGGGTCCTTGGGACCCCGACAGTCAGTCAGTGTCCTGCTGCGCGCGCGCGCGCGGCGGCGCT  195
             |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Cp     1082  GTGGGTCCTTGGGACCCCGCAGTCAGTGGTGCTGCTGCGCGCAGAGGTGCACATTGACAGCT  1023

Db      196  GAGAGCCACGGCGTAGGAGAGACCACGGGGGTTCACGCCGCGCGCGGG-CAGCCAGGGAGCCGGGAT  254
```

```
Cp     1022  GAGAGGCCACACGGTAGGAGACCACGGGGTTCACGCCCGCGCCGCGGCGGGCCGCGGCCGCAGGGCCAGCCGGGGCCAGCCGAGCCCGGAT  963
             ||||||||| |||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db      255  GGACTCGAAGGCGCACATCGCGGTAGTTGCACACCACCTGAGGCCAGGGCGGC-AGGACCC  313
             |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Cp      962  GGACTCGAAGGCGCACATCGCGGTAGTTGCACACCACCTGAGGCCAGGGCGGCAGGACCC  903

Db      314  -TGCAGCACGCGCGGGTCATGGTGGGGGCCAGTAGC-GGCACAGATGGGTGGTGTGTGACGGTGAT  371
             ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Cp      902  CTGCAGCACGCGCGGGTCATGGTGGGGGCCAGTAGCCGGCACAGATGGGTGGTGTTGACGGTGAT  843

Db      372  GGCACACGGGCGGCAGCCTCCTTCTCCACAGCCCAGGGTGGCATTGATGGGGCG-ACCGTG  430
             ||||||||||||||||||||||||| |||||||||||||||||||||||| |||||||||
Cp      842  G-CACACGGGCGGCAGCCCCTTCCTTCCACAGCCCAGGGTGGCATTGATGATGGGGCCACGGTG  784

Db      431  G  431
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Cp      783  G  783
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RESULT  14

LOCUS        AA232905        400 bp       mRNA         EST        06-AUG-1997
DEFINITION   zr46c04.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 666438 3'
             similar to gb:J00117 CHORIOGONADOTROPIN BETA CHAIN PRECURSOR
             (HUMAN);.
ACCESSION    AA232905
NID          g1855917
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
             Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
             Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
             Homo.
REFERENCE    1  (bases 1 to 400)
AUTHORS      Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
             Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
             Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
             White,Y., Wylie,T., Waterston,R. and Wilson,R.
TITLE        WashU-Merck EST Project 1997
JOURNAL      Unpublished (1997)
COMMENT      Contact: Wilson RK
             Washington University School of Medicine
             4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
             Tel: 314 286 1800
             Fax: 314 286 1810
             Email: est@watson.wustl.edu
             This clone is available royalty-free through LLNL ; contact the
             IMAGE Consortium (info@image.llnl.gov) for further information.
             Insert Length: 834  Std Error: 0.00
             Seq primer: -41m13 fwd. ET from Amersham
             High quality sequence stop: 361.
FEATURES             Location/Qualifiers
     source          1..400
                     /organism="Homo sapiens"
                     /note="Organ: mixed (see below); Vector: pT7T3D-Pac
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; Equal amounts of plasmid DNA from three
                     normalized libraries (melanocyte 2NbHM, pregnant uterus
                     NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
                     were made in vitro. Following HAP purification, this DNA
                     was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from pools of
                     5,000 clones made from the same 3 libraries. The pools
                     consisted of I.M.A.G.E. clones 260232-265223,
                     340488-345479, and 484488-489479."
                     /db_xref="taxon:9606"
                     /clone="666438"
                     /clone_lib="Soares NhHMPu S1"
                     /tissue_type="Pooled human melanocyte, fetal heart, and
                     pregnant uterus"
                     /lab_host="DH10B"
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FEATURES                                                              COMMENT  Contact: Wilson RK
                                                                               Washu-Merck EST Project
                                                                               Washington University School of Medicine
                                                                               4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                               Tel: 314 286 1800
                                                                               Fax: 314 286 1810
                                                                               Email: estewatson.wustl.edu
                                                                               This clone is available royalty-free through LLNL ; contact the
                                                                               IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                               Insert Length: 957  Std Error: 0.00
                                                                               Seq primer: mob.REGA+ET
                                                                               High quality sequence stop: 346.
                                                                               Location/Qualifiers
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TITLE   The Washu-Merck EST Project
JOURNAL   Unpublished (1995)

REFERENCE   1 (bases 1 to 531)
AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
             Holmen,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
             Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
             Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
             Wilson,R.

SOURCE   human.
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata;
             Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.

KEYWORDS   EST.
NID   g138299
ACCESSION   W71989
DEFINITION   zd66b03.s1 Soares fetal heart NbHH19w Homo sapiens cDNA clone
             345581 3' similar to gb:J00117 CHORIOGONADOTROPIN BETA CHAIN
             PRECURSOR (HUMAN).

LOCUS   W71989   531 bp   mRNA   EST   17-OCT-1996
RESULT   15

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Query Match      29.5%;   Score 354;   DB 25;   Length 400;
Best Local Similarity  97.2%;   Pred. No. 0.00e+00;
Matches  375;   Conservative   0;   Mismatches  9;   Indels  2;  Gaps  2;

ORIGIN
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Db    17  TTATTGTGGGAGGATCGGGTGTCCGGAGGCGCCCGGAGTCGGGATGGGCTTGGGAAGGCT 76
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Cp  1202  TTATTGTGGGAGGATCGGGTGTCCGGAGGCGCCCGGAGTCGGGATGGGCTTGGGAAGGCT 1143

Db    77  GGGGGGAGTGGCGTTTTGAGGAAGAGGAGAGTCCTGGAAGGGGGTCATCACAGGTCAAGG 136
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp  1142  GGGGGGAGGGGGGCCTTTGAGGAAGAGGAGAGTCCTGGAACGGGGGTCATCACAGGTCAAGG 1083

Db   137  GTGGTCCTTGGGACACCCGAGTCAGTCAGTGGTGCTGCGGGGGCAGGAGGCACATTGACAGCT 196
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp  1082  GTGGTCCTTGGGACCCCGCAGTCAGTCGTGCTGCGGGGGCAGGAGGTGCACATTGACAGCT 1023

Db   197  GAGAGCCACGCGGGTAGGAGACCACACGGGTTCACGCCGCGGCGCAGGGAGCCCGGAT 256
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp  1022  GAGAGCCACACGGGTAGGAGACCACACGGGTTCACGCCGCGGCGCAGGGAGCCCGGAT 963

Db   257  GGACTCGAAGCCGCACATCGCGTAGTTGCACCACCACCTGAGCGACGAGTCAG-AGCCC 315
          ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Cp   962  GGACTCGAAGCCGCACATCGCGTAGTTGCACCACCACCTGAGCGACGAGTCAGGGAGGACCCC 903

Db   316  CTGCAGCACGCGGGTCATGGTGGGGTAGC--GGCACAGATAGTGGTGTTGACGGTGAT 374
          ||||||||||||||||||||||||||   |||||||||||||||||||||||||||
Cp   902  CTGCAGCACGCGGGTCATGGTGGGGAGTAGCCGGCACAGATAGTGGTGTTGACGGTGAT 843

Db   375  GCACACGCGGGCAGCCCCTCCTTCTCCA 400
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Cp   842  GCACACGCGGGCAGCCCTTCCTTCTCTCCA 817
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source   1 ..531
                /organism="Homo sapiens"
                /note="Organ: heart; Vector: pT7T3D (Pharmacia) with a
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                TGTTACCAATCTGAAGTGGAGACCGGCGCCACTCTTTTTTTTTTTTTTTT 3'],
                double-stranded cDNA was size selected, ligated to Eco RI
                adapters (Pharmacia), digested with Not I and cloned into
                the Not I and Eco RI sites of a modified pT7T3 vector
                (Pharmacia). Library went through one round of
                normalization to a Cot = 5. Library constructed by
                M.Fatima Bonaldo. This library was constructed from the
                same fetus as the fetal lung library, Soares fetal lung
                NbHL19W."
                /db_xref="taxon:9606"
                /clone="345581"
                /clone_lib="Soares fetal heart NbHH19W"
                /sex="unknown"
                /dev_stage="19 weeks"
                /lab_host="DH10B (ampicillin resistant)"
                complement(<1. .>531)

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Query Match      29.1%;   Score 350;   DB 16;   Length 531;
Best Local Similarity  93.1%;   Pred. No. 0.00e+00;
Matches  391;   Conservative   0;   Mismatches  25;   Indels  4;  Gaps  4;

ORIGIN
mRNA            102 a      125 c      193 g       93 t
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Db    18  TTATTGTGGGAGGATCGGGTGTCCGGAGGCGCCCGGAGTCGGGATGGGACTTGGAAGGCT 77
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Cp  1202  TTATTGTGGGAGGATCGGGTGTCCGGAGGCGCCCGGAGTCGGGATGGGCTTGGAAGGCT 1143

Db    78  NNNGGGAGGGGGCCTTTGAGGAAGAGGAGAGTCCTGGAAAGCGGGGTCATCACAGGTCAAGG 137
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp  1142  GGGGGGAGGGGGGCCTTTGAGGAAGAGGAGAGTCCTGGAAGCGGGGTCATCACAGGTCAAGG 1083

Db   138  GTGGTCNTTGGGACCCC-GCAGTCAGTGGTGCTGCGGGGGCAGGAGGTGCACATTGACAGCT 196
          ||||||  |||||||| ||||||||||||||||||||||||||||||||||||||||||||
Cp  1082  GTGGTCCTTGGGACCCCGCAGTCAGTGGTGCTGCGGGGGCAGGAGGTGCACATTGACAGCT 1023

Db   197  GAGAGCCACGCGGTAGGAGGACCACACGGGTTCACGCCGCGGCGCAGGGAGCCGGAT 256
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp  1022  GAGAGCCACACGGGTAGGAGGACCACACGGGTTCACGCCGCGGCGCAGGGAGCCGGAT 963

Db   257  GGACTCGAAGCCGCACATCCGCGTAGTTGCACCACCACCTGAGCGACGAAGACCCCC 316
          |||||||||||||||||||||||||||||||||||||||||||||| |||||
Cp   962  GGACTCGAAGCCGCACATCGCGTAGTTGCACCACCACCTGAGCGACGAGGGAGGAGGACCCC 903

Db   317  TTGCAGCACGCGGGTCATGGTGGGGCAGTAAACGGGCACACAGATNGTGGTGTTTGACGGTTG 376
          ||||||||||||||||||||||||||  |||||||||||||||| ||||||||||| |||||
Cp   902  CTGCAGCACGCGGGTCATGGTGGGGAGTAGCCGGCACAGATAGTGGTGTT-GACGGT-G 845

Db   377  ATGCANACGGGGCAGCC-TCCTTCTCCACACAGCCAAGGTGGCATTGATGGGGGGGGAACGT 435
          ||||| ||||||||||| |||||||||||||||||||||||| ||| |||||| ||||
Cp   844  ATGCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGATGGGGCGGCCACCGT 785
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Search completed: Wed May  6 13:37:32 1998
Job time : 1115 secs.
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*****************************************************
  |\/| |_)  /``  |_)   /``  |_|
  |  | |    `-,  |    `-,  | |         (TM)
*****************************************************
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MPsrch.pp   protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 6 08:56:17 1998; MasPar time 9.51 Seconds
                                        482.526 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-4
Description: (1-307) from US08804166.pep
Perfect Score: 2341
Sequence: 1 SRTSLLLAFGLLCLPWLQEG........PSLPSPSRLPGPSDTPILPQ 307

Scoring table: PAM 150
                Gap 11

Searched: 120837 seqs, 14945552 residues

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database: a-geneseq31
              1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
              8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
              14:part14 15:part15 16:part16 17:part17 18:part18
              19:part19 20:part20 21:part21 22:part22 23:part23
              24:part24 25:part25 26:part26

Statistics: Mean 32.496; Variance 135.826; scale 0.239

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                          SUMMARIES

Result   %   Query
No.   Score Match Length DB   ID   Description   Pred. No.

  1   2341 100.0   307 26 W33358 TBP(20-161)/hCG-beta   9.21e-224
  2   2022   86.4   336 26 W33350 TBP(20-190)/hCG-beta   4.77e-191
  3   1321   56.4   256 26 W33357 TBP(20-161)/hCG-alpha   1.84e-119
  4   1289   55.1   285 26 W33359 Native 30 kD TNF inhi   3.29e-116
  5   1124   48.0   161   5 R27496 Truncated TNF-alpha   1.82e-99
  6   1124   48.0   199   3 R24080 Truncated TNF-alpha   1.82e-99
  7   1124   48.0   309 13 R70108 TNF-R-GBPH fusion pro   1.82e-99
  8   1124   48.0   371   2 R07409 Tumour Necrosis Facto   1.82e-99
  9   1124   48.0   451 13 R70107 TNF-R-GBP 130 fusion   1.82e-99
 10   1124   48.0   455   8 R42059 Lambda derived TNF-R.   1.82e-99
 11   1124   48.0   455 13 R10986 30KD TNF inhibitor pr   1.82e-99
 12   1124   48.0   455   2 R20787 TNF-alpha binding pro   1.82e-99
 13   1124   48.0   455 14 R75084 p55 TNF-R.   1.82e-99
 14   1124   48.0   455   2 R07451 Human Tumour Necrosis   1.82e-99
 15   1124   48.0   455   4 R11082 Human 55kD TNF-bindin   1.82e-99
 16   1124   48.0   547   4 R70104 TNF-R-GBPH fusion pro   1.82e-99
 17   1124   48.0   884 13 R70109 TNF-R-GBP 130 fusion   1.82e-99
 18   1124   48.0   900 13 R70103 TNF-R-GBP 130 fusion   1.82e-99
 19   1124   48.0 1245 13 R70106 TNF-R-P1, vivax Duffy   1.82e-99
 20   1124   48.0 1604 13 R70105 TNF-R-EBA 175 fusion   1.82e-99
 21   1124   48.0   433   8 R51032 Mutant p55 tumour nec   7.38e-99
 22   1124   48.0   443   8 R51033 Mutant p55 tumour nec   7.38e-99
 23   1118   47.8   455   8 R51034 Mutant p55 tumour nec   7.38e-99
 24   1118   47.8   455   8 R42197 Mutant p55 tumour nec   7.38e-99
 25   1110   47.4   455   8 R12550 Type I TNF receptor.   4.76e-98
 26   1030   44.0   165   3 R15043 Human chorionic gonad   5.90e-90
 27   1025   43.8   145   6 R30999 Human chorionic gonad   1.89e-89
 28   1022   43.7   145   3 R15074 hCG histidine substit   3.80e-89
 29   1022   43.6   145   3 R15171 hCG methionine subst   4.79e-89
 30   1021   43.6   145 25 R31200 Human chorionic gonad   6.04e-89
 31   1021   43.6   145   3 R15120 hCG/hLH chimera, A5.   4.79e-89
 32   1021   43.6   145   3 R15117 hCG histidine substit   4.79e-89
 33   1020   43.6   145   3 R15169 hCG/hLH chimera, A3a.   6.04e-89
 34   1020   43.6   145   3 R15116 hCG methionine substi   6.04e-89
 35   1021   43.6   265 15 R86247 Single chain gonadotr   4.79e-89
 36   1021   43.6   265 15 R86259 Single chain gonadotr   4.79e-89
 37   1018   43.5   145   3 R15173 hCG histidine substit   9.63e-89
 38   1015   43.4   145   3 R15172 hCG histidine substit   1.93e-88
 39   1015   43.4   181 15 R86258 Human CG beta-subunit   1.93e-88
 40   1016   43.4   181 15 R86249 Human CG beta-subunit   1.53e-88
 41   1014   43.4   145 24 R15168 Partially deglycosyla   2.44e-88
 42   1013   43.3   145   3 R15103 hCG/hLH chimera, D7.   3.08e-88
 43   1013   43.3   145   3 R15170 hCG methionine substi   3.08e-88
 44   1013   43.3   145 24 R27687 Chorionic gonadotroph   3.08e-88
 45   1013   43.3   145 24 R27682 Chorionic gonadotroph   3.08e-88
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                              ALIGNMENTS

RESULT   1
ID   W33358   standard; Protein; 307 AA.
AC   W33358;
DT   19-MAR-1998 (first entry)
DE   TBP(20-161)/hCG-beta fusion protein.
KW   Fusion protein; thrombopoietin; TPO; human chorionic gonadotrophin;
KW   beta subunit; hCG-beta.
OS   Homo sapiens.
FH   Key   Location/Qualifiers
FT   CDS   279..1202
FT   /*tag= a
PN   WO9730161-A1.
PD   21-AUG-1997.
PF   20-FEB-1997; U02315.
PR   20-FEB-1996; US-011936.
PA   (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
PI   Campbell RK, Chappel SC, Jameson BA;
PT   Hybrid dimeric protein comprising two co-expressed units - each
PT   based on receptor or ligand and a subunit of a heterodimeric
PT   hormone, especially FSH, for inducing follicular maturation
PS   Example; Pages 34-35; 60pp; English.
DR   WPI; 97-425036/39.
DR   N-PSDB; T94008.
CC   A novel fusion protein comprises 2 dimer forming co-expressed amino
CC   acid sequences, each consisting of a homodimeric or heterodimeric
CC   receptor chain or ligand, with ligand-receptor binding activity,
CC   bound directly or via a peptide linker to a subunit of a
CC   heterodimeric protein hormone capable of forming a heterodimer with
CC   the hormone's other subunits. The fusion protein, e.g. the
CC   thrombopoietin (TPO)/human chorionic gonadotrophin-beta subunit
CC   (hCG-beta) fusion protein denoted by the present sequence,
CC   significantly increases the biological activity of the hormone
CC   component, reducing the requirement for hormone itself and the
CC   number of injections needed.
SQ   Sequence   307 AA;

Query Match   100.0%; Score 2341; DB 26; Length 307;
Best Local Similarity   100.0%;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 srtslllafgllclpwlqegsadsvcpggkyihpqnnsicctkchkgtylyndcpgppgqd 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 SRTSLLLAFGLLCLPWLQEGSADSVCPGGKYIHPQNNSICCTKCHKGTYLYNDCPGPPGQD 60

RESULT 2

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ID   W33360    standard; Protein; 336 AA.
AC   W33360;
DT   19-MAR-1998  (first entry)
DE   TBP(20-190)/hCG-beta fusion protein.
KW   Fusion protein; thrombopoietin; TPO; human chorionic gonadotrophin;
KW   beta subunit; hCG-beta.
OS   Homo sapiens.
PN   WO9730161-A1.
PD   21-AUG-1997.
PF   20-FEB-1997; U02315.
PR   20-FEB-1996; US-011936.
PA   (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
PI   Campbell RK, Chappel SC, Jameson BA;
PS   Example; Pages 39-40; 60pp; English.
PT   A novel fusion protein comprises 2 dimer forming co-expressed amino
PT   acid sequences, each consisting of a homodimeric or heterodimeric
PT   receptor chain or ligand, with ligand-receptor binding activity,
PT   bound directly or via a peptide linker to a subunit of a
PT   heterodimeric protein hormone capable of forming a heterodimer with
PT   the hormone's other subunits. The fusion protein, e.g. the
PT   thrombopoietin (TPO)/human chorionic gonadotrophin-beta subunit
PT   (hCG-beta) fusion protein denoted by the present sequence,
PT   significantly increases the biological activity of the hormone
PT   component, reducing the requirement for hormone itself and the
PT   number of injections needed.
DR   N-PSDB; T94022.
DR   WPI; 97-425036/39.
CC   -
SQ   Sequence   336 AA;

Query Match             86.4%;  Score 2022; DB 26;  Length 336;
Best Local Similarity   91.4%;
Matches   307;  Conservative    0;  Mismatches    0;  Indels   29;  Gaps    1;

Qy      1 srtslllafgllclpwlqegsadsvcpqgkylhpqnnsicctkchkgtylyndcpgpggqd 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 SRTSLLLAFGLLCLPWLQEGSADSVCPQGKYLHPQNNSICCTKCHKGTYLYNDCPGPGGQD 60

Qy     61 tdcrecesgsftasenhlrhclscsskcrkemgqveisssctvdrdtvcgcrknqyrhywse 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TDCRECESGSFTASENHLRHCLSCSSKCRKEMGQVEISSSCTVDRDTVCGCRKNQYRHYWSE 120

Qy    121 nlfgcfncslclngtvhlscqekqntvctchagfflrenecvscagaprcrpinatlav 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 NLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCAGAPRCRPINATLAV 180

Qy    181 ekegcpvcitvnttlcagycptmtrvlgqvylpalpqvvcnyrdvrfesirlpgcprgvnp 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 EKEGCPVCITVNTTICAGYCPTMTRVLGQVLPALPQVVCNYRDVRFESIRLPGCPRGVNP 240

Qy    241 vvsyavalscqcalcrrsttdcggpkdhpltcddprfqdsssskapps1pspsr1pgps 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 VVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPSLPSPSRLPGPS 300

Qy    301 dtpllpq 307
          |||||||
Db    301 DTPILPQ 307
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RESULT 3

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ID   W33357    standard; Protein; 256 AA.
AC   W33357;
DT   19-MAR-1998  (first entry)
DE   TBP(20-161)/hCG-alpha fusion protein.
KW   Fusion protein; thrombopoietin; TPO; human chorionic gonadotrophin;
KW   alpha subunit; hCG-alpha.
OS   Homo sapiens.
PN   WO9730161-A1.
PD   21-AUG-1997.
PF   20-FEB-1997; U02315.
PR   20-FEB-1996; US-011936.
PA   (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
PI   Campbell RK, Chappel SC, Jameson BA;
PS   Example; Pages 32-33; 60pp; English.
PT   Hybrid dimeric protein comprising two co-expressed units - each
PT   based on receptor or ligand and a subunit of a heterodimeric
PT   hormone, especially FSH, for inducing follicular maturation
PT   A novel fusion protein comprises 2 dimer forming co-expressed amino
PT   acid sequences, each consisting of a homodimeric or heterodimeric
PT   receptor chain or ligand, with ligand-receptor binding activity,
PT   bound directly or via a peptide linker to a subunit of a
PT   heterodimeric protein hormone capable of forming a heterodimer with
PT   the hormone's other subunits. The fusion protein, e.g. the
PT   thrombopoietin (TPO)/human chorionic gonadotrophin-alpha subunit
PT   (hCG-alpha) fusion protein denoted by the present sequence,
PT   significantly increases the biological activity of the hormone
PT   component, reducing the requirement for hormone itself and the
PT   number of injections needed.
DR   N-PSDB; T94007.
DR   WPI; 97-425036/39.
SQ   Sequence   256 AA;

Query Match             56.4%;  Score 1321; DB 26;  Length 256;
Best Local Similarity   98.8%;
Matches   169;  Conservative    1;  Mismatches    1;  Indels   0;  Gaps    0;

Qy    165 ------------AGAGPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVL 211
                      |||||||||||||||||||||||||||||||||||||||||||||||||
Db    212 PALPQVVCNRDVRFESIRLPGCPRGVNPVVSIAVALSCQCALCRRSTTDCGGPKDHPLT 271

Qy    212 PALPQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLT 271
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    272 CDDPRFQDSSSSKAPPSLPSPSRLPGPSDTPILPQ 307

Qy    301 cddprfqdsssskapps1pspsr1pgpsdtpllpq 336
          |||||||||||||||||||||||||||||||||||
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RESULT 4

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ID   W33359    standard; Protein; 285 AA.
AC   W33359;
DT   19-MAR-1998  (first entry)
DE   TBP(20-190)/hCG-alpha fusion protein.
KW   Fusion protein; thrombopoietin; TPO; human chorionic gonadotrophin;
KW   alpha subunit; hCG-alpha.
OS   Homo sapiens.
PN   WO9730161-A1.
PD   21-AUG-1997.
PF   20-FEB-1997; U02315.
PR   20-FEB-1996; US-011936.

Query Match             98.8%;  Score 1321; DB 26;  Length 256;
Best Local Similarity   56.4%;
Matches   169;  Conservative    1;  Mismatches    1;  Indels   0;  Gaps    0;

Qy    121 nlfgcfncslclngtvhlscqekqntvctchagfflrenecvscagaaapgc 171
          |||||||||||||||||||||||||||||||||||||||||||||||||:|
Db    121 NLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCAGAGPRC 171

Qy     61 tdcrecesgsftasenhlrhclscsskcrkemgqveisssctvdrdtvcgcrknqyrhywse 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TDCRECESGSFTASENHLRHCLSCSSKCRKEMGQVEISSSCTVDRDTVCGCRKNQYRHYWSE 120

Qy      1 srtslllafgllclpwlqegsadsvcpqgkylhpqnnsicctkchkgtylyndcpgpggqd 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 SRTSLLLAFGLLCLPWLQEGSADSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQD 60
```

PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
PI Campbell RK, Chappel SC, Jameson BA;
DR WPI; 97-425036/39.
DR N-PSDB; T94021.
PT Hybrid dimeric protein comprising two co-expressed units - each
PT based on receptor or ligand and a subunit of a heterodimeric
PT hormone, especially FSH, for inducing follicular maturation
PS Example; Pages 37-38; 60pp; English.
CC A novel fusion protein comprises 2 dimer forming co-expressed amino
CC acid sequences, each consisting of a homodimeric or heterodimeric
CC receptor chain or ligand, with ligand-receptor binding activity,
CC bound directly or via a peptide linker to a subunit of a
CC heterodimeric protein capable of forming a heterodimer with
CC the hormone's other subunits. The fusion protein, e.g. the
CC thrombopoietin (TPO)/human chorionic gonadotrophin-alpha subunit
CC (hCG-alpha) fusion protein denoted by the present sequence,
CC significantly increases the biological activity of the hormone
CC component, reducing the requirement for hormone itself and the
CC number of injections needed.
SQ Sequence 285 AA;

Query Match   55.1%; Score 1289; DB 26; Length 285;
Best Local Similarity 98.8%;
Matches 163; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db   1 srtslllafgilclpwlqegsadsvcpqgkylhpqnnsicctkchkgtylyndcpgppgqd 60
         |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Qy   1 SRTSLLLAFGILCLPWLQEGSADSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQD 60

Db   61 tdcrecesgsftasenhlrhclscsksckrkemgqvelssctvdrdtvcgcrknqyrhywse 120
         ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Qy   61 TDCRECESGSFTASENHLRHCLSCSKSCKRKEMGQVEISSCTVDRDTVCGCRKNQYRHWSE 120

Db 121 nlfqcfnctlclngtvhlscqekqntvctchagffllrenecvscs 165
         |||||||| |||||||||||||||||||||||||||:|||||||
Qy 121 NLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCA 165

RESULT 5
ID   R27496 standard; protein; 161 AA.
AC   R27496;
DT   09-MAR-1993 (first entry)
DE   Native 30 kD TNF inhibitor.
KW   Tumour necrosis factor; ethylene glycol; pharmokinetic;
KW   adult respiratory distress syndrome; rheumatoid arthritis;
KW   septic shock; pulmonary fibrosis; spacer.
OS   Homo sapiens.
PN   WO9216221-A.
PD   01-OCT-1992.
PF   13-MAR-1992; U00122.
PR   15-MAR-1991; US-669862.
PR   17-JAN-1992; US-822296.
PA   (SYND) SYNERGEN INC.
PI   Armes LG, Brewer MT, Evans RJ, Kohno T, Thompson RC;
DR   WPI; 92-348933/42.
PT   New ethylene glycolated polypeptide(s) with improved
PT   pharmacokinetic properties - for treating e.g. TNF and IL-1
PT   mediated diseases, e.g. adult respiratory distress syndrome,
PT   rheumatoid arthritis, septic shock etc.
PS   Claim 54; Fig 2; 100pp; English.
CC   The sequence shows a native 30 kD TNF inhibitor which may be
CC   modified to contain at least one non-native cysteine residue, pref.
CC   at positions 1, 14, 105, 111 and/or 165. The non-native cysteine is
CC   joined to a non-peptidic polymer, pref. monomethoxy PEG via
CC   thio-ether bonds. Two such TNF inhibitor mols. may be linked via
CC   this non-peptidic spacer. The modified polypeptides show improved
CC   pharmokinetic properties, i.e. increased mol. wt. hence reduced
CC   clearance rate following s.c. or systemic administration, increased
CC   sol. of native TNF inhibitors, and reduced antigenicity. The
CC   polypeptides may be used for treatment of TNF mediated diseases such
CC   as adult respiratory distress syndrome, pulmonary fibrosis, rheumatoid
CC   arthritis, inflammatory bowel disease and septic shock. The same
CC   method may be applied to the interleukin-1 receptor antagonist
CC   Il-1ra.
SQ   Sequence   161 AA;   See also R27495.

Query Match   48.0%; Score 1124; DB 5; Length 161;
Best Local Similarity 99.3%; Pred. No. 1.82e-99;
Matches 142; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db   1 dsvcpqgkylhpqnnsicctkchkgtylyndcpgppgqdtdcrecesgsftasenhlrhcl 60
         |||||||| |||||||||||||||||||||||||||| ||||||||||||||||||||||
Qy   23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db   61 scsksckrkemgqvelssctvdrdtvcgcrknqyrhywse 120
         |||||| |||||| ||||||||||||||||||||
Qy   83 SCSKRKEMGQVEISSCTVDRDTVCGCRKNQYRHWSENLFQCFNCSLCLNGTVHLSCQE 142

Db 121 kqntvctchagffllrenecvscs 143
         ||||||||||||||:|||||||
Qy 143 KQNTVCTCHAGFFLRENECVSCA 165

RESULT 6
ID   R24080 standard; protein; 199 AA.
AC   R24080;
DT   05-NOV-1992 (first entry)
DE   Truncated TNF-alpha 55kD receptor.
KW   Tumour necrosis factor alpha; extracellular binding domain;
KW   treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
KW   malaria; viral meningitis; graft versus host disease;
KW   autoimmune disease; rheumatoid arthritis.
OS   Homo sapiens.
PN   WO9207076-A.
PD   30-APR-1992.
PF   18-OCT-1991; G01826.
PR   18-OCT-1990; GB-0022648.
PA   (CHAR-) CHARING CROSS SUNLEY RES CENT.
PI   Brennan FM, Feldmann M, Gray PW, Turner MJC;
DR   WPI; 92-167156/20.
DR   N-PSDB; Q24441.
PT   New polypeptide capable of binding human TNF alpha - comprises
PT   first three cysteine-rich subdomains of TNF alpha receptor for
PT   treating autoimmune disease, septic shock, HIV etc.
PS   Example; Fig 7; 43pp; English.
CC   This sequence is a truncated TNF-alpha receptor derivative, as encoded
CC   in pTNFRecd. This was produced as described in Q24440.
CC   This derivative lacks the 81 carboxyl terminal residues of the
CC   cytoplasmic domain. The derivative could be used in the
CC   regulation of TNF-alpha mediated responses by binding and
CC   sequestering human TNF-alpha e.g. in the treatment of pulmonary
CC   diseases, septic shock, HIV infection, malaria, viral meningitis,
CC   graft versus host disease and autoimmune diseases, esp. rheumatoid
CC   arthritis.
CC   See also Q24440-51, R24000, R24080-84, R27585, Q29236-8
SQ   Sequence   199 AA;

Query Match   48.0%; Score 1124; DB 4; Length 199;
Best Local Similarity 99.3%; Pred. No. 1.82e-99;
Matches 142; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db   41 dsvcpqgkylhpqnnsicctkchkgtylyndcpgppgqdtdcrecesgsftasenhlrhcl 100
         |||||||| |||||||||||||||||||||||||||| ||||||||||||||||||||||
Qy   23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db 101 scsksckrkemgqvelssctvdrdtvcgcrknqyrhywsenlfqcfnctlclngtvhlscqe 160
         |||||| |||||| ||||||||||||||||||||||||||| |||||||||||||||
Qy   83 SCSKRKEMGQVEISSCTVDRDTVCGCRKNQYRHWSENLFQCFNCSLCLNGTVHLSCQE 142

Db 161 kqntvctchagffllrenecvscs 183
         ||||||||||||||:|||||||
Qy 143 KQNTVCTCHAGFFLRENECVSCA 165

RESULT 7
ID   R70108 standard; protein; 309 AA.

RESULT 8

```
AC   R70108;
DT   10-NOV-1995 (first entry)
DE   TNF-R-GBPH fusion protein.
KW   Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;
KW   red blood cell; cytokine receptor; glycophorin binding peptide 130;
KW   tumour necrosis factor receptor; TNF-R;
KW   GBP 130; GBPH; glycophorin binding peptide homologue; glycophorin A;
OS   Chimeric Homo sapiens.
OS   Chimeric Plasmodium falciparum.
FH   Key             Location/Qualifiers
FT   misc_difference 230..269
FT                   /label= repeat_region
FT                   /note= "can be repeated n times, where n is a real
FT                   number"
PN   WO9506737-A.
PD   09-MAR-1995;
PF   01-SEP-1994; G01900.
PF   03-SEP-1993; GB-018350.
PR   23-AUG-1994; GB-0170021.
PA   (PREN/) PRENDERGAST K F.
PI   Prendergast KF;
DR   WPI; 95-115452/15.
PT   New hybrid peptide(s) for binding cytokine(s) - comprising a
PT   malaria parasite peptide capable of binding a red blood cell and
PT   a receptor peptide.
PS   Example A; Page 54-55; 93pp; English.
CC   Hybrid peptides for binding cytokines, comprising a malaria parasite
CC   (Plasmodium falciparum) peptide (capable of binding to a red blood
CC   cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples
CC   of these hybrid peptides. R70108 is a fusion of tumour necrosis factor
CC   receptor (in accordance with H Loetscher et al Cell, Vol. 61, 351-359)
CC   and glycophorin binding protein (GBP) homologue (GBPH). The
CC   use of cytokine receptors not normally found on RBCs means that the
CC   cytokine can bind harmlessly to the RBC without deleterious effect.
CC   The RBC protects the hybrid peptides from excretion from the kidney, and
CC   due to steric hindrance prevents the cytokines binding to a receptor in
CC   another cell. GBP 130 or GBPH are the prefd. malaria parasite peptides
CC   used, others include EBA 175 (175 kDa erythrocyte binding antigen), PMMSA
CC   (pre major merozoite surface antigen) and the Duffy binding receptor
CC   molecule (eg. exhibited by Plasmodium vivax). These peptides bind to
CC   pref. glycophorin A, B and C, sialo glycoproteins, found on the surface
CC   of RBCs. The hybrid peptides are thus used to lower the levels of free
CC   cytokines in the circulation to reduce pathological damage.
SQ   Sequence 309 AA;

Query Match             48.0%;  Score 1124;  DB 13;  Length 309;
Best Local Similarity   99.3%;                         Pred. No.1.82e-99;
Matches  142;  Conservative   1;  Mismatches   0;  Indels   0;  Gaps   0;

Qy     20 dsvcpqgkylhpqnnsiccctkchkgtylyndcpgpgqddtcdcrecesgsftasenhlrhcl 79
          ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDDTCRECESGSFTASENHLRHCL 82

Qy     80 scskcrkemgqveisscctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 139
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     83 SCSKCRKEMGQVEISSCCTVDRDTVCGCRKNQYRHWSENLFQCFNCSLCLNGTVHLSCQE 142

Qy    140 kqntvctchagffirenecvscs 162
          |||||||||||||||||||||||:
Db    143 KQNTVCTCHAGFFLRENECVSCA 165
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RESULT 9

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ID   R70107 standard; Protein; 451 AA.
AC   R70107;
DT   10-NOV-1995 (first entry)
DE   TNF-R-GBP 130 fusion protein.
KW   Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;
KW   red blood cell; cytokine receptor; glycophorin binding peptide 130;
KW   GBP 130; GBPH; glycophorin binding peptide homologue; glycophorin A;
OS   Chimeric Homo sapiens.
OS   Chimeric Plasmodium falciparum.
PN   WO9506737-A.
PD   09-MAR-1995;
PF   01-SEP-1994; G01900.
PF   03-SEP-1993; GB-018350.
PR   23-AUG-1994; GB-0170021.
PA   (PREN/) PRENDERGAST K F.
PI   Prendergast KF;
DR   WPI; 95-115452/15.
PT   New hybrid peptide(s) for binding cytokine(s) - comprising a
PT   malaria parasite peptide capable of binding a red blood cell and
PT   a receptor peptide.
PS   Example A; Page 53-54; 93pp; English.
CC   Hybrid peptides for binding cytokines, comprising a malaria parasite
CC   (Plasmodium falciparum) peptide(capable of binding to a red blood
CC   cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples
CC   of these hybrid peptides. R70107 is a fusion of tumour necrosis factor
CC   receptor (in accordance with H Loetscher et al Cell, Vol. 61, 351-359)
CC   and glycophorin binding protein (GBP) 130. The use of cytokine
CC   receptors not normally found on RBCs means that the cytokine can bind
CC   harmlessly to the RBC without deleterious effect. The RBC protects the
CC   hybrid peptides from excretion from the kidney, and due to steric
CC   hindrance prevents the cytokines binding to a receptor in another cell.
CC   GBP 130 or GBPH (GBP homologue) are the prefd. malaria parasite peptides
CC   used, others include EBA 175 (175 kDa erythrocyte binding antigen) and the Duffy binding
CC   PMMSA (pre major merozoite surface antigen) and the Duffy binding

Query Match             48.0%;  Score 1124;  DB 2;  Length 371;
Best Local Similarity   99.3%;                        Pred. No.1.82e-99;
Matches  142;  Conservative   1;  Mismatches   0;  Indels   0;  Gaps   0;

Qy     41 dsvcpqgkylhpqnnsiccctkchkgtylyndcpgpgqddtcdcrecesgsftasenhlrhcl 100
          ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDDTCRECESGSFTASENHLRHCL 82

Qy    101 scskcrkemgqveisscctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     83 SCSKCRKEMGQVEISSCCTVDRDTVCGCRKNQYRHWSENLFQCFNCSLCLNGTVHLSCQE 142

Qy    161 kqntvctchagffirenecvscs 183
          |||||||||||||||||||||||:
Db    143 KQNTVCTCHAGFFLRENECVSCA 165
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PF   06-APR-1990; 106624.
PF   21-APR-1989; DE-913101.
PR   21-JUN-1989; DE-920282.
PA   (BOEH ) BOEHRINGER INGELHEIMINT.
PA   Hauptmann R, Himmler A, Maurer-Fogy I, Stratowa C;
     WPI; 90-321987/43.
DR   N-PSDB; Q06282.
PI   Prendergast KF;
PT   DNA encoding TNF binding protein and TNF - receptor - used in
PT   tumour treatment and to understand mechanism to TNF action
PT   Disclosure; Fig 1(1-3); 51pp; German.
CC   Clone pTNF-BP15 was used to construct pADTNF-BP, for transfection of
CC   e.g. COS7 cells. The expressed proteins are useful
CC   prophylactically and therapeutically to control disorders which
CC   involve the damaging effects of TNF-alpha or -beta (e.g. infectious or
CC   parasitic diseases, shock, cachexia, autoimmune diseases, adult
CC   respiratory distress syndrome etc., or side effects of treatment with
CC   TNG-alpha). They can also be used as diagnostic reagents for
CC   assaying TNF and in study of TNF-receptor interactions.
CC   See also Q06282-Q06285.
SQ   Sequence 371 AA;
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RESULT   8
ID   R07449 standard; protein; 371 AA.
AC   R07449;
DT   29-JAN-1991 (first entry)
DE   Tumour Necrosis Factor-Binding Protein from pTNF-BP15 cDNA.
KW   Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
KW   pTNF-BP15; infectious disease; parasitic disease; cachexia;
OS   Homo sapiens.
KW   autoimmune disease; shock.
PN   EP-393438-A;
PD   24-OCT-1990.
```

CC   receptor molecule (eg. exhibited by Plasmodium vivax). These peptides
CC   bind to pref. glycophorin A, B and C, sialo glycoproteins, found on
CC   the surface of RBCs. The hybrid peptides are thus used to lower
CC   the levels of free cytokines in the circulation to reduce pathological
CC   damage.
SQ   Sequence 451 AA;

Query Match   48.0%; Score 1124; DB 13; Length 451;
Best Local Similarity   99.3%;   Pred. No. 1.82e-99;
Matches 142; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Db   20 dsvcpggkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 79
          ||||| ||||||||||||||||||||||| ||||||||||| ||||||| |||||||||||
Qy   23 DSVCPQGKYIHPQNNSICCTKCHKGIYLYNDCPGPGGQDTDCRECESSGSFTASENHLRHCL 82

Db   80 scskcrkemgqveisscctvdrdtvcgcrknqyrhywsenlfqcfncslcngtvhlscqe 139
          ||||||||||||||| |||||||||||||||||||||||||||| ||||| |||||||||
Qy   83 SCSKCRKEMGQVEISSCCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db   140 kqntvctchagfflrenecvscs 162
          ||||||||||||||||||||||:
Qy   143 KQNTVCTCHAGFFLRENECVSCA 165

RESULT 10
ID   R42059 standard; Protein; 455 AA.
AC   R42059;
DT   29-APR-1994 (first entry)
DE   Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;
DE   Lambda derived TNF-R.
KW   IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;
KW   rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;
KW   pulmonary fibrosis; silicosis; allograft; xenograft; rejection;
KW   graft verses host disease; sepsis; inflammation; allergy;
OS   Homo sapiens.
OS   autoimmune dysfunction.
FH   Lambda-gt10-7ctnfbp.
FH   Key   Location/Qualifiers
FT   peptide   1..40
FT   /note= "Signal peptide"
FT   protein   41..455
FT   /note= "Mature hTNF-R"
PN   WO9319777-A.
PD   14-OCT-1993.
PF   26-MAR-1993; US02938.
PR   30-MAR-1992; US-860710.
PA   (IMMV) IMMUNEX CORP.
PI   Smith CA;
WPI; 93-336592/42.
N-PSDB; Q49932.
PT   New fusion protein tumour necrosis factor and human interleukin-1
PT   receptor - useful in therapy, diagnosis and assays of e.g.
PT   rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.
The linker may comprise 5-100 amino acids selected from Gly, Asp,
Ser, Thr and Ala. These linkers separate the individual moieties
by such a distance that each component of the fusion protein is
capable of folding into the secondary or tertiary structure required
for its biological activity. These fusion proteins may be used in
therapy, diagnosis and assays for conditions mediated by TNF or IL-1,
particularly in conditions in which both TNF and IL-1 play a causitive
role. They may be used to treat cachexia, rheumatoid arthritis,
diabetes, multiple sclerosis, pulmonary fibrosis and silicosis,
cerebral malaria, allograft and xenograft rejection in graft verses
host disease, sepsis, septic shock, inflammation, allergies and
formulae:

TNF-R-linker-TNF-R-linker-IL-1R
IL-1R-linker-TNF-R-linker-TNF-R or
TNF-R-linker-TNF-R

The sequences given in R42060-61 represent human tumour necrosis
factor receptor (TNF-R) and the sequences in R42060-61 represent
human interleukin-1 receptor (IL-1R). These sequences were used in
the production of a fusion protein which conformed to one of the

Disclosure: Page 57-59; 85pp; English.

CC   autoimmune dysfunctions.
SQ   Sequence 455 AA;

Query Match   48.0%; Score 1124; DB 8; Length 455;
Best Local Similarity   99.3%;   Pred. No. 1.82e-99;
Matches 142; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Db   41 dsvcpggkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
          ||||| ||||||||||||||||||||||| ||||||||||| ||||||| |||||||||||
Qy   23 DSVCPQGKYIHPQNNSICCTKCHKGIYLYNDCPGPGGQDTDCRECESSGSFTASENHLRHCL 82

Db   101 scskcrkemgqveisscctvdrdtvcgcrknqyrhywsenlfqcfncslcngtvhlscqe 160
          ||||||||||||||| |||||||||||||||||||||||||||| ||||| |||||||||
Qy   83 SCSKCRKEMGQVEISSCCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db   161 kqntvctchagfflrenecvscs 183
          ||||||||||||||||||||||:
Qy   143 KQNTVCTCHAGFFLRENECVSCA 165

RESULT 11
ID   R10986 standard; Protein; 455 AA.
AC   R10986;
DT   13-MAY-1991 (first entry)
DE   30kD TNF inhibitor precursor.
KW   Tumour necrosis factor; inhibitor.
OS   Homo sapiens.
FH   Key   Location/Qualifiers
FT   cleavage_site   40..41
FT   /note=" cleavage gives active protein "
PN   AU9058976-A.
PD   24-JAN-1991.
PF   16-JUL-1990; 058976.
PR   18-JUL-1989; US-381080.
PR   11-DEC-1989; US-450329.
PR   07-FEB-1990; US-479661.
PA   (SYNE-) SYNERGEN INC.
WPI; 91-073847/11.
N-PSDB; Q10883.
PT   Tumour necrosis factor inhibitor - for suppression of TNF-alpha
PT   and -beta, useful as therapeutic agent.
Disclosure: Fig 21; 142pp; English.
The sequence comprises the entire 30 kD TNF inhibitor. The clone
from which the sequence was deduced was isolated from a cDNA
library prepd. from RNA form U937 cells treated with PMA/PHA.
The whole gene can be inserted into expression vectors for prepn.
of TNF inhibitor for use in the treatment of inflammatory and
degenerative diseases. The active protein is claimed (Claim 8).
See also R10984 and R11001.
SQ   Sequence 455 AA;

Query Match   48.0%; Score 1124; DB 2; Length 455;
Best Local Similarity   99.3%;   Pred. No. 1.82e-99;
Matches 142; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Db   41 dsvcpggkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
          ||||| ||||||||||||||||||||||| ||||||||||| ||||||| |||||||||||
Qy   23 DSVCPQGKYIHPQNNSICCTKCHKGIYLYNDCPGPGGQDTDCRECESSGSFTASENHLRHCL 82

Db   101 scskcrkemgqveisscctvdrdtvcgcrknqyrhywsenlfqcfncslcngtvhlscqe 160
          ||||||||||||||| |||||||||||||||||||||||||||| ||||| |||||||||
Qy   83 SCSKCRKEMGQVEISSCCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db   161 kqntvctchagfflrenecvscs 183
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Qy   143 KQNTVCTCHAGFFLRENECVSCA 165

RESULT 12
ID   R20787 standard; Protein; 455 AA.
AC   R20787;
DT   11-MAY-1992 (first entry)
DE   TNF-alpha binding protein.

```
PN   GB224569-A.
PD   05-FEB-1992.
PF   15-JUN-1990;
PR   15-JUN-1990; GB-013410.
PA   (CHAR-) CHARING CROSS SUN,E.
PI   Feldman M, Gray P, Turner M, Brennan F;
DR   WPI; 92-043613/06.
DR   N-PSDB; Q20973.
PT   New tumour necrosis factor alpha binding protein and polypeptide
PT   - useful in treating cachexia, sepsis and auto immune diseases
PT   e.g. rheumatoid arthritis
PS   Disclosure: Fig 1; 25pp; English.
CC   The amino acid sequence is that of tumour necrosis factor alpha
CC   binding protein which contains the extracellular domain of human TNF
CC   alpha receptor. It is soluble and can be used in the regulation of
CC   TNF-mediated responses by binding and sequestering the cytokine. It
CC   can therefore be used therapeutically to treat disorders such as
CC   cachexia, sepsis and autoimmune diseases, specifically rheumatoid
CC   arthritis.
KW   Tumour necrosis factor alpha; autoimmune diseases; cachectin;
KW   extracellular domain.
OS   Homo sapiens.
FH
FH   Key             Location/Qualifiers
FT   peptide         1..40
FT                   /note= "signal peptide"
FT   peptide         41..455
FT                   /note= "mature peptide"
FT   domain          30..199
FT                   /note= "extracellular domain"
FT   domain          212..234
FT                   /note= "transmembrane domain"
FT   modified_site   145..147
FT                   /note= "potential N-glycosylation site"
FT   modified_site   151..153
FT                   /note= "potential N-glycosylation site"
SQ   Sequence 455 AA;

Query Match             48.0%;  Score 1124;  DB 4;  Length 455;
Best Local Similarity   99.3%;  Pred. No. 1.82e-99;
Matches  142;  Conservative  1;  Mismatches  0;  Indels  0;  Gaps  0;

Db   41  dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
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Qy   23  DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL  82

Db  101  scskcrkengqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
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Qy   83  SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db  161  kqntvctchagfflrenecvscs 183
         |||||||||||||||||||||||:
Qy  143  KQNTVCTCHAGFFLRENECVSCA 165


RESULT  13
ID   R75084 standard; protein; 455 AA.
AC   R75084;
DT   19-JAN-1996  (first entry)
DE   p55 TNF-R.
KW   p55; tumour necrosis factor receptor; TNF-R; human; murine; chimera;
KW   epidermal growth factor receptor; EGF-R; protease; inhibitor;
KW   phorbol myristate acetate; PMA.
OS   Homo sapiens.
FH
FH   Key             Location/Qualifiers
FT   peptide         41..53
FT                   /note= "N terminus of soluble p55 TNF-R"
FT   modified_site   54..56
FT                   /note= "glycosylation site"
FT   modified_site   145..147
FT                   /note= "glycosylation site"
FT   modified_site   161..163
FT                   /note= "glycosylation site"
FT   peptide         193..210
FT                   /note= "glycosylation site"
FT   region          198..210
FT                   /note= "peptide used in creation of chimeras"
FT   misc_difference 201
FT                   /note= "spacer region"
FT   misc_difference 202
FT                   /note= "major C terminus for soluble p55 TNF-R"
FT   misc_difference 203
FT                   /note= "essential for shedding reaction"
FT   region          212..234
FT                   /note= "minor C terminus for soluble p55 TNF-R"
FT   region          212..234
FT                   /note= "transmembrane region"
SQ   Sequence 455 AA;
PN   AU9475742-A.
PD   04-MAY-1995.
PF   11-OCT-1994;
PR   12-OCT-1993; IL-107268.
PA   (YEDA ) YEDA RES & DEV CO LTD.
PI   Batkin M, Brakebusch C, Varfolomeev E, Wallach D;
DR   WPI; 95-194342/26.
DR   N-PSDB; Q90513.
PT   New protease capable of cleaving soluble tumour necrosis factor
PT   (TNF) receptor - from cell-bound TNF- receptor, useful for
PT   antagonising deleterious effects of TNF.
PS   Disclosure: Fig 1; 40pp; English.
CC   This sequence represents human p55 tumour necrosis factor (TNF-R).
CC   Expression of this receptor is regulated by shedding of the extracellular
CC   receptor fragment. The p55 TNF-R can be shed in response to different
CC   inducing agents, e.g. phorbol myristate acetate (PMA), depending on cell
CC   type. The only region of the receptor whose structure affects the
CC   shedding response is the spacer region (see R75012) in the extracellular
CC   domain. This region is located close to a site of cleavage of the
CC   molecule, and links the Cys rich module to the transmembrane domain. The
CC   spacer region of the encoded protein was used to create the chimera
CC   between human p55 TNF-R and murine epidermal growth factor receptor
CC   (EGF-R) that are represented by R75007-11. This spacer region was
CC   subjected to deletion mutations (R75013-25) and substitutions
CC   (R75026-47). Of the spacer region, the most important residues are
CC   Asn 172, Val 173, Lys 174 and Gly 175, with Val 173 being the most
CC   important of these. The shedding of the receptor is independent of the
CC   side chain identity of these residues, with the exception of Val 173.
CC   dependence on the identity of Val 173. Mutations which alter the
CC   conformation of the protein adversely affect the shedding process.
CC   The mutations shown in R75013-47 were introduced in order to create an
CC   inhibitor of a protease that is capable of cleaving the soluble TNF-R
CC   from the cell bound TNF-R. Fragments of these inhibitors can be seen in
CC   R75017-9, R75025, R75033-5 and R75042-3. These protease inhibitors can
CC   be used for enhancing TNF function.

Query Match             48.0%;  Score 1124;  DB 14;  Length 455;
Best Local Similarity   99.3%;  Pred. No. 1.82e-99;
Matches  142;  Conservative  1;  Mismatches  0;  Indels  0;  Gaps  0;

Db   41  dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
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Qy   23  DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL  82

Db  101  scskcrkengqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
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Qy   83  SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db  161  kqntvctchagfflrenecvscs 183
         |||||||||||||||||||||||:
Qy  143  KQNTVCTCHAGFFLRENECVSCA 165


RESULT  14
ID   R07451 standard; protein; 455 AA.
AC   R07451;
DT   29-JAN-1991  (first entry)
DE   Human Tumour Necrosis Factor-Receptor from lambdaTNF-R2 cDNA insert.
KW   Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
KW   infectious disease; parasitic disease; shock; lambdaTNF-R2; raTNF-R8.
KW   autoimmune disease; cachexia;
```

```
OS   Homo sapiens.
PN   EP-393438-A.
PD   24-OCT-1990.
PF   06-APR-1990; 106624.
PR   21-APR-1989; DE-911301.
PR   21-APR-1989; DE-920282.
PR   21-JUN-1989; DE-920282.
PI   (BOEH ) BOEHRINGER INGELHEIM INT.
PI   Hauptmann R, Himmler A, Maurer-Fogy I, Stratowa C;
DR   WPI; 90-321987/43.
DR   N-PSDB; Q06285.
PI   N-PSDB; Q06285.
PT   DNA encoding TNF binding protein and TNF- receptor - used in
PT   tumour treatment and to understand mechanism to TNF action
PS   Disclosure: Fig 91(1-2); 51pp; German.
CC   raTNF-R8 (Q06284) was used to screen the HS913T cDNA library.
CC   LambdaTNF-R2 encodes the complete human TNF-R2 and was used to
CC   construct a plasmid (pADTNF-R) expressing the product the same way
CC   as pADTNF-BP (see Q06282). The expressed proteins are useful
CC   prophylactically and therapeutically to control disorders which
CC   involve the damaging effects of TNF-alpha or -beta (e.g. infectious or
CC   parasitic diseases, shock, cachexia, autoimmune diseases, adult
CC   respiratory distress syndrome etc., or side effects of treatment with
CC   TNG-alpha). They can also be used as diagnostic reagents for
CC   assaying TNF and in study of TNF-receptor interactions.
CC   See also Q06282-Q06285.
SQ   Sequence   455 AA;

Query Match        48.0%;  Score 1124;  DB 2;  Length 455;
Best Local Similarity  99.3%;  Pred. No. 1.82e-99;
Matches  142;  Conservative  1;  Mismatches  0;  Indels  0;  Gaps  0;

Db   41  dsvcpqgkylhpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl  100
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Qy   23  DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL  82

Db  101  scskcrkemgqveisscvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe  160
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Qy   83  SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE  142

Db  161  kqntvctchagfflrenecvscs  183
         |||||||||||||||||||||:
Qy  143  KQNTVCTCHAGFFLRENECVSCA  165
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```
RESULT  15
ID   R11082 standard; Protein; 455 AA.
AC   R11082;
DT   24-MAY-1991 (first entry)
DE   Human 55kD TNF-binding protein.
KW   Tumour Necrosis Factor; binding proteins; septic shock;
KW   autoimmune glomerulonephritis; lymphokine; cytokine.
FH   Key            Location/Qualifiers
FT   modified_site      54
FT                  /label= putative N-glycosylation site
FT   modified_site      145
FT                  /label= putative N-glycosylation site
FT   modified_site      151
FT                  /label= putative N-glycosylation site
FT   modified_site      270
FT                  /label= putative N-glycosylation site
FT   region         212..230
FT                  /label= putative N-glycosylation site
FT   region         1..28
FT                  /label= transmembrane region
FT   peptide        1..28
FT                  /label= signal peptide
PN   EP-417563-A.
PD   20-MAR-1991.
PF   31-AUG-1990; 116707.
PR   12-SEP-1989; CH-003319.
PR   08-MAR-1990; CH-000746.
PR   20-APR-1990; CH-001347.
PA   (HOFF ) HOFFMANN-LA ROCHE AG.
PA   (HOFF )
PI   Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;
PI   Schlaeger EJ;
DR   WPI; 91-081851/12.
```

```
DR   N-PSDB; Q10955.
PT   Insoluble tumour necrosis factor binding proteins - and DNA
PT   encoding them, useful in pharmaceutical prods. and for antibody
PT   prodn.
PS   Claim 1: Fig 1; 26pp; German.
CC   Partial amino acid sequences were determined for the 55 and 75kD
CC   TNF-BPs (see R11072-R11081) and oligonucleotide primers were
CC   synthesised based on these partial sequences. The primers were used
CC   to produce a cDNA fragment for use as aprobe to screen a human
CC   placental cDNA bank constructed in lambda gt11. Positive clones were
CC   identified and sequenced. DNA constructs comprising the TNF-BP coding
CC   sequence may also contain a fragment encoding a human Ig domain.
CC   Recombinant constructs are used to transform cells to confer
CC   improved TNF-binding properties.
CC   See also Q10956.
SQ   Sequence   455 AA;

Query Match        48.0%;  Score 1124;  DB 2;  Length 455;
Best Local Similarity  99.3%;  Pred. No. 1.82e-99;
Matches  142;  Conservative  1;  Mismatches  0;  Indels  0;  Gaps  0;

Db   41  dsvcpqgkylhpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl  100
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Qy   23  DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL  82

Db  101  scskcrkemgqveisscvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe  160
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Qy   83  SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE  142

Db  161  kqntvctchagfflrenecvscs  183
         |||||||||||||||||||||:
Qy  143  KQNTVCTCHAGFFLRENECVSCA  165

Search completed: Wed May  6 08:57:56 1998
Job time : 99 secs.
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|  _____||    ___||   _   ||   | ||  |       ||  |_|  |   (TM)
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*********************************************************************
*                                                                   *
*   M P S R C H                                                (TM)  *
*                                                                   *
*   Release 3.0.5AA John F. Collins, Biocomputing Research Unit.    *
*   Copyright (c) 1993-1997 University of Edinburgh, U.K.           *
*   Distribution rights by Oxford Molecular Ltd                     *
*                                                                   *
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MPsrch_pp   protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 6 08:55:24 1998:   MasPar time 13.64 Seconds
                                            821.959 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-4
Description: (1-307) from US08804166.pep
Perfect Score: 2341
Sequence: 1 SRTSLLLAFGLLCLPWLQEG............PSLPSPSRLPGPSDTPILPQ 307

Scoring table: PAM 150
                   Gap 11

Searched: 120446 seqs, 3653193 residues

Post-processing: Minimum Match 0%
                   Listing first 45 summaries

Database: pir56
                   1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 42.076; Variance 82.446; scale 0.510

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                                SUMMARIES

Result   %   Query
No.   Score Match Length DB ID   Description   Pred. No.
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  1   1124   48.0   158   5   1EXTB   tumor necrosis factor   2.76e-207
  2   1124   48.0   455   1   GQHUT1   tumor necrosis factor   2.76e-207
  3   1118   47.8   160   5   1EXTA   tumor necrosis factor   5.28e-206
  4   1114   47.6   142   5   1NCFB   tumor necrosis factor   3.78e-205
  5   1105   47.2   139   5   ITNRR   tumor necrosis factor   3.17e-203
  6   1098   46.9   140   5   1NCFA   tumor necrosis factor   9.90e-202
  7   1030   44.0   145   2   I37412   tumor necrosis factor   9.90e-202
  8   1030   44.0   165   1   KTHUB   beta-gonadotropin - h   6.00e-187
  9   1024   43.7   145   2   I37231   chorlogonadotropin be   8.16e-187
 10   1030   44.0   165   1   KTHUB   beta-gonadotropin - h   6.00e-186
 11   955   40.8   461   2   JC4302   tumor necrosis factor   2.83e-171
 12   857   36.6   165   1   KTBAB   chorlogonadotropin be   1.63e-150
 13   841   35.9   454   2   I57826   chorlogonadotropin be   3.90e-147
 14   841   35.9   454   2   GQMST1   tumor necrosis factor   3.90e-147
 15   809   34.6   461   1   GORTT1   tumor necrosis factor   2.19e-140
 16   803   34.3   110   5   1XULB   chorionic gonadotropi   4.02e-139
 17   803   34.3   110   5   1HCNB   Human chorionic gonad   4.02e-139
 18   803   34.3   110   5   1HRPB   chorionic gonadotropi   4.02e-139
 19   740   31.6   121   2   I37994   beta-LH - human (frag   9.96e-126
 20   709   30.3   115   2   UTHUB   beta-LH - human (frag   2.16e-119
 21   614   26.2   141   1   UTBOB   lutropin beta chain -   1.30e-99
 22   613   26.2   141   2   I46949   luteinizing hormone b   1.30e-99
 23   596   25.5   119   2   KTHOB   chorlogonadotropin b   6.93e-96
 24   598   25.5   141   1   UTPGB   lutropin beta chain p   2.67e-96
 25   597   25.5   141   1   UTRTB   lutropin beta chain -   4.31e-96
 26   595   25.4   118   2   PN0139   lutropin beta chain -   1.12e-95
 27   594   25.4   141   2   UTSHB   lutropin beta chain p   1.80e-95
 28   587   25.1   138   2   S00512   lutropin beta chain p   5.02e-94
 29   585   25.0   118   2   PN0141   lutropin beta chain p   1.30e-93
 30   582   24.9   141   1   JC4527   luteinizing hormone b   5.41e-93
 31   430   18.4   144   1   UTCAB   gonadotropin II beta   1.39e-53
 32   427   18.2   141   2   B60626   gonadotropin II beta cha   3.18e-49
 33   426   18.2   146   2   S16763   gonadotropin beta cha   2.22e-61
 34   420   17.9   119   2   S09344   gonadotropin II beta   3.52e-61
 35   416   17.9   119   2   C36179   gonadotropin II beta   5.64e-60
 36   411   17.6   113   2   S15232   gonadotropin II beta cha   3.58e-58
 37   407   17.4   142   2   S15232   gonadotropin II beta   5.68e-57
 38   405   17.3   112   2   S21196   lutropin beta chain -   1.42e-56
 39   403   17.2   140   2   A48166   gonadotropin II beta cha   1.42e-55
 40   398   17.0   142   2   A25800   gonadotropin II beta cha   1.39e-53
 41   388   16.6   142   2   I50143   lutropin II beta   2.18e-49
 42   366   15.6   158   2   A61091   gonadotropin II beta cha   3.09e-48
 43   361   15.4   147   2   I50994   gonadotropin II beta cha   3.09e-48
 44   357   15.2   166   2   I51242   luteinizing hormone b   1.89e-47
 45   350   15.0   159   2   I51373   luteinizing hormone b   4.51e-46
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RESULT                                      ALIGNMENTS
ENTRY

   1      1EXTB          #type complete

PDB_TITLE         tumor necrosis factor receptor extracellular domain, chain B
TITLE             extracellular domain of the 55kda tumor necrosis factor
                  receptor. crystallized at ph3.7 in P 21 21.
ORGANISM          #formal_name Homo sapiens #common_name man
                  expressed in Escherichia coli, the construct contains
#note             residues 12 to 172 of the mature sequence of the entire
                  receptor. residue 11 is mutated to met as a result of the
                  expression system

REFERENCE         A65560
#authors          Naismith, J.H.; Sprang, S.R.
#submission       submitted to the Brookhaven Protein Data Bank, July 1996
#cross-references PDB:1EXT

REFERENCE         TN026251
#authors          Naismith, J.H.; Devine, T.Q.; Brandhuber, B.J.; Sprang, S.R.
#journal          J. Biol. Chem. (1995) 270:13303
#title            Crystallographic evidence for dimerization of unliganded
                  tumor necrosis factor receptor.

REFERENCE         TN026252
#authors          Rodseth, L.E.; Brandhuber, B.; Devine, T.Q.; Eck, M.J.; Hale,
                  K.; Naismith, J.H.; Sprang, S.R.
#journal          J. Mol. Biol. (1994) 239:332
#title            Two crystal forms of the extracellular domain of type 1 tumor
                  necrosis factor receptor.

REFERENCE         A40737
#authors          Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
                  H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
#journal          Cell (1993) 73:431-445
#title            Crystal structure of the soluble human 55 kd TNF
                  receptor-human TNFbeta complex: implications for TNF
                  receptor activation.

COMMENT           Resolution: 1.85 angstroms
COMMENT           Determination: X-ray diffraction
COMMENT           R-value: no refinement
KEYWORDS          binding protein; cytokine; signalling protein
FEATURE
                  68-70        #region helix (right hand 3-10)\
                  143-145      #region helix (right hand 3-10)\
                  9-11,19-21   #region beta sheet\
                  133-136,139-142 #region beta sheet\
                  27-31,41-44  #region beta sheet\
                  73-76,85-87  #region beta sheet\
                  92-98,101-106 #region beta sheet\
                  113-117,126-129 #region beta sheet\
                  5-19         #disulfide_bonds\
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```
20-33      #disulfide_bonds//
23-42      #disulfide_bonds//
45-60      #disulfide_bonds//
63-78      #disulfide_bonds//
66-86      #disulfide_bonds//
88-104     #disulfide_bonds//
107-119    #disulfide_bonds//
110-127    #disulfide_bonds//
129-140    #disulfide_bonds//
143-156    #disulfide_bonds//
146-152    #disulfide_bonds/
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SUMMARY   #length 158 #molecular-weight 17827 #checksum 5022

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Query Match      48.0%;  Score 1124;  DB 5;  Length 158;
Best Local Similarity 99.3%;
Matches  142;  Conservative  1;  Pred. No. 2.76e-207;  Mismatches  0;  Indels  0;  Gaps  0;

Db    2  DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL   61
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Db   62  SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE  121
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   83  SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE  142

Db  122  KQNTVCTCHAGFFLRENECVSCS   144
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Qy  143  KQNTVCTCHAGFFLRENECVSCA   165
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RESULT    2
ENTRY     GGHUT1       #type complete
TITLE     tumor necrosis factor receptor type 1 precursor - human ALTERNATE_NAMES
CONTAINS  tumor necrosis factor alpha inhibitor; tumor necrosis factor
          binding protein 1 (TNF blocking factor)
ORGANISM  *formal_name Homo sapiens #common_name man
DATE      30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
          24-Oct-1997
ACCESSIONS A38208; A34899; A34900; A36555; C35555; A38281; S12057;
           JT0758; A60231; A38258; A60594; A35010; JC2404
REFERENCE A38208
          #authors Fuchs, P.; Strehl, S.; Dworzak, M.; Himmler, A.; Ambros, P.F.
          #journal Genomics (1992) 13:219-224
          #title Structure of the human TNF receptor 1 (p60) gene (TNFR1) and
                 localization to chromosome 12p13.
          #accession A38208
          ##molecule_type DNA
          ##residues 1-455 ##label FUC
          ##cross-references GB:M75864; GB:M75865; GB:M75866; NID:g339748;
                 PID:g339750
REFERENCE A34899
          #authors Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus,
                 M.; Tabuchi, H.; Lesslauer, W.
          #journal Cell (1990) 61:351-359
          #title Molecular cloning and expression of the human 55 kd tumor
                 necrosis factor receptor.
          #accession A34899
          ##molecule_type mRNA
          ##residues 1-455 ##label LOE
          ##cross-references GB:M58286; NID:g339753; PID:g339754
          ##experimental_source placenta
          #note part of this sequence, including the amino end of the
                 mature protein, confirmed by protein sequencing
REFERENCE A34900
          #authors Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.;
                 Wong, G.H.W.; Gatanaga, T.; Granger, G.A.; Lentz, R.; Raab,
                 H.; Kohr, W.J.; Goeddel, D.V.
          #journal Cell (1990) 61:361-370
          #title Molecular cloning and expression of a receptor for human
                 tumor necrosis factor.
          #cross-references MUID:90035285
```

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          #accession A34900
          ##molecule_type mRNA
          ##residues 1-455 ##label SCH
          ##cross-references GB:M33294; NID:g339744; PID:g339745
REFERENCE A36555
          #authors Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.;
                 Pfizenmaier, K.; Lantz, M.; Olsson, I.; Hauptmann, R.;
                 Stratowa, C.; Adolf, G.R.
          #journal DNA Cell Biol. (1990) 9:705-715
          #title Molecular cloning and expression of human and rat tumor
                 necrosis factor receptor chain (p60) and its soluble
                 derivative, tumor necrosis factor-binding protein.
          #cross-references MUID:91090841
          #accession A36555
          ##molecule_type mRNA
          ##residues 1-455 ##label HIM
          ##cross-references GB:M63121; NID:g339755; PID:g339756
          #accession C35555
          ##molecule_type protein
          ##residues 30-38;41-53,'X','55-79,'XX','82-94,'NK','X','100-104;
                 107-128;162-167,'X','169-201 ##label HI2
                 the purified protein, called tumor necrosis factor
          #note binding protein, is a soluble derivative of the
                 receptor
REFERENCE A38281
          #authors Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann,
                 M.
          #journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:7380-7384
          #title Cloning of human tumor necrosis factor (TNF) receptor cDNA
                 and expression of recombinant soluble TNF-binding protein.
          #cross-references MUID:91017509
          #accession A38281
          ##molecule_type mRNA
          ##residues 1-455 ##label GRA
          ##cross-references GB:M37764
          #note the authors translated the codon TGG for residue 371 as
                 Thr, AAG for residue 372 as Leu, and GAC for residue
                 427 as Asn
REFERENCE S12057
          #authors Nophar, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang,
                 R.; Aderka, D.; Holtmann, H.; Wallach, D.
          #journal EMBO J. (1990) 9:3269-3278
          #title Soluble forms of tumor necrosis factor receptors (TNF-Rs).
                 The cDNA for the type I TNF-R, cloned using amino acid
                 sequence data of its soluble form, encodes both the cell
                 surface and a soluble form of the receptor.
          #cross-references MUID:91006021
          #accession S12057
          ##molecule_type mRNA
          ##residues 1-455 ##label NOP
          ##cross-references EMBL:X55513; NID:g37223; PID:g37224
          #note parts of soluble TNF binding protein 1, including its
                 amino and carboxyl ends, were confirmed by protein
                 sequencing
REFERENCE JT0758
          #authors Kemper, O.; Wallach, D.
          #journal Gene (1993) 134:209-216
          #title Cloning and partial characterization of the promoter for the
                 human p55 tumor necrosis factor (TNF) receptor.
          #accession JT0758
          ##molecule_type DNA
          ##residues 1-13 ##label KEM
REFERENCE A60231
          #authors Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer,
                 J.M.
          #journal Eur. J. Immunol. (1990) 20:1167-1174
          #title Tumor necrosis factor inhibitor: purification, NH-2-terminal
                 amino acid sequence and evidence for anti-inflammatory and
                 immunomodulatory activities.
          #cross-references MUID:90292116
          #accession A60231
          ##molecule_type protein
          ##residues 41-43,'X','45-53,'X','55-57 ##label SEC
```

REFERENCE
#authors A38258
Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci III,
J.A.; Jeffes, E.W.B.; Lentz, R.; Tomich, J.; Yamamoto,
R.S.; Granger, G.A.
#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:8781-8784
#title Purification and characterization of an inhibitor (soluble
tumor necrosis factor receptor) for tumor necrosis factor
and lymphotoxin obtained from the serum ultrafiltrates of
human cancer patients.
#cross-references MUID:91062364
#accession A38258
##molecule_type protein
##residues 41-60 ##label GAT

REFERENCE A60594
#authors Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thysell, H.;
Grubb, A.; Adolf, G.
#journal Eur. J. Haematol. (1989) 42:270-275
#title Isolation and characterization of a tumor necrosis factor
binding protein from urine.
#accession A60594
##molecule_type protein
##residues 41-43,'X',45-53,'V',55-57,'XK',60 ##label OLS

REFERENCE A35010
#authors Engelmann, H.; Novick, D.; Wallach, D.
#journal J. Biol. Chem. (1990) 265:1531-1536
#title Two tumor necrosis factor-binding proteins purified from
human urine. Evidence for immunological cross-reactivity
with cell surface tumor necrosis factor receptors.
#cross-references MUID:90110215
#accession A35010
##molecule_type protein
##residues 41-45 ##label ENG

REFERENCE JC2404
#authors Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.
#journal Biosci. Biotechnol. Biochem. (1994) 58:2266-2268
#title Amino acid sequence of natural tumor necrosis factor alpha
inhibitor purified from human urine.
#accession JC2404
##molecule_type protein
##residues 41-53,'X',55-144,'X',146-150,'X',152-186,'X',188-201
##label KAJ

COMMENT This protein is one of two known receptors for both TNF-alpha
(cachectin) and TNF-beta (lymphotoxin).
##experimental_source urine

GENETICS
#gene GDB:TNFR1
##cross-references GDB:125913; OMIM:191190
##map_position 12p13.2-12p13.2
#introns 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1

CLASSIFICATION
#superfamily tumor necrosis factor receptor type 1; NGF
receptor repeat homology

KEYWORDS
duplication; glycoprotein; receptor; transmembrane protein

FEATURE
1-21   #domain signal sequence #status predicted #label SIG\
22-455   #product tumor necrosis factor receptor type 1 #status
            predicted #label MAT\
30-211   #domain extracellular #status predicted #label EXT\
41-201   #product TNF binding protein 1 (tumor necrosis factor
            alpha inhibitor) #status experimental #label TBP1\
44-82   #domain NGF receptor repeat homology #label NG1\
84-126   #domain NGF receptor repeat homology #label NG2\
127-167   #domain NGF receptor repeat homology #label NG3\
168-196   #domain NGF receptor repeat homology #label NG4\
212-234   #domain transmembrane #status predicted #label MEM\
235-455   #domain intracellular #status predicted #label INT\
54,145,151 #binding_site carbohydrate (Asn) (covalent) #status
            predicted

SUMMARY
#length 455 #molecular-weight 50494 #checksum 153

Query Match   48.0%;   Score 1124;   DB 1;   Length 455;

Best Local Similarity 99.3%;   Pred. No. 2.76e-207;
Matches 142; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db   41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL  82

Db  101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db  161 KQNTVCTCHAGFFLRENECVSCS 183
         |||||||||||||||||||||||
Qy  143 KQNTVCTCHAGFFLRENECVSCA 165
```

RESULT 3

ENTRY 1EXTA   #type complete
TITLE tumor necrosis factor receptor extracellular domain, chain A
PDB_TITLE extracellular domain of the 55kda tumor necrosis factor
receptor. crystallized at ph3.7 in p 21 21 21.
ORGANISM #formal_name Homo sapiens #common_name man
#note expressed in Escherichia coli, the construct contains
residues 12 to 172 of the mature sequence of the entire
receptor. residue 11 is mutated to met as a result of the
expression system

REFERENCE A65560
#authors Naismith, J.H.; Sprang, S.R.
#submission submitted to the Brookhaven Protein Data Bank, July 1996
#cross-references PDB:1EXT

REFERENCE TN026248
#authors Naismith, J.H.; Devine, T.Q.; Brandhuber, B.J.; Sprang, S.R.
#journal J. Biol. Chem. (1995) 270:13303
#title Crystallographic evidence for dimerization of unliganded
tumor necrosis factor receptor.

REFERENCE TN026249
#authors Rodseth, L.E.; Brandhuber, B.; Devine, T.Q.; Eck, M.J.; Hale,
K.; Naismith, J.H.; Sprang, S.R.
#journal J. Mol. Biol. (1994) 239:332
#title Two crystal forms of the extracellular domain of type 1 tumor
necrosis factor receptor.

REFERENCE A40737
#authors Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
#journal Cell (1993) 73:431-445
#title Crystal structure of the soluble human 55 kd TNF
receptor-human TNFbeta complex: implications for TNF
receptor activation.

COMMENT Resolution: 1.85 angstroms
COMMENT Determination: X-ray diffraction
COMMENT R-value: no refinement
KEYWORDS binding protein; cytokine; signalling protein

FEATURE
66-68   #region helix (right hand 3-10)\
141-143   #region helix (right hand 3-10)\
151-154   #region helix (right hand alpha)\
7-9,17-19   #region beta sheet\
131-134,137-140   #region beta sheet\
25-29,39-42   #region beta sheet\
71-74,83-85   #region beta sheet\
90-96,99-104   #region beta sheet\
111-115,124-127   #region beta sheet\
3-17   #region beta sheet\
18-31   #region beta sheet\
21-40   #region beta sheet\
43-58   #region beta sheet\
61-76   #region beta sheet\
64-84   #region beta sheet\
86-102   #disulfide_bonds\
105-117   #disulfide_bonds\
108-125   #disulfide_bonds\
127-138   #disulfide_bonds\

```
SUMMARY
        141-154                                   #disulfide_bonds\
        144-150                                   #disulfide_bonds
        #length 160         #molecular-weight 18065         #checksum 2297

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Best Local Similarity  99.3%;    Pred. No. 5.28e-205;
Matches      141;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db    1 SVCPQGKYIHPQNNSICICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLS 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   24 SVCPQGKYIHPQNNSICICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLS 83

Db   61 CSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEK 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   84 CSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEK 143

Db  121 QNTVCTCHAGFFLRENECVSCS 142
        ||||||||||||||||||||||:
Qy  144 QNTVCTCHAGFFLRENECVSCA 165

RESULT       4
ENTRY        1NCFB               #type complete
TITLE        tumor necrosis factor receptor 55 kd extracellular domain
             contains residues 12 172 of the mature receptor sequence,
             chain B - hu
ALTERNATE_NAMES    stnfr1; type 1 receptor
ORGANISM     #formal_name Homo sapiens #common_name man
             expressed in Escherichia coli, residue 11 is mutated to met
             as a result of the expression system
REFERENCE    A66195
    #authors Naismith, J.H.; Sprang, S.R.
    #submission submitted to the Brookhaven Protein Data Bank, October 1994
    #cross-references PDB:1NCF
REFERENCE    TN029041
    #authors Rodseth, L.E.; Brandhuber, B.; Devine, T.O.; Eck, M.J.; Hale,
             K.; Naismith, J.H.; Sprang, S.R.
    #journal  J. Mol. Biol. (1994) 239:332
    #title    Two crystal forms of the extracellular domain of type 1 tumor
              necrosis factor receptor.
REFERENCE    A40737
    #authors Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
             H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
    #journal  Cell (1993) 73:431-445
    #title    Crystal structure of the soluble human 55 kd TNF
              receptor-human TNFbeta complex: implications for TNF
              receptor activation.
COMMENT      Resolution: 2.25 angstroms
COMMENT      Determination: X-ray diffraction
KEYWORDS     R-value: no refinement
FEATURE      binding protein; cytokine; signalling protein
        2-16                                      #disulfide_bonds\
        17-30                                     #disulfide_bonds//
        20-39                                     #disulfide_bonds\
        42-57                                     #disulfide_bonds\
        60-75                                     #disulfide_bonds//
        63-83                                     #disulfide_bonds\
        85-101                                    #disulfide_bonds//
        104-116                                   #disulfide_bonds\
        107-124                                   #disulfide_bonds//
        126-137                                   #disulfide_bonds\
SUMMARY
        #length 142         #molecular-weight 16046         #checksum 1225

Query Match            47.4%;    Score 1114;   DB 5;   Length 142;
Best Local Similarity  99.3%;    Pred. No. 3.78e-205;
Matches      140;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db    1 VCPQGKYIHPQNNSICICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   25 VCPQGKYIHPQNNSICICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC 84
```

```
Db   61 SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQ 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   85 SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQ 144

Db  121 NTVCTCHAGFFLRENECVSCS 141
        |||||||||||||||||||||:
Qy  145 NTVCTCHAGFFLRENECVSCA 165

RESULT       5
ENTRY        1TNRR               #type complete
TITLE        tumor necrosis factor receptor type 1 (P55 extracellular
             receptor-human TNFbeta complex: implications for TNF
             receptor activation.
ORGANISM     #formal_name Homo sapiens #common_name man
             recombinant form expressed in Baculovirus SF9
REFERENCE    A52442
    #authors Banner, D.W.
    #submission submitted to the Brookhaven Protein Data Bank, May 1994
    #cross-references PDB:1TNR
REFERENCE    A40737
    #authors Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
             H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
    #journal  Cell (1993) 73:431-445
    #title    Crystal structure of the soluble human 55 kd TNF
    #authors D'arcy, A.; Banner, D.W.; Janes, W.; Winkler, F.K.;
             Loetscher, H.; Schoenfeld, H.J.; Zulauf, M.; Gentz, R.;
             Lesslauer, W.
    #journal  J. Mol. Biol. (1993) 229:555
    #title    Crystallization and preliminary analysis of tnf-beta and a
             tnf-beta-55 kd tnf receptor complex.
COMMENT      Resolution: 2.85 angstroms
COMMENT      Determination: X-ray diffraction
KEYWORDS     Complex(lymphokineRECEPTOR)
FEATURE
        1-15                                      #disulfide_bonds\
        16-29                                     #disulfide_bonds//
        19-38                                     #disulfide_bonds\
        41-56                                     #disulfide_bonds\
        59-74                                     #disulfide_bonds//
        62-82                                     #disulfide_bonds\
        84-100                                    #disulfide_bonds//
        103-115                                   #disulfide_bonds\
        106-123                                   #disulfide_bonds//
        125-136                                   #disulfide_bonds\
SUMMARY
        #length 139         #molecular-weight 15746         #checksum 5235

Query Match            47.2%;    Score 1105;   DB 5;   Length 139;
Best Local Similarity  100.0%;   Pred. No. 3.17e-203;
Matches      139;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db    1 CPQGKYIHPQNNSICICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCS 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   26 CPQGKYIHPQNNSICICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCS 85

Db   61 KCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQN 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   86 KCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQN 145

Db  121 TVCTCHAGFFLRENECVSC 139
        |||||||||||||||||||
Qy  146 TVCTCHAGFFLRENECVSC 164

RESULT       6
ENTRY        1NCFA               #type complete
TITLE        tumor necrosis factor receptor 55 kd extracellular domain
             contains residues 12 172 of the mature receptor sequence,
             chain A - hu
ALTERNATE_NAMES    stnfr1; type 1 receptor
```

ORGANISM   #formal_name Homo sapiens #common_name man
  #note   expressed in Escherichia coli, residue 11 is mutated to met
      as a result of the expression system
REFERENCE   A66195
  #authors   Naismith, J.H.; Sprang, S.R.
  #submission   submitted to the Brookhaven Protein Data Bank, October 1994
  #cross-references PDB:1NCF
REFERENCE   TN023039
  #authors   Rodseth, L.E.; Brandhuber, B.; Devine, T.O.; Eck, M.J.; Hale,
      K.; Naismith, J.H.; Sprang, S.R.
  #journal   J. Mol. Biol. (1994) 239:332
  #title   Two crystal forms of the extracellular domain of type 1 tumor
      necrosis factor receptor.
REFERENCE   A40737
  #authors   Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
      H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
  #journal   Cell (1993) 73:431-445
  #title   Crystal structure of the soluble human 55 kd TNF
      receptor-human TNFbeta complex: implications for TNF
      receptor activation.
COMMENT   Resolution: 2.25 angstroms
COMMENT   Determination: X-ray diffraction
COMMENT   R-value: no refinement
KEYWORDS   binding protein; cytokine; signalling protein
FEATURE
  5-19   #disulfide_bonds\
  20-33   #disulfide_bonds\
  23-42   #disulfide_bonds\
  45-60   #disulfide_bonds\
  63-78   #disulfide_bonds\
  66-86   #disulfide_bonds\
  88-104   #disulfide_bonds\
  107-119   #disulfide_bonds\
  110-127   #disulfide_bonds\
  129-140   #disulfide_bonds
SUMMARY   #length 140 #molecular-weight 15889 #checksum 6622

Query Match   46.9%;   Score 1098;   DB 5;   Length 140;
Best Local Similarity 100.0%;
Matches   139;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Db      2 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 61
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db     62 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db    122 KQNTVCTCHAGFFLRENEC 140
          |||||||||||||||||||
Qy    143 KQNTVCTCHAGFFLRENEC 161
```

RESULT   7
ENTRY   I37412   #type fragment
TITLE   beta-gonadotropin - human (fragment)ORGANISM #formal_name Homo
DATE   21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change
      09-May-1997
ACCESSIONS   I37412
REFERENCE   I37231
  #authors   Talmadge, K.; Vamvakopoulos, N.C.; Fiddes, J.C.
  #journal   Nature (1984) 307:37-40
  #title   Evolution of the genes for the beta subunits of human
      chorionic gonadotropin and luteinizing hormone.
  #cross-references MUID:84093590
  #accession I37412
    ##status preliminary; translated from GB/EMBL/DDBJ
    ##molecule_type DNA
    ##residues 1-145 ##label RES
    ##cross-references EMBL:X00265; NID:g31719
GENETICS

  #introns 41/3
CLASSIFICATION   #superfamily pituitary glycoprotein hormone beta chain
SUMMARY   #length 145 #checksum 2358

Query Match   44.0%;   Score 1030;   DB 2;   Length 145;
Best Local Similarity 100.0%;   Pred. No. 3.16e-187;
Matches   139;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

```
Db      7 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 66
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

Db     67 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPP 126
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPP 288

Db    127 SLPSPSRLPGPSDTPILPQ 145
          |||||||||||||||||||
Qy    289 SLPSPSRLPGPSDTPILPQ 307
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RESULT   8
ENTRY   KTHUB   #type complete
TITLE   choriogonadotropin beta chain precursor - humanALTERNATE_NAMES   chor
ORGANISM   #formal_name Homo sapiens #common_name man
DATE   23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change
      20-Mar-1998
ACCESSIONS   A93230; I69972; I55224; I55250; I70007; I70008; A92303;
      A92181; A92142; PC10116; A61097; B56873; A01502
REFERENCE   A93230
  #authors   Fiddes, J.C.; Goodman, H.M.
  #journal   Nature (1980) 286:684-687
  #title   The cDNA for the beta-subunit of human chorionic gonadotropin
      suggests evolution of a gene by readthrough into the
      3'-untranslated region.
  #cross-references MUID:81012134
  #accession A93230
    ##status translated from GB/EMBL/DDBJ
    ##molecule_type mRNA
    ##residues 1-165 ##label FID
    ##cross-references GB:J00117; GB:M38559; GB:M54963; NID:g180436;
      PID:g180437
REFERENCE   I55224
  #authors   Policastro, P.; Ovitt, C.E.; Hoshina, M.; Fukuoka, H.;
      Boothby, M.R.; Boime, I.
  #journal   J. Biol. Chem. (1983) 258:11492-11499
  #title   The beta subunit of human chorionic gonadotropin is encoded
      by multiple genes.
  #cross-references MUID:84008141
  #accession I69972
    ##status translated from GB/EMBL/DDBJ
    ##molecule_type DNA
    ##residues 1-165 ##label POL
    ##cross-references GB:K03189; NID:g180450; PID:g180453
    ##note clone CG-beta-e
  #accession I55224
    ##status translated from GB/EMBL/DDBJ
    ##molecule_type DNA
    ##residues 1-23,'M',25-136,'A',138-165 ##label PO2
    ##cross-references GB:K03183; NID:g180442; PID:g180444
    ##note clone CG-beta-a
REFERENCE   I55250
  #authors   Policastro, P.F.; Daniels-McQueen, S.; Carle, G.; Boime, I.
  #journal   J. Biol. Chem. (1986) 261:5907-5916
  #title   A map of the hCG beta-LH beta gene cluster.
  #cross-references MUID:86195987
  #accession I55250
    ##status preliminary; translated from GB/EMBL/DDBJ
    ##molecule_type DNA
    ##residues 1-5 ##label PO3
    ##cross-references GB:M13504; NID:g180419; PID:9463088
    ##note CG-beta-3 gene
  #accession I70007

```
##status           preliminary; translated from GB/EMBL/DDBJ
##molecule_type    DNA
##residues         1-5 ##label PO4
##cross-references GB:M13505; NID:g180429; PID:g463089
##note             CG-beta-6 gene
*accession         I70008
##status           preliminary; translated from GB/EMBL/DDBJ
##molecule_type    DNA
##residues         1-5 ##label RE5
##cross-references GB:M13503; NID:g180432; PID:g463090
##note             CG-beta-7 gene
*accession         A92303
REFERENCE
##authors          Birken, S.; Fetherston, J.; Canfield, R.; Boime, I.
##journal          J. Biol. Chem. (1981) 256:1816-1823
##title            The amino acid sequences of the prepeptides contained in the
                   alpha and beta subunits of human choriogonadotropin.
*accession         A92303
##molecule_type    protein
##residues         1-20 ##label BIR
##note             the identity of the residue at position 19 could not be
                   determined
REFERENCE
##authors          Morgan, F.J.; Birken, S.; Canfield, R.E.
##journal          J. Biol. Chem. (1975) 250:5247-5258
##title            The amino acid sequence of human chorionic gonadotropin. The
                   alpha subunit and beta subunit.
*accession         A92181
##molecule_type    protein
##residues         21-165 ##label MOR
REFERENCE
##authors          Carlsen, R.B.; Bahl, O.P.; Swaminathan, N.
##journal          J. Biol. Chem. (1973) 248:6810-6827
*accession         A92142
##molecule_type    protein
##residues         21-22,'Q',24-73,'ZL',76-140,142-157,'PB',160-165,'SLP'
REFERENCE
##authors          Shi, Z.P.; Du, G.G.; Li, W.X.; Liu, X.J.; Li, S.Z.; Xu, Y.S.;
                   Wang, Y.
##journal          Chinese Biochem. J. (1990) 6:558-562
##title            The immunological characteristics of the enzymatic fragments
                   of human chorionic gonadotropin beta-subunit.
*accession         PC1016
##molecule_type    protein
##residues         21-165 ##label SHI
##note             article in Chinese with English abstract
REFERENCE
##authors          Birken, S.; Armstrong, E.G.; Kolks, M.A.G.; Cole, L.A.;
                   Agosto, G.M.; Krichevsky, A.; Vaitukaitis, J.L.; Canfield,
                   R.E.
##journal          Endocrinology (1988) 123:572-583
##title            Structure of the human chorionic gonadotropin beta-subunit
                   fragment from pregnancy urine.
*accession         A61097
##molecule_type    protein
##residues         26-32,'X',34-49,'X',51-60,75-112 ##label BI2
##note             this material from pregnancy urine lacks sialic acid in
                   its carbohydrate and has been processed further from
                   the mature form into two chains linked by disulfide
                   bonds
REFERENCE
##authors          Kardana, A.; Bagshawe, K.D.; Coles, B.; Read, D.; Taylor, M.
##journal          Br. J. Cancer (1993) 67:686-692
##title            Characterisation of UGP and its relationship with beta-core
                   fragment.
*accession         A56873
##cross-references MUID:93229246
##accession        B56873
##molecule_type    protein
##residues         26-28,'X',30-32,'X',34-42,'X',44-45,'X',47-48,75-76,'X',
                   78-91,'G',93-102 ##label KAR
```

```
##note             experimental_source urine
##note             sequence modified after extraction from NCBI backbone
                   this material was designated urinary gonadotrophin
                   peptide (peak 2)
REFERENCE
##authors          Lapthorn, A.J.; Harris, D.C.; Littlejohn, A.; Lustbader,
                   J.W.; Canfield, R.E.; Machin, K.J.; Morgan, F.J.; Isaacs,
                   N.W.
##title            Nature (1994) 369:455-461
##title            Crystal structure of human chorionic gonadotropin.
##contents         annotation: X-ray crystallography, 3.0 angstroms; correction
                   of disulfide bonds
GENETICS
##gene             GDB:CGB
##cross-references GDB:119055; OMIM:118860
##map_position     19q13.3-19q13.3
##introns          5/3; 61/3
##note             the choriogonadotropin beta chain locus contains six genes
                   (or pseudogenes)
CLASSIFICATION     *superfamily pituitary glycoprotein hormone beta chain
KEYWORDS           glycoprotein; hormone; pituitary
FEATURE
1-20               #domain signal sequence #status experimental #label SIG\
21-165             *product choriogonadotropin beta chain #status
                   experimental #label MAT\
29-77,43-92,46-130,
54-108,58-110,
113-120,           #disulfide_bonds #status experimental\
33,50              #binding_site carbohydrate (Asn) (covalent) #status
                   experimental\
138,150            #binding_site carbohydrate (Ser) (covalent) #status
                   predicted\
141,147,152,158    #binding_site carbohydrate (Ser) (covalent) #status
                   experimental
SUMMARY            #length 165 #molecular-weight 17739 #checksum 6523
```

```
Query Match       44.0%;  Score 1030;  DB 1;  Length 165;
Best Local Similarity 100.0%;
Matches 139;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
                  Pred. No. 3.16e-187;

Qy   27  PRCRPINATLAVEKEGCPVCIIVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES  86
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  169  PRCRPINATLAVEKEGCPVCIIVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

Qy   87  IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 146
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  229  IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 288

Qy  147  SLPSPSRLPGPSDTPILPQ 165
         |||||||||||||||||||
Db  289  SLPSPSRLPGPSDTPILPQ 307
```

```
RESULT   9
ENTRY              I37231          #type fragment
TITLE              beta-gonadotropin - human (fragment)ORGANISM     #formal_name Ho
DATE               21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change
                   09-May-1997
ACCESSIONS         I37231
REFERENCE
##authors          Talmadge, K.; Vamvakopoulos, N.C.; Fiddes, J.C.
##journal          Nature (1984) 307:37-40
##title            Evolution of the genes for the beta subunits of human
                   chorionic gonadotropin and luteinizing hormone.
*accession         I37231
##cross-references MUID:84093590
##accession        I37231
##status           preliminary; translated from GB/EMBL/DDBJ
##molecule_type    DNA
##residues         1-145 ##label RES
##cross-references EMBL:X00266; NID:g29907
GENETICS
##introns          41/3
```

CLASSIFICATION #superfamily pituitary glycoprotein hormone beta chain
SUMMARY #length 145 #checksum 2349

```
Query Match
Best Local Similarity   43.7%;   Score 1024;   DB 2;   Length 145;
Matches 138;   Conservative 99.3%;   Pred. No. 6.00e-186;   Mismatches 1;   Indels 0;   Gaps 0;

Db     7  PRCRPINATLAVEKEGCPVCITVNTIICAGYCPTMRVLQGVLPALPQVVCNYRDVRFES   66
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   169  PRCRPINATLAVEKEGCPVCITVNTIICAGYCPTMRVLQGVLPALPQVVCNYRDVRFES   228

Db    67  IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQOASSSSKAPP  126
          |||||||||||||||||||||||| |||||||||||||||||||| ||||||||||||
Qy   229  IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPP   288

Db   127  SLPSPSRLPGPSDTPILPQ  145
          |||||||||||||||||||
Qy   289  SLPSPSRLPGPSDTPILPQ  307
```

RESULT 10

ENTRY JC4302 #type complete

TITLE tumor necrosis factor receptor p55 - pigORGANISM
DATE 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change
12-Dec-1997

ACCESSIONS JC4302; PC4093
REFERENCE JC4302
#authors Suter, B.; Pauli, U.
#journal Gene (1995) 163:263-266
#title Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.
#molecule_type mRNA
#residues 1-461 ##label SUT
#cross-references GB:U19994; NID:g1141752; PID:g1141753
GENETICS
#gene tnfr
CLASSIFICATION #superfamily tumor necrosis factor receptor type 1; NGF receptor repeat homology
KEYWORDS glycoprotein; kidney; receptor; transmembrane protein; tumor
FEATURE
1-29 #domain signal sequence #status predicted #label SIG\
30-461 #product tumor necrosis factor receptor p55 #status predicted #label MAT\
44-194 #domain extracellular cysteine rich #status predicted #label EXT\
44-82 #domain NGF receptor repeat homology #label NG1\
211-231 #domain transmembrane #status predicted #label TM\
361-447 #domain signal transduction #status predicted #label SIT\
54,145,151 #binding_site carbohydrate (Asn) (covalent) #status predicted

SUMMARY #length 461 #molecular-weight 50696 #checksum 8079

```
Query Match
Best Local Similarity   40.8%;   Score 955;   DB 2;   Length 461;
Matches 114;   Conservative 80.3%;   Pred. No. 2.83e-171;   Mismatches 12;   Indels 12;   Gaps 0;

Db    41  ESLCPQGKYISHPQNRSICCTKCHKGTYLHNDCLGPGLDTDCRECDNGTFTASENHLTQCL  100
          :||:|| |||| |::|||||:||||||||||: ||| | |||||||::| |||||:|:|||
Qy    23  DSVCPQGKYIHPQNNSICCTRCHKGTYLYNDCPGPGQDTDCRECESGSFTASENLHRCL    82

Db   101  SCSKCRSEMSQVEISPCTVDRDTVCGCRKNQYRKRWSETLFQCLNCSLCPNGTVQLPCLE  160
          ||||||:||.|||||.||||||||||||||||||:.||||:|| ||||| |||| ||||:|
Qy    83  SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHVWSENLFQCFNCSLCLNGTVHLSCQE  142

Db   161  KQDTICNCHSGFFLRDKECVSC  182
          |||:||  ||:|||||:::||||
Qy   143  KQNTVCTCHAGFFLRENECVSC  164
```

RESULT 11

ENTRY KTBAB #type complete

TITLE choriogonadotropin beta chain precursor - olive baboonORGANISM
#common_name olive baboon
DATE 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change
03-May-1996
ACCESSIONS A25808
REFERENCE A25808
#authors Crawford, R.J.; Tregear, G.W.; Niall, H.D.
#journal Gene (1986) 46:161-169
#title The nucleotide sequences of baboon chorionic gonadotropin beta-subunit genes have diverged from the human.
#cross-references MUID:87106851
#molecule_type mRNA
#residues 1-165 ##label CRA
COMMENT There are at least five copies of CG-related genes and at least two of these are expressed in the baboon placenta.
CLASSIFICATION #superfamily pituitary glycoprotein hormone beta chain
KEYWORDS glycoprotein; hormone; placenta; pregnancy maintenance
FEATURE
1-20 #domain signal sequence #status predicted #label SIG\
21-165 #product choriogonadotropin beta chain #status predicted #label CGB\
29-77,43-92,46-130, #disulfide_bonds #status predicted\
54-108,58-110,
113-120
33,50 #binding_site carbohydrate (Asn) (covalent) #status predicted\
#binding_site carbohydrate (Ser) (covalent) #status
140,147,152 predicted

SUMMARY #length 165 #molecular-weight 17592 #checksum 4960

```
Query Match
Best Local Similarity   36.6%;   Score 857;   DB 1;   Length 165;
Matches 113;   Conservative 81.3%;   Pred. No. 1.63e-150;   Mismatches 14;   Indels 12;   Gaps 0;

Db    27  PLCRPINATLAAAEKEACPVCVTVNTVNTIICAGYCPTMMRVLQAVLPPVPQVVCVREVRFES   86
          |:|||||||||::::||:|||||.|||:|:|:|||||||||:|||.||||:|:|||||:::||||:||
Qy   169  PRCRPINATLAVEKEGCPVCITVNTIICAGYCPTMRVLQGVLPALPQVVCNYRDVRFES      228

Db    87  IRLPGCPPGVDMVSVPVALSCRCALCRRSTSDCGGPRDHPLITCDDPNLQASSSSKDPPP  146
          |||||||.|.:.:|:.:|||||:|||||||:||||||:|||:|||||.::|:|||||:|||
Qy   229  IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPP   288

Db   147  SPPSPSRLLEPAGTPFLPQ  165
          |.|||||| |.|.||:|||
Qy   289  SLPSPSRLPGPSDTPILPQ  307
```

RESULT 12

ENTRY I57826 #type complete

TITLE tumor necrosis factor receptor - mouseORGANISM
DATE 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
23-May-1997
ACCESSIONS I57826
REFERENCE I57826
#authors Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M.
#journal Mol. Immunol. (1993) 30:165-176
#title Genomic organization and promoter function of the murine tumor necrosis factor receptor beta gene.
#cross-references MUID:93156721
#accession I57826
#status preliminary; translated from GB/EMBL/DDBJ
#molecule_type DNA
#residues 1-454 ##label RES
#cross-references GB:M76556; NID:g202100; PID:g202102

GENETICS
 #gene   TNFR-2
 #intron   13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; 353/1
CLASSIFICATION *superfamily tumor necrosis factor receptor type 1; NGF
               receptor repeat homology
KEYWORDS   cytokine receptor
SUMMARY   #length 454 #molecular-weight 50030 #checksum 4267
 Query Match   Best Local Similarity 35.9%; Score 841; DB 2; Length 454;
 Matches 101; Conservative 23; Mismatches 19; Indels 0; Gaps 0;

Qy   41 DSICPQGKYVHSKNNSICCTKCHKGTYLVSDCPSPGRDTVCRECEKGTFTASQNYLRQCL 100
        |:|||:|||:|: ||||:|||:| |||:||||||:|::||||||:|||:|:||| ||:||
Db   23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Qy   83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142
        ||||||||:|||||||||||||||||| ||| ||||:|||| ||||:|||| :|||:||
Db 101 SCKTCRKEMSQVEISPCQADKDTVCGCKENQFQRYLSETHFQCVDCSPCFNGTVTIPCKE 160

Qy 143 KQNTVCTCHAGFFLRESECVPCSCA 165
        ||||||||||||||||||||:||
Db 161 TQNTVCNCHAGFFLRESECVPCS 183

ACCESSIONS A38634; B40254; S16677; S19021; I54532
REFERENCE
 #authors   Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice,
             G.C.; Wong, G.H.W.; Chen, E.Y.; Goeddel, D.V.
 #journal   Proc. Natl. Acad. Sci. U.S.A. (1991) 88:2830-2834
 #title   Cloning and expression of cDNAs for two distinct murine tumor
             necrosis factor receptors demonstrate one receptor is
             species specific.
 #cross-references MUID:91187885
 #accession A38634

```
COMMENT      This protein is one of two known receptors for both TNF-alpha
             (cachectin) and TNF-beta (lymphotoxin).
CLASSIFICATION  #superfamily tumor necrosis factor receptor receptor type 1; NGF
                receptor repeat homology
KEYWORDS     duplication; glycoprotein; receptor; transmembrane protein
FEATURE
       1-29    #domain signal sequence #status predicted #label SIG\
      30-461   #product tumor necrosis factor receptor type 1 #status
               predicted #label MAT\
      30-211   #domain extracellular #status predicted #label EXT\
      30-201   #product tumor necrosis factor receptor binding protein #status
               predicted #label TBP\
      44-82    #domain NGF receptor repeat homology #label NG1\
      84-126   #domain NGF receptor repeat homology #label NG2\
     127-167   #domain NGF receptor repeat homology #label NG3\
     168-204   #domain NGF receptor repeat homology #label NG4\
     212-234   #domain transmembrane #status predicted #label MEM\
     235-461   #domain intracellular #status predicted #label INT\
   54,151,201  #binding_site carbohydrate (Asn) (covalent) #status
               predicted
SUMMARY      #length 461 #molecular-weight 50969 #checksum 1617

Query Match        34.6%;  Score 809;  DB 1;  Length 461;
Best Local Similarity   68.5%;  Pred. No. 2.19e-140;
Matches   98;  Conservative   21;  Mismatches  24;  Indels   0;  Gaps   0;

Db    41  DNLCPQGKYAHPKNNSICCTKCHKGTYLVSDCPSPGQETVCVCDKGTFTASQNHVRQCL  100
          |::||||||  ||  ||||||||:||||||:::||||||:  |::||||:|:|||:|:
Qy    23  DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRICL  82

Db   101  SCKTCREKMFQVEISPCKADMDTVCGCKKNQFQRYLSETHFQCVDCSPCFNGTVTIPCKE  160
          | ||||||||||||:||:||  |||:||:|:|  |:|||||||:|:||
Qy    83  SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE  142

Db   161  KQNTVCNCHAGFFLSGNECTPCS  183
          |||||| |||||||||| ||| :|:
Qy   143  KQNTVCTCHAGFFLRENECVSCA  165

RESULT 15
ENTRY    1XULB       #type complete
TITLE       chorionic gonadotropin, chain B - humanPDB_TITLE    theoretical mod
            receptor complexed with human chorionic gonadotropin
ORGANISM    #formal_name Homo sapiens #common_name man
REFERENCE   A66957
  #authors  Jiang, X.; Dreano, M.; Buckler, D.R.; Cheng, S.; Ythier, A.;
            Wu, H.; Hendrickson, W.A.; El Tayar, N.
  #submission submitted to the Brookhaven Protein Data Bank, December 1996
  #cross-references PDB:1XUL
REFERENCE   TN032625
  #authors  Jiang, X.; Dreano, M.; Buckler, D.R.; Cheng, S.; Ythier, A.;
            Wu, H.; Hendrickson, W.A.; El Tayar, N.
  #journal  Structure (London) (1996) 3:1341
  #title    Structural predictions for the ligand-binding region of
            glycoprotein hormone receptors and the nature of
            hormone-receptor interactions structure.
REFERENCE   TN032626
  #authors  Wu, H.; Lustbader, J.W.; Liu, Y.; Canfield, R.E.;
            Hendrickson, W.A.
  #journal  Structure (London) (1994) 2:545
  #title    Structure of human chorionic gonadotropin at 2.6 a resolution
            from mad analysis of the selenomethionyl protein.
COMMENT     Resolution: not applicable
            Determination: theoretical model
KEYWORDS    complex; glycoprotein hormone receptor glycoprotein; hormone;
            phosphorylation; receptor
FEATURE
   - 97-101,26-39,9-17  #region beta sheet\
     54-59,86-91        #region beta sheet\
     61-67,78-84        #region beta sheet\
       8-56             #disulfide_bonds\
      22-71             #disulfide_bonds\
      25-109            #disulfide_bonds\
      33-87             #disulfide_bonds\
      37-89             #disulfide_bonds\
      92-99             #disulfide_bonds\
SUMMARY     #length 110 #molecular-weight 11906 #checksum 6414

Query Match        34.3%;  Score 803;  DB 5;  Length 110;
Best Local Similarity  100.0%;  Pred. No. 4.02e-139;
Matches  105;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Db     6  PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES  65
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   169  PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES  228

Db    66  IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCD  110
          |||||||||||||||||||||||||||||||||||||||||||||
Qy   229  IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCD  273

Search completed: Wed May  6 08:55:58 1998
Job time : 34 secs.
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MPsrch (TM)

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|  \  /  ||  __  | |  __  | |  __  |  |  ____||  | |  |
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|        ||  ____| |  __  / | ____/   | |  __ |   _   |
|  |\/|  || |      | |  \  \| |       | |_|  ||  | |  |
|__|  |__||_|      |_|   \__|_|        \____/ |__| |__|
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****
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****

MPsrch.pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 6 08:53:11 1998; MasPar time 9.09 seconds
                  846.789 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-4.pep
Description: (1-307) from US08804166.pep
Perfect Score: 2341
Sequence: 1 SRTSLLLAFGLLCLPWLQEG..........PSLPSPSRLPGPSDTPILPQ 307

Database: swiss-prot35
                  1:swiss1

Post-processing: Minimum Match 0%
                  Listing first 45 summaries

Searched: 69112 seqs, 25083644 residues

Scoring table: PAM 150
                  Gap 11

Statistics: Mean 43.895; Variance 73.304; scale 0.599

                  Pred. No. is the number of results predicted by chance to have a
                  score greater than or equal to the score of the result being printed,
                  and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1124	48.0	455	1	TNR1_HUMAN	TUMOR NECROSIS FACTOR	2.90e-242
2	1030	44.0	165	1	CGHB_HUMAN	CHORIOGONADOTROPIN BET	8.92e-219
3	955	40.8	461	1	TNR1_PIG	TUMOR NECROSIS FACTOR	4.23e-200
4	857	36.6	165	1	CGHB_PAPAN	CHORIOGONADOTROPIN BET	8.42e-176
5	841	35.9	454	1	CGHB_PAPAN	CHORIOGONADOTROPIN BET	7.59e-172
6	809	34.6	461	1	TNR1_MOUSE	TUMOR NECROSIS FACTOR	5.98e-164
7	740	31.6	461	1	TNR1_RAT	TUMOR NECROSIS FACTOR	5.55e-147
8	709	30.3	164	1	LSHB_HUMAN	LUTROPIN BETA CHAIN PR	2.18e-139
9	630	26.9	169	1	CGHB_EQUAS	CHORIOGONADOTROPIN BET	3.88e-120
10	614	26.2	141	1	CGHB_CALJA	CHORIOGONADOTROPIN BET	2.18e-116
11	613	26.2	169	1	LSHB_EQUAS	LUTROPIN/CHORIOGONADOT	5.13e-116
12	602	25.7	141	1	LSHB_BOVIN	LUTROPIN BETA CHAIN PR	2.94e-116
13	598	25.5	141	1	LSHB_HORSE	LUTROPIN/CHORIOGONADOT	2.36e-113
14	597	25.5	141	1	LSHB_SHEEP	LUTROPIN BETA CHAIN PR	2.19e-112
15	595	25.4	141	1	LSHB_PIG	LUTROPIN BETA CHAIN PR	3.82e-112
16	587	25.1	118	1	LSHB_RAT	LUTROPIN BETA CHAIN (L	1.16e-111
17	585	25.0	138	1	LSHB_BALAC	LUTROPIN BETA CHAIN PR	9.94e-110
18	542	23.2	105	1	LSHB_CANFA	LUTROPIN BETA CHAIN (L	3.02e-109
19	430	18.4	144	1	LSHB_PHYCA	LUTROPIN BETA CHAIN PR	6.71e-99
20	427	18.2	141	1	LSHB_MOUSE	GONADOTROPIN BETA CHAI	2.64e-72
21	426	18.2	146	1	LSHB_CYPCA	GONADOTROPIN BETA CHAI	1.33e-71
22	416	17.8	142	1	GTHB_HYPMO	GONADOTROPIN BETA CHAI	2.29e-71
23	411	17.6	138	1	GTHB_CTEID	GONADOTROPIN BETA CHAI	5.02e-69
24	411	17.6	142	1	GTH2_ONCKE	GONADOTROPIN BETA-II C	7.39e-68
25	407	17.4	113	1	GTHB_CLAGA	GONADOTROPIN BETA CHAI	7.39e-68
26	405	17.3	112	1	GTH2_ONCMA	GONADOTROPIN BETA-II C	6.34e-67
27	403	17.2	140	1	GTHB_MURCI	GONADOTROPIN BETA CHAI	1.85e-66
28	398	17.0	142	1	LSHB_RANCA	LUTROPIN BETA CHAIN (L	5.42e-66
29	388	16.6	142	1	GTH2_ANGAN	GONADOTROPIN BETA-II C	1.66e-65
30	371	15.8	128	1	GTHB_ONCTS	GONADOTROPIN BETA CHAI	1.42e-62
31	357	15.2	115	1	GTHB_CORAU	GONADOTROPIN BETA-II C	6.78e-58
32	355	15.2	115	1	LSHB_STRCA	LUTROPIN BETA CHAIN (L	2.16e-55
33	350	15.0	159	1	GTH2_THUOB	GONADOTROPIN BETA-II C	6.78e-55
34	328	14.0	166	1	LSHB_COTJA	LUTROPIN BETA CHAIN PR	9.48e-54
35	320	13.7	138	1	LSHB_MELGA	LUTROPIN BETA CHAIN PR	9.76e-49
36	319	13.6	136	1	LSHB_CANFA	LUTROPIN BETA CHAIN PR	6.31e-47
37	318	13.6	138	1	GTH2_FUNHE	GONADOTROPIN BETA-II C	1.79e-46
38	318	13.5	138	1	TSHB_PIG	THYROTROPIN BETA CHAIN	3.00e-46
39	317	13.5	138	1	TSHB_BOVIN	THYROTROPIN BETA CHAIN	5.05e-46
40	316	13.5	138	1	TSHB_HUMAN	THYROTROPIN BETA CHAIN	1.06e-46
41	305	13.0	130	1	TSHB_MOUSE	THYROTROPIN BETA CHAIN	1.50e-43
42	303	12.9	130	1	TSHB_RAT	THYROTROPIN BETA CHAIN	4.22e-43
43	297	12.7	118	1	FSHB_RAT	FOLLITROPIN BETA CHAIN	5.28e-42
44	289	12.3	129	1	FSHB_SHEEP	FOLLITROPIN BETA CHAIN	5.63e-40
45	281	12.0	129	1	FSHB_HUMAN	FOLLITROPIN BETA CHAIN	3.35e-38

RESULT 1

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ID   TNR1_HUMAN     STANDARD;      PRT;   455 AA.
AC   P19438;
DT   01-FEB-1991 (REL. 17, CREATED)
DT   01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DT   01-NOV-1991 (REL. 35, LAST ANNOTATION UPDATE)
DE   TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (TUMOR NECROSIS FACTOR
DE   BINDING PROTEIN 1) (TBP1) (P60) (TNF-R1) (P55) (CD120A).
GN   TNFR1 OR TNFAR.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PLACENTA;
RX   MEDLINE; 90235284.
RA   LOETSCHER H., PAN Y.-C.E., LAHM H.-W., GENTZ R., BROCKHAUS M.,
RA   TABUCHI H., LESSLAUER W.;
RL   CELL 61:351-359(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PLACENTA;
RX   MEDLINE; 90235285.
RA   SCHALL T.J., LEWIS M., KOLLER K.J., LEE A., RICE G.C., WONG G.H.W.,
RA   GETANAGA T., GRANGER G.A., LENTZ R., RAAB H., KOHR W.J., GOEDDEL D.V.;
RL   CELL 61:361-370(1990).
RN   [3]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 41-53; 110-124 AND 199-201.
RA   NOPHAR Y., KEMPER O., BRAKEBUSCH C., ENGELMANN H., ZWANG R.,
RA   ADERKA D., HOLTMANN H., WALLACH D.;
RL   EMBO J. 9:3269-3278(1990).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91090841.
RA   HIMMLER A., MAURER-FOGY I., KROENKE M., SCHEURICH P., PFIZENMAIER K.,
RA   LANTZ M., OLSSON I., HAUPTMANN R., STRATOWA C., ADOLF G.R.;
RL   DNA CELL BIOL. 9:705-715(1990).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PLACENTA;
RX   MEDLINE; 91017509.
RA   GRAY P.W., BARRETT K., CHANTRY D., TURNER M., FELDMAN M.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 87:7380-7384(1990).
RN   [6]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 92250049.
RA   FUCHS P., STREHL S., DWORZAK M., HIMMLER A., AMBROS P.F.;
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ALIGNMENTS

ID	Description	Pred. No.
GTH2_ONCMA	GONADOTROPIN BETA-II C	7.39e-68
GTHB_MURCI	GONADOTROPIN BETA CHAI	6.34e-67
LSHB_RANCA	LUTROPIN BETA CHAIN (L	1.85e-66
GTH2_ANGAN	GONADOTROPIN BETA-II C	5.42e-66
GTHB_ONCTS	LUTROPIN BETA CHAIN (L	1.91e-65
GTHB_CORAU	GONADOTROPIN BETA-II C	1.42e-62
LSHB_MOUSE	LUTROPIN BETA CHAIN (L	1.50e-43
LSHB_STRCA	LUTROPIN BETA CHAIN (L	1.22e-58
GTH2_THUOB	GONADOTROPIN BETA-II C	2.16e-55
LSHB_COTJA	LUTROPIN BETA CHAIN PR	6.78e-55
LSHB_MELGA	LUTROPIN BETA CHAIN PR	9.48e-54
LSHB_CANFA	LUTROPIN BETA CHAIN PR	9.76e-49
GTHB_MOUSE	GONADOTROPIN BETA CHAIN	1.06e-47
GTH2_FUNHE	GONADOTROPIN BETA-II C	6.31e-47
TSHB_MOUSE	THYROTROPIN BETA CHAIN	1.06e-46
TSHB_HUMAN	THYROTROPIN BETA CHAIN	5.05e-46
TSHB_BOVIN	THYROTROPIN BETA CHAIN	3.00e-46
TSHB_RAT	THYROTROPIN BETA CHAIN	1.79e-46
TSHB_PIG	THYROTROPIN BETA CHAIN	1.79e-46
FSHB_MOUSE	FOLLITROPIN BETA CHAIN	1.50e-43
FSHB_RAT	FOLLITROPIN BETA CHAIN	4.22e-43
FSHB_HORSE	FOLLITROPIN BETA CHAIN	5.28e-42
FSHB_SHEEP	FOLLITROPIN BETA CHAIN	5.63e-40
FSHB_HUMAN	FOLLITROPIN BETA CHAIN	3.35e-38

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RL   GENOMICS 13:219-224(1992).
RN   [7]
RP   SEQUENCE OF 41-45.
RX   MEDLINE; 90110215.
RA   ENGELMANN H., NOVICK D., WALLACH D.;
RL   J. BIOL. CHEM. 265:1531-1536(1990).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211.
RX   MEDLINE; 93258809.
RA   BANNER D.W., D'ARCY A., JANES W., GENTZ R., SCHOENFELD H.-J.,
RA   BROGER C., LOETSCHER H., LESSLAUER W.;
RL   CELL 73:431-445(1993).
RN   [9]

RP   X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.
RX   MEDLINE; 97094982.
RA   NAISMITH J.H., DEVINE T.Q., KOHNO T., SPRANG S.R.;
RL   STRUCTURE 4:1251-1262(1996).
-!-  FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC   RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC   AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC   PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC   SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC   PROTEASES) MEDIATING APOPTOSIS.
-!-  SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC   HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC   PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC   WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC   PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC   TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC   ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC   NF-KAPPA B SIGNALING.
-!-  SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!-  SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR   EMBL; X55313; G37224; -.
DR   EMBL; M33294; G339745; -.
DR   EMBL; M58286; G339754; -.
DR   EMBL; M63121; G339756; -.
DR   EMBL; M75866; G339750; -.
DR   EMBL; M75865; G339750; JOINED.
DR   EMBL; M60275; G339760; JOINED.
DR   EMBL; A21522; G579600; -.
DR   PIR; A34899; GQHUTI.
DR   PIR; A35010; A35010.
DR   PIR; S12057; S12057.
DR   PIR; A38208; A38208.
DR   PDB; ITNR; 31-JUL-94.
DR   PDB; 1NCF; 07-DEC-95.
DR   PDB; 1EXT; 11-JAN-97.
DR   MIM; 191190; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS00050; TNFR_NGFR_2; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS;
KW   3D-STRUCTURE.
FT   SIGNAL        1     21
FT   CHAIN        22    455       TUMOR NECROSIS FACTOR RECEPTOR 1.
FT   CHAIN        41    291       TUMOR NECROSIS FACTOR BINDING PROTEIN 1.
FT   DOMAIN       22    211       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    212    234       POTENTIAL.
FT   DOMAIN      235    455       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       43    196       4 X TNFR-CYS.
FT   REPEAT       43     82       TNFR-CYS 1.
FT   REPEAT       83    125       TNFR-CYS 2.
FT   REPEAT      126    166       TNFR-CYS 3.
FT   REPEAT      167    196       TNFR-CYS 4.
FT   DOMAIN      356    441       DEATH DOMAIN.
FT   DISULFID     44     58
FT   DISULFID     59     72
FT   DISULFID     62     81
FT   DISULFID     84     99
FT   DISULFID    102    117
FT   DISULFID    105    125
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FT   DISULFID    127    143
FT   DISULFID    146    158
FT   DISULFID    149    166
FT   DISULFID    168    179
FT   DISULFID    182    191
FT   DISULFID    185    195
FT   CARBOHYD     54     54       POTENTIAL.
FT   CARBOHYD    145    145       POTENTIAL.
FT   CARBOHYD    151    151       POTENTIAL.
FT   CONFLICT    412    412       MISSING (IN REF. 4).
FT   CONFLICT    443    446       GPAA -> APP (IN REF. 4).
SQ   SEQUENCE   455 AA;  50494 MW;  CE0EA06F CRC32;

Query Match    48.0%;  Score 1124;  DB 1;  Length 455;
Best Local Similarity  99.3%;  Pred. No. 2.90e-242;
Matches  142;  Conservative  1;  Mismatches  0;  Indels  0;  Gaps  0;

Db    41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGGSFTASENHLRHCL 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGGSFTASENHLRHCL 82

Db   101 SCSKCRKEMGQVEISSCTVRDTVCGCRKNQYRHWSENLFQCFNCSLCLNGTVHLSCQE 160
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Qy    83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHWSENLFQCFNCSLCLNGTVHLSCQE 142

Db   161 KQNTVCTCHAGFFLRENECVSCS 183
          |||||||||||||||||||||| :
Qy   143 KQNTVCTCHAGFFLRENECVSCA 165
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RESULT 2
ID   CGHB_HUMAN      STANDARD;      PRT;     165 AA.
AC   P01233;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (CHORIONIC GONADOTROPHIN BETA
DE   SUBUNIT).
GN   CGB.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 81012134.
RA   FIDDES J.C., GOODMAN H.M.;
RL   NATURE 286:684-687(1980).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 84093590.
RA   TALMADGE K., VANVAKOPOULOS N.C., FIDDES J.C.;
RL   NATURE 307:37-40(1984).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 84008141.
RA   POLICASTRO P., OVITT C.E., HOSHINA M., FUKUOKA H., BOOTHBY M.R.,
RA   BOIME I.;
RL   J. BIOL. CHEM. 258:11492-11499(1983).
RN   [4]
RP   SEQUENCE OF 1-20.
RX   MEDLINE; 81117268.
RA   BIRKEN S., FETHERSTON J., CANFIELD R.E., BOIME I.;
RL   J. BIOL. CHEM. 256:1816-1823(1981).
RN   [5]
RP   SEQUENCE OF 21-165.
RX   MEDLINE; 7521304.
RA   MORGAN F.J., BIRKEN S., CANFIELD R.E.;
RL   J. BIOL. CHEM. 250:5247-5258(1975).
RN   [6]
RP   PRELIMINARY SEQUENCE OF 21-165.
RX   MEDLINE; 74011267.
RA   CARLSEN R.B., BAHL O.P., SWAMINATHAN N.;
RL   J. BIOL. CHEM. 248:6810-6827(1973).
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RN   [7]
RP   SEQUENCE OF 1-5 FROM N.A.
RX   MEDLINE; 8619587.
RA   POLICASTRO P.F., DANIELS-MCQUEEN S., CARLE G., BOIME I.;
RL   J. BIOL. CHEM. 261:5907-5916(1986).
RN   [8]
RP   PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.
RX   MEDLINE; 81215630.
RA   MISE T., BAHL O.P.;
RL   J. BIOL. CHEM. 256:6587-6592(1981).
RN   [9]
RP   DISULFIDE BONDS.
RX   MEDLINE; 90094415.
RA   SACCUZO BEEBE J., MOUNTJOY K., KRZESICKI R.F., PERINI F.,
RA   RUDDON R.W.;
RL   J. BIOL. CHEM. 265:312-317(1990).
RN   [10]
RP   STRUCTURE OF CARBOHYDRATES.
RX   MEDLINE; 92314469.
RA   WEISSHAAR G., HIYAMA J., RENWICK A.G.C.;
RL   GLYCOBIOLOGY 1:393-404(1991).
RN   [11]
RP   X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RX   MEDLINE; 94261179.
RA   LAPTHORN A.J., HARRIS D.C., LITTLEJOHN A., LUSTBADER J.W.,
RA   CANFIELD R.E., MACHIN K.J., MORGAN F.J., ISAACS N.W.;
RL   NATURE 369:455-461(1994).
CC   -!- FUNCTION: STIMULATES THE OVARIES TO SYNTHESIZE THE STEROIDS THAT
CC       ARE ESSENTIAL FOR THE MAINTENANCE OF PREGNANCY.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- TISSUE SPECIFICITY: PLACENTA.
CC   -!- DEVELOPMENTAL STAGE: MADE BY THE FIRST TRIMESTER PLACENTA.
DR   EMBL; J00117; G180437; -.
DR   EMBL; M13504; G463088; -.
DR   EMBL; M13505; G463089; -.
DR   EMBL; M13503; G463090; -.
DR   EMBL; K03189; G180453; -.
DR   EMBL; K03187; G180453; JOINED.
DR   EMBL; K03188; G180453; JOINED.
DR   PIR; A01502; KTHUB.
DR   PDB; 1HCN; 30-SEP-94.
DR   PDB; 1HRP; 01-NOV-94.
DR   MIM; 118860;
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL; 3D-STRUCTURE.
FT   SIGNAL        1     20
FT   CHAIN        21    165       CHORIOGONADOTROPIN BETA CHAIN.
FT   DISULFID     29     77
FT   DISULFID     43     92
FT   DISULFID     46    130
FT   DISULFID     54    108
FT   DISULFID     58    110
FT   DISULFID    113    120
FT   DISULFID     33     33
FT   CARBOHYD     50     50
FT   CARBOHYD    141    141
FT   CARBOHYD    147    147
FT   CARBOHYD    152    152
FT   CARBOHYD    158    158
FT   VARIANT     137    137       D -> A (IN GENE 6).
FT   SEQUENCE    165 AA;  17739 MW;  FF1D4802 CRC32;
SO
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Db    27  PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES    86
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   169  PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES   228
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Query Match             44.0%;  Score 1030;  DB 1;  Length 165;
Best Local Similarity  100.0%;  Pred. No. 8.92e-219;
Matches  139;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;
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Db    87  IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPP   146
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   229  IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPP   288

Db   147  SLPSPSRLPGPSDTPILPQ   165
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Qy   289  SLPSPSRLPGPSDTPILPQ   307
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RESULT   3
ID   TNR1_PIG      STANDARD;      PRT;   461 AA.
AC   P50555;
DT   01-OCT-1996 (REL. 34, CREATED)
DT   01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
GN   TNFR1.
OS   SUS SCROFA (PIG).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; ARTIODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 96011645.
RA   PAULI U.H.;
RL   GENE 163:263-266(1995).
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC       RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC       AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC       PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC       SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC       PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC       HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC       PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC       WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC       PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC       TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC       ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR   EMBL; U19994; G1141753; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS00050; TNFR_NGFR_2; 2.
DR   PROSITE; PS00017; DEATH_DOMAIN; 1.
KW   RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS.
FT   SIGNAL         1     21       POTENTIAL.
FT   CHAIN         22    461       TUMOR NECROSIS FACTOR RECEPTOR 1.
FT   DOMAIN        22    210       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     211    233       POTENTIAL.
FT   DOMAIN       234    461       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN        43    195       4 X TNFR-CYS.
FT   REPEAT        43     82       TNFR-CYS 1.
FT   REPEAT        83    125       TNFR-CYS 2.
FT   REPEAT       126    166       TNFR-CYS 3.
FT   REPEAT       167    195       TNFR-CYS 4.
FT   DOMAIN       362    447       DEATH DOMAIN.
FT   DISULFID      44     58       BY SIMILARITY.
FT   DISULFID      58     72       BY SIMILARITY.
FT   DISULFID      59     81       BY SIMILARITY.
FT   DISULFID      62     99       BY SIMILARITY.
FT   DISULFID      84    117       BY SIMILARITY.
FT   DISULFID     102    125       BY SIMILARITY.
FT   DISULFID     105    127       BY SIMILARITY.
FT   DISULFID     143    143       BY SIMILARITY.
FT   DISULFID     146    158       BY SIMILARITY.
FT   DISULFID     149    166       BY SIMILARITY.
FT   DISULFID     168    179       BY SIMILARITY.
FT   DISULFID     182    190       BY SIMILARITY.
FT   DISULFID     185    194       BY SIMILARITY.
FT   CARBOHYD      54     54       POTENTIAL.
FT   CARBOHYD      86     86       POTENTIAL.
FT   CARBOHYD     145    145       POTENTIAL.
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FT   CARBOHYD       151    151    POTENTIAL.
SQ   SEQUENCE       461 AA;  50696 MW;  8E2C350A CRC32;
     Query Match             40.8%;  Score 955;  DB 1;  Length 461;
     Best Local Similarity   80.3%;  Pred. No. 4.23e-200;
     Matches  114;  Conservative  16;  Mismatches  12;  Indels   0;  Gaps   0;

Db          41  ESLCPQGKYSHPQNRSICCITKCHKGTYLIHNDCLGPGLDTDCRECDNGTFTASENHLTQCL 100
                 ::|:|||||::|||||::|||||||||||||||:|||||||||||::|||::|||||||:||
Qy           1  DSVCPQGKYIHPQNNSICCITKCHKGTYLIYNDCPGPGQDTDCRECESGSFTASENHLRHCL  60

Db         101  SCSKCRSEMSQVEISPCTVDRDTVCGCRKNQYRKYWSETLFQCLNCSLCPNGTVQLPCLE 160
                ||:|||||:||||||::|||||||||||||||||||||||:|||||||||||||||||||
Qy          23  SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHWSENLFQCFNCSLCLNGTVHLSCQE 142

Db         161  KQDTICNCHSGFFLRDKECVSC 182
                ||||||||||:||||||||:|||
Qy         143  KQNTVCTCHAGFFLRENECVSC 164
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RESULT 4

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ID   CGHB_PAPAN     STANDARD;      PRT;   165 AA.
AC   P07434;
DT   01-APR-1988 (REL. 07, CREATED)
DT   01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (CHORIONIC GONADOTROPHIN BETA
DE   SUBUNIT).
GN   CGB.
OS   PAPIO ANUBIS (OLIVE BABOON).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 87106851.
RA   CRAWFORD R.J., TREGEAR G.W., NIALL H.D.;
RL   GENE 46:161-169(1986).
CC   -!- FUNCTION: STIMULATES THE OVARIES TO SYNTHESIZE THE STEROIDS THAT
CC       ARE ESSENTIAL FOR THE MAINTENANCE OF PREGNANCY.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- TISSUE SPECIFICITY: PLACENTA.
CC   -!- THERE ARE AT LEAST FIVE COPIES OF CG-RELATED GENES AND AT LEAST
CC       TWO OF THESE ARE EXPRESSED IN THE BABOON PLACENTA.
DR   EMBL; M14966; G176573; -.
PIR; A25808; KTBAB.
HSSP; P01233; 1HCN.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL         1     20         BY SIMILARITY.
FT   CHAIN          21    165        CHORIOGONADOTROPIN BETA CHAIN.
FT   DISULFID       29    77         BY SIMILARITY.
FT   DISULFID       43    92         BY SIMILARITY.
FT   DISULFID       46    130        BY SIMILARITY.
FT   DISULFID       54    108        BY SIMILARITY.
FT   DISULFID       58    110        BY SIMILARITY.
FT   DISULFID       113   120        BY SIMILARITY.
FT   CARBOHYD       33    33         BY SIMILARITY.
FT   CARBOHYD       50    50         BY SIMILARITY.
FT   CARBOHYD       141   141        BY SIMILARITY.
FT   CARBOHYD       147   147        BY SIMILARITY.
FT   CARBOHYD       152   152        BY SIMILARITY.
SQ   SEQUENCE       165 AA;  17592 MW;  78987D30 CRC32;
     Query Match             36.6%;  Score 857;  DB 1;  Length 165;
     Best Local Similarity   81.3%;  Pred. No. 8.42e-176;
     Matches  113;  Conservative  14;  Mismatches  12;  Indels   0;  Gaps   0;

Db          27  PLCRPINATLAAEKEACPVCVTVNTICAGYCPTMMRVLQAVLPPVPQVVCNYREVRFES 86
                |||||||||||::|:||||||::|:|:|||||||||::|||||||:||:||||:|||||
Qy         169  PRCRPINATLAVEKEGCPVCITVNTICAGYCPTMVRVLQGVLPALPQVVCNYRDVRFES 228
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RESULT 5

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ID   TNR1_MOUSE     STANDARD;      PRT;   454 AA.
AC   P25118;
DT   01-MAY-1992 (REL. 22, CREATED)
DT   01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
GN   TNFR1 OR TNFR-1.
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91187885.
RA   LEWIS M., TARTAGLIA L.A., LEE A., BENNETT G.L., RICE G.C.,
RA   WONG G.H., CHEN E.Y., GOEDDEL D.V.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 88:2830-2834(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91246168.
RA   GOODWIN R.G., ANDERSON D., JERZY R., DAVIS T., BRANNAN C.I.,
RA   COPELAND N.G., JENKINS N.A., SMITH C.A.;
RL   MOL. CELL. BIOL. 11:3020-3026(1991).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91285014.
RA   BARRETT K., TAYLOR-FISHWICK D.A., COPE A.P., KISSONERGHIS A.M.,
RA   GRAY P.W., FELDMANN M., FOXWELL B.M.J.;
RL   EUR. J. IMMUNOL. 21:1649-1656(1991).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=SPLEEN;
RX   MEDLINE; 92039815.
RA   ROTHE J.G., BROCKHAUS M., GENTZ R., LESSLAUER W.;
RL   IMMUNOGENETICS 34:338-340(1991).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 94245292.
RA   BEBO B.F., LINTHICUM D.S.;
RL   IMMUNOGENETICS 39:450-451(1994).
RN   [6]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 93156721.
RA   ROTHE J., BLUETHMANN H., GENTZ R., LESSLAUER W., STEINMETZ M.;
RL   MOL. IMMUNOL. 30:165-175(1993).
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC       RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC       AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC       PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC       SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC       PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC       HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC       PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC       WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC       PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC       TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC       ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR   EMBL; M60468; G199826; -.
DR   EMBL; M59377; G202097; -.
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Db          87  IRLPGCPPGVDPMVSVPVALSCRCALCRRSTSDCGGPKDHPLTCDDPNLQASSSKDPPP 146
                |||||||| |||:|||  :||:|| ||||| |||:||||||||||||||||   |||||||
Qy         229  IRLPGCPRGVNPVVSTAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPP 288

Db         147  SPPSPSRLLEPAGTPFLPQ 165
                |||||||| |: ||:||||
Qy         289  SLPSPSRLPGPSDTPLPQ 307
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EMBL; X59238; G53579; -.
EMBL; X57796; G54849; -.
EMBL; L26349; G430733; -.
EMBL; M76655; G202102; -.
EMBL; M88067; G202102; JOINED.
EMBL; M76655; G202102; JOINED.
PIR; A38634; GOMST1.
PIR; S16677; S16677.
PIR; S19021; S19021.
HSSP; P19438; 1TNR.
MGD; MGI:98781; TNFR1.
PROSITE; PS00652; TNFR_NGFR_1; 3.
PROSITE; PS50050; TNFR_NGFR_2; 3.
PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS.
FT   SIGNAL        1     21
FT   CHAIN        22    454    TUMOR NECROSIS FACTOR RECEPTOR 1.
FT   DOMAIN       22    212    EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    213    235    POTENTIAL.
FT   DOMAIN      236    454    CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       43    196    4 X TNFR-CYS.
FT   REPEAT       43     82    TNFR-CYS 1.
FT   REPEAT       83    125    TNFR-CYS 2.
FT   REPEAT      126    166    TNFR-CYS 3.
FT   REPEAT      167    196    TNFR-CYS 4.
FT   DOMAIN      356    441    DEATH DOMAIN.
FT   DISULFID     44     58    BY SIMILARITY.
FT   DISULFID     59     72    BY SIMILARITY.
FT   DISULFID     62     81    BY SIMILARITY.
FT   DISULFID     84     99    BY SIMILARITY.
FT   DISULFID    102    117    BY SIMILARITY.
FT   DISULFID    105    125    BY SIMILARITY.
FT   DISULFID    127    143    BY SIMILARITY.
FT   DISULFID    146    158    BY SIMILARITY.
FT   DISULFID    149    166    BY SIMILARITY.
FT   DISULFID    168    179    BY SIMILARITY.
FT   DISULFID    182    191    BY SIMILARITY.
FT   DISULFID    185    195    BY SIMILARITY.
FT   CARBOHYD     54     54    POTENTIAL.
FT   CARBOHYD    151    151    POTENTIAL.
FT   CARBOHYD    202    202    POTENTIAL.
FT   CONFLICT    394    394    R -> G (IN REF. 6).
SQ   SEQUENCE    454 AA;  50129 MW;  4B6EEC09 CRC32;

Query Match      35.9%;  Score 841;  DB 1;  Length 454;
Best Local Similarity 70.6%;  Pred. No. 7.59e-172;
Matches 101;  Conservative 23;  Mismatches 19;  Indels 0;  Gaps 0;

Db   41  DSLCPQGKYVHSKNNSICCTKCHKGTIYLVSDCPSPGRDTVCRECEKGTFTASQNYLRQCL 100
         |::||||||:|| :|||||||||||||:||| |||:|||| ||||||:|:|||||:| ||:|
Qy   23  DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRCL 82

Db  101  SCKTCRKEMSQVEISPCQADKDTVCGCRKENQFQRYLSETHFQCVDCSPCFNGTVTIPCKE 160
         |||:||||| ||:|||| ::|:||||||||||||:| :|| ||| ||:||:|||||:||::|
Qy   83  SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db  161  TONTVCNCHAGFFLRESECVPCS 183
         ||||||:|||||||||||||:|:
Qy  143  KONTVCTCHAGFFLRESECVPCS 165
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RESULT  6
ID   TNFR1_RAT    STANDARD;    PRT;    461 AA.
AC   P22934;
DT   01-AUG-1991 (REL. 19, CREATED)
DT   01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
GN   TNFR1 OR TNFR-1.
OS   RATTUS NORVEGICUS (RAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
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RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91090841.
RA   HIMMLER A., MAURER-FOGY I., KROENKE M., SCHEURICH P., PFIZENMAIER K.,
RA   LANTZ M., OLSSON I., HAUPTMANN R., STRATOWA C., ADOLF G.R.;
RL   DNA CELL BIOL. 9:705-715(1990).
-!-  FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC   RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC   AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC   PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC   SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC   PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
-!-  SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC   HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC   PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC   WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC   PROTEINS SUCH AS TRAF2, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC   TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC   ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC   NF-KAPPA B SIGNALING (BY SIMILARITY).
-!-  SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!-  SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
EMBL; M63122; G207362; -.
EMBL; G207362; -.
PIR; B36555; B36555.
HSSP; P19438; 1TNR.
PROSITE; PS00652; TNFR_NGFR_1; 3.
PROSITE; PS50050; TNFR_NGFR_2; 3.
PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS.
FT   SIGNAL        1     21    POTENTIAL.
FT   CHAIN        22    455    TUMOR NECROSIS FACTOR RECEPTOR 1.
FT   DOMAIN       22    211    EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    212    234    POTENTIAL.
FT   DOMAIN      235    461    CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       43    196    4 X TNFR-CYS.
FT   REPEAT       43     82    TNFR-CYS 1.
FT   REPEAT       83    125    TNFR-CYS 2.
FT   REPEAT      126    166    TNFR-CYS 3.
FT   REPEAT      167    196    TNFR-CYS 4.
FT   DOMAIN      363    448    DEATH DOMAIN.
FT   DISULFID     44     58    BY SIMILARITY.
FT   DISULFID     59     72    BY SIMILARITY.
FT   DISULFID     62     81    BY SIMILARITY.
FT   DISULFID     84     99    BY SIMILARITY.
FT   DISULFID    102    117    BY SIMILARITY.
FT   DISULFID    105    125    BY SIMILARITY.
FT   DISULFID    127    143    BY SIMILARITY.
FT   DISULFID    146    158    BY SIMILARITY.
FT   DISULFID    149    166    BY SIMILARITY.
FT   DISULFID    168    179    BY SIMILARITY.
FT   DISULFID    182    191    BY SIMILARITY.
FT   DISULFID    185    195    BY SIMILARITY.
FT   CARBOHYD     54     54    POTENTIAL.
FT   CARBOHYD    151    151    POTENTIAL.
FT   CARBOHYD    201    201    POTENTIAL.
SQ   SEQUENCE    461 AA;  50969 MW;  82768B08 CRC32;

Query Match      34.6%;  Score 809;  DB 1;  Length 461;
Best Local Similarity 68.8%;  Pred. No. 5.98e-164;
Matches 98;  Conservative 21;  Mismatches 24;  Indels 0;  Gaps 0;

Db   41  DNLCPQGKYAHPKNNSICCTKCHKGTIYLVSDCPSPGQETVCEVCGCDKGTFTASQNHVRQCL 100
         |::||||||:|| :||||||||||||||||| |||||:|| |: | ||:|||||::||:|||
Qy   23  DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRCL 82

Db  101  SCKTCRKEMFQVEISPCKRADMDTVCGCKRKQNQFQRYLSETHFQCVDCSPCFNGTVTIPCKE 160
         |||:|||||| ||:||| : |:||||||:|:|| :|| ||| ||:||:|||||:||::|
Qy   83  SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db  161  KQNTVCNCHAGFFLSGNECTPCS 183
         |||||| ||||||| :|||: |:
Qy  143  KONTVCTCHAGFFLRENECVSCA 165
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RESULT 7

ID   LSHB_HUMAN   STANDARD;   PRT;   141 AA.
AC   P01229;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT   01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE   LUTROPIN BETA CHAIN PRECURSOR (LUTEINIZING HORMONE) (LSH-B) (LH-B).
GN   LHB.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 84093590.
RA   TALMADGE K., VAMVAKOPOULOS N.C., FIDDES J.C.;
RL   NATURE 307:37-40(1984).
RN   [2]
RP   SEQUENCE OF 21-141.
RX   MEDLINE; 76062547.
RA   SAIRAM M.R., LI C.H.;
RL   BIOCHIM. BIOPHYS. ACTA 412:70-81(1975).
RN   [3]
RP   PRELIMINARY SEQUENCE OF 21-141.
RX   MEDLINE; 73090987.
RA   SHOME B., PARLOW A.F.;
RL   J. CLIN. ENDOCRINOL. METAB. 36:618-621(1973).
RN   [4]
RP   PRELIMINARY PARTIAL SEQUENCE.
RX   MEDLINE; 73221227.
RA   CLOSSET J., HENNEN G., LEQUIN R.M.;
RL   FEBS LETT. 29:97-100(1973).
RN   [5]
RP   STRUCTURE OF CARBOHYDRATE.
RX   MEDLINE; 91122088.
RA   WEISSHAAR G., HIYAMA J., RENWICK A.G.C., NIMTZ M.;
RL   EUR. J. BIOCHEM. 195:257-268(1991).
RN   [6]
RP   STRUCTURE BY NMR OF 58-77.
RX   MEDLINE; 92357029.
RA   KEUTMANN H.T., HUA Q.-X., WEISS M.A.;
RL   MOL. ENDOCRINOL. 6:904-913(1992).
RN   [7]
RP   VARIANT ARG-74.
RX   MEDLINE; 92085985.
RA   WEISS J., AXELROD L., WHITCOMB R.W., HARRIS P.E., CROWLEY W.F.,
RA   JAMESON J.L.;
RL   NEW ENGL. J. MED. 326:179-183(1992).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC   THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC   CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC   LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- TISSUE SPECIFICITY: PITUITARY.
CC   -!- DISEASE: DEFECTS IN LHB ARE A CAUSE OF HYPOGONADISM WHICH IS
CC   CHARACTERIZED BY INFERTILITY AND PSEUDOHERMAPHRODITISM.
DR   EMBL; X00264; E28368; -.
DR   EMBL; S71273; E91454; -.
DR   PIR; A01497; UTHUB.
DR   HSSP; P01233; 1HCN.
DR   MIM; 152780; -.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL; PSEUDOHERMAPHRODITISM;
KW   DISEASE MUTATION.
FT   SIGNAL   1   20
FT   CHAIN   21   141   LUTROPIN BETA CHAIN.
FT   DISULFID   29   77   BY SIMILARITY.
FT   DISULFID   43   92   BY SIMILARITY.
FT   DISULFID   46   130   BY SIMILARITY.
FT   DISULFID   54   108   BY SIMILARITY.
FT   DISULFID   58   110   BY SIMILARITY.
FT   DISULFID   113   120   BY SIMILARITY.
FT   CARBOHYD   50   50   BY SIMILARITY.

FT   VARIANT   74   74   Q -> R (IN HYPOGONADISM; LACK OF
FT   RECEPTOR-BINDING).
FT   CONFLICT   39   39   E -> Q (IN REF. 2).
FT   CONFLICT   76   76   MISSING (IN REF. 2).
FT   CONFLICT   132   135   HPQL -> A245776F CRC32;
FT   SEQUENCE   141 AA; 15345 MW; A245776F CRC32;

Query Match   31.6%; Score 740; DB 1; Length 141;
Best Local Similarity   84.4%;
Matches   92; Conservative   12; Mismatches   5; Indels   0; Gaps   0;

Db   27 PWCHPINAILAVEKEGCPVCITVNTTICAGYCPTMMRVLQAVLPPLPQVVCTYRDVRFES 86
               :|:|:||||:|||||:||||::||||||||||||:|||||:|||||||||||||||||||
Qy   169 PRCRPINATLAVEKEGCCPVCITVNTTICAGYCPTMRVLQGVLPALPQVVCNYRDVRFES 228

Db   87 IRLPGCPRGVDPVVSFPVALSCRCGPCRRSTSDCGGPKDHPLTCDDPRF 135
               ||||||||||||||||||:||||||||:|||||||||||||||||| |
Qy   229 IRLPGCPRGVNPVVSVAVALSCQCALCRRSTDCGGPKDHPLTCDDPRF 277

RESULT 8

ID   CGHB_CALJA   STANDARD;   PRT;   164 AA.
AC   P51500;
DT   01-OCT-1996 (REL. 34, CREATED)
DT   01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (CHORIONIC GONADOTROPHIN BETA
DE   SUBUNIT).
GN   CGB.
OS   CALLITHRIX JACCHUS (COMMON MARMOSET).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PLACENTA;
RX   MEDLINE; 96115012.
RA   SIMULA A.P., AMATO F., FAAST R., LOPATA A., BERKA J., NORMAN R.J.;
RL   BIOL. REPROD. 53:380-389(1995).
CC   -!- FUNCTION: STIMULATES THE OVARIES TO SYNTHESIZE THE STEROIDS THAT
CC   ARE ESSENTIAL FOR THE MAINTENANCE OF PREGNANCY.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC   CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC   LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- TISSUE SPECIFICITY: PLACENTA.
DR   EMBL; U04447; G606607; -.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL   1   20   BY SIMILARITY.
FT   CHAIN   21   164   CHORIOGONADOTROPIN BETA CHAIN.
FT   DISULFID   29   77   BY SIMILARITY.
FT   DISULFID   43   92   BY SIMILARITY.
FT   DISULFID   46   130   BY SIMILARITY.
FT   DISULFID   54   108   BY SIMILARITY.
FT   DISULFID   58   110   BY SIMILARITY.
FT   DISULFID   113   120   BY SIMILARITY.
FT   CARBOHYD   113   113   BY SIMILARITY.
FT   CARBOHYD   50   50   BY SIMILARITY.
FT   CARBOHYD   146   146   BY SIMILARITY.
FT   CARBOHYD   151   151   BY SIMILARITY.
SQ   SEQUENCE   164 AA; 17712 MW; E36A4DB3 CRC32;

Query Match   30.3%; Score 709; DB 1; Length 164;
Best Local Similarity   64.7%; Pred. No. 2.18e-139;
Matches   90; Conservative   25; Mismatches   23; Indels   1; Gaps   1;

Db   27 PLCRPVNAILAAEKEGCPVCVAFNTTICAGYCSSMRVLQTILPPLPQSVCNYHELRFTS 86
               |||::|| :||:|| ||||||:|:|||||||| ||:||:|||||||| ||| |||||:
Qy   169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMRVLQGVLPALPQVVCNYRDVRFES 228

Db   87 VRLPGCRPGVDPVVSMPVALSCRCGICRRSYSDCGSLRNEPLGCYSTFQDSSS-KDPPR 145
               :||||| |||:||:|||||||||:|| ||:||:|||| |:||||:|||| || ||
Qy   169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMRVLQGVLPALPQVVCNYRDVRFES 228

Db   87 IRLPGCPRGVNPVVSVAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 288

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Db   146  NLTSPSQLLEPADPPLVPQ 164
          :||:||| |:|:|||:|
Qy   289  SLPSPSRLPGPSDTIPLPQ 307


RESULT  9
ID   LSHB_EQUAS         STANDARD;     PRT;    169 AA.
AC   P19794;
DT   01-FEB-1991 (REL. 17, CREATED)
DT   01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   LUTROPIN/CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (LSH-B/CG-B).
GN   LHB.
OS   EQUUS ASINUS (DONKEY).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PERISSODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   CHOPINEAU M., COMBARNOUS Y., ALLEN W.R., STEWART F.;
RL   SUBMITTED (JUL-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN   [2]
RP   PRELIMINARY SEQUENCE OF 105-169 FROM N.A.
RC   TISSUE=PLACENTA;
RX   MEDLINE; 9062634.
RA   LEIGH S.E.A., STEWART F.;
RL   J. MOL. ENDOCRINOL. 4:143-150(1990).
RN   [-]
RP   SEQUENCE FROM N.A.
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
RX   EMBL; X80116; G510971; -.
EMBL; X53669; E27544; ALT_SEQ.
RA   LEIGH S.E.A., STEWART F.;
RL   PIR; S15676; S15676.
RP   HSSP; P01233; 1HCN.
PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL        1     20        BY SIMILARITY.
FT   CHAIN        21    169        LUTROPIN/CHORIOGONADOTROPIN BETA CHAIN.
FT   DISULFID     29     77        BY SIMILARITY.
FT   DISULFID     43     92        BY SIMILARITY.
FT   DISULFID     46    130        BY SIMILARITY.
FT   DISULFID     54    108        BY SIMILARITY.
FT   DISULFID     58    110        BY SIMILARITY.
FT   DISULFID    113    120        BY SIMILARITY.
FT   CARBOHYD    113     33        PROBABLE.
SQ   SEQUENCE   169 AA;  17943 MW;  9D4B5421 CRC32;
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Query Match             26.9%;    Score 630;   DB 1;   Length 169;
Best Local Similarity   63.4%;    Pred. No. 3.88e-120;
  Matches   85;  Conservative  21;  Mismatches  23;  Indels  5;  Gaps  4;

Qy   27   PLCRPINATLAAEKEACPICIIFTTSICAGYCRSMVRVMPAALPPIPQPVCTYRELRFGS  86
          |||||||||||||||||:||||||:||||:|||||::|| :|||||| ||||||||
Db   169  PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES  228

Qy   87   IRLPGCPPGVDPMVSFPVALSCHGPCRLKTTDCGGPRDHPLACA-P--QTSSSCKDPPS  143
          ||||||||||  |||||||  | |||||  ||||||  | |  |||| |  | |:|:::
Db   229  IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP  288

Qy   144  QPLTSTPTPGAS  157
          ::||: ||:|
Db   289  -SLPSPS-RLPGPS  300
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RESULT  10
ID   LSHB_BOVIN         STANDARD;     PRT;    141 AA.
AC   P04651;
DT   13-AUG-1987 (REL. 05, CREATED)
DT   01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   LUTROPIN BETA CHAIN PRECURSOR (LUTEINIZING HORMONE) (LSH-B) (LH-B).
GN   LHB.
OS   BOS TAURUS (BOVINE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; ARTIODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 85207729.
RA   VIRGIN J.B., SILVER B.J., THOMASON A.R., NILSON J.H.;
RL   J. BIOL. CHEM. 260:7072-7077(1985).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 85182575.
RA   MAURER R.A.;
RL   J. BIOL. CHEM. 260:4684-4687(1985).
RN   [3]
RP   SEQUENCE OF 21-139.
RX   MEDLINE; 74075724.
RA   MAGHUIN-ROGISTER G., HENNEN G.;
RL   EUR. J. BIOCHEM. 39:235-253(1973).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   EMBL; M10077; G163301; -.
EMBL; M11506; G163299; -.
PIR; A01499; UTBOB.
HSSP; P01233; 1HCN.
PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   HORMONE; SIGNAL; GLYCOPROTEIN.
FT   SIGNAL        1     20
FT   CHAIN        21    141        LUTROPIN BETA CHAIN.
FT   DISULFID     29     77        BY SIMILARITY.
FT   DISULFID     43     92        BY SIMILARITY.
FT   DISULFID     46    130        BY SIMILARITY.
FT   DISULFID     54    108        BY SIMILARITY.
FT   DISULFID     58    110        BY SIMILARITY.
FT   DISULFID    113    120        BY SIMILARITY.
FT   CARBOHYD    113     33        BY SIMILARITY.
FT   CONFLICT      1      2        MISSING (IN REF. 2).
FT   CONFLICT     74     74        Q -> E (IN REF. 3).
FT   CONFLICT    112    112        P -> S (IN REF. 2).
FT   CONFLICT    122    122        GP -> PG (IN REF. 3).
FT   CONFLICT    126    126        Q -> E (IN REF. 3).
SQ   SEQUENCE   141 AA;  15202 MW;  82879D1F CRC32;
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Query Match             26.2%;    Score 614;   DB 1;   Length 141;
Best Local Similarity   64.9%;    Pred. No. 2.94e-116;
  Matches   72;  Conservative  22;  Mismatches  17;  Indels  0;  Gaps  0;

Qy   27   PLCQPINATLAAEKEACPVCIIFTTSICAGYCPSMKRVLPVILPPMPQRVCTYHELRFAS  86
          | :|||||||||:||||||:|||||:||||||:| || ||||||| || || |:||||
Db   169  PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES  228

Qy   87   VRLPGCPPGVDPMVSFPVALSCHGGPCRLSSTDCGGPRTQPLACDHPPLPD  137
          :||||||  ||||||:||||||  |:|| ||||||| || :|  | ||: |
Db   229  IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQD  279
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RESULT  11
ID   LSHB_HORSE         STANDARD;     PRT;    169 AA.
AC   P08751; P01234;
DT   01-AUG-1988 (REL. 08, CREATED)
DT   01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   LUTROPIN/CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (LSH-B/CG-B).
GN   LHB.
OS   EQUUS CABALLUS (HORSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PERISSODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
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Column 1

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RX   MEDLINE; 92357035.
RA   SHERMAN G.B., WOLFE M.W., FARMERIE T.A., CLAY C.M.,
RA   THREADGILL D.S., SHARP D.C., NILSON J.H.;
RL   MOL. ENDOCRINOL. 6:951-959(1992).
RN   [2]
RP   SEQUENCE OF 21-169.
RX   MEDLINE; 87250476.
RA   BOUSFIELD G.R., LIU W.-K., SUGINO H., WARD D.N.;
RL   J. BIOL. CHEM. 262:8610-8620(1987).
RN   [3]
RP   SEQUENCE OF 21-169.
RX   MEDLINE; 87250475.
RA   SUGINO H., BOUSFIELD G.R., MOORE W.T. JR., WARD D.N.;
RL   J. BIOL. CHEM. 262:8603-8609(1987).
RN   [4]
RP   CHORIOGONADOTROPIN, PARTIAL SEQUENCE.
RA   WARD D.N., MOORE W.T. JR., WARD D.N., BURLEIGH B.D.;
RL   J. PROTEIN CHEM. 1:263-280(1982).
RN   [5]
RP   STRUCTURE OF CARBOHYDRATES.
RX   MEDLINE; 90235854.
RA   DAMM J.B.L., HARD K., KAMERLING J.P., VAN DEDEM G.W.K.,
RA   VLIEGENTHART J.F.G.;
RL   EUR. J. BIOCHEM. 189:175-183(1990).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- PTM: AT LEAST FOUR O-GLYCOSYLATION SITES ARE PRESENT.
DR   EMBL; S41704; G252741; -.
DR   PIR; A01503; KTHOB.
DR   PIR; A29304; A29304.
DR   PIR; A29305; A29305.
DR   PIR; A41917; A41917.
DR   HSSP; P01233; 1HCN.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL        1     20
FT   CHAIN        21    169       LUTROPIN/CHORIOGONADOTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   CARBOHYD     33     33       GLYCAN SHOWING A REMARKABLY STRUCTURAL
FT                                HETEROGENEITY.
SQ   SEQUENCE   169 AA;  17865 MW;  9AB1CAA3 CRC32;

Query Match     26.2%;  Score 613;  DB 1;  Length 169;
Best Local Similarity   62.7%;
Matches  84;  Conservative  22;  Mismatches  23;  Indels   5;  Gaps   4;

Db    27 PLCRPINATLAAEKEACPICITFTTSICAGYCPSMVRVMPAALPAIPQPVCTYRELRFAS 86
          |||||||||||||||:|||  |||||||||||| ::|||  || ||:|| || ||| ||||
Qy   169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

Db    87 IRLPGCPGVDPMVSFPVALSCHGPCQIKTTDCGVFRDQPLACA-P--QASSSSKDPPS 143
          |||||||| | | ||| || |||:| |||| ||| ||||| | |
Qy   229 IRLPGCPRQVNPVVSYAVALSCCQALCRSSTTDCGGPKDHPLTCDDPRRQDSSSSSKAPP 288

Db   144 QPLTSTSTPTPGAS 157
          :| |||
Qy   289 -SLPSPS-RLPGPS 300
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Column 2

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DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   LUTROPIN BETA CHAIN PRECURSOR (LUTEINIZING HORMONE) (LSH-B) (LH-B).
OS   OVIS ARIES (SHEEP).
GN   LHB.
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; ARTIODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 93351742.
RA   BROWN P., MCNEILLY J.R., WALLACE R.M., MCNEILLY A.S., CLARK A.J.;
RL   MOL. CELL. ENDOCRINOL. 93:157-165(1993).
RN   [2]
RP   SEQUENCE OF 21-139.
RC   TISSUE=PITUITARY;
RX   MEDLINE; 90245669.
RA   D'ANGELO-BERNARD G., MOUMNI M., JUTISZ M., COUNIS R.;
RL   NUCLEIC ACIDS RES. 18:2175-2175(1990).
RN   [3]
RP   SEQUENCE OF 21-139.
RX   MEDLINE; 72211145.
RA   LIU W.-K., NAHM H.S., SWEENEY C.M., HOLCOMB G.N., WARD D.N.;
RL   J. BIOL. CHEM. 247:4365-4381(1972).
RN   [4]
RP   SEQUENCE OF 21-139.
RA   SAIRAM M.R., SAMY T.S.A., PAPKOFF H., LI C.H.;
RL   ARCH. BIOCHEM. BIOPHYS. 153:572-586(1972).
RN   [5]
RP   STRUCTURE OF CARBOHYDRATE.
RX   MEDLINE; 91006170.
RA   WEISSHAAR G., HIYAMA J., RENWICK A.G.C.;
RL   EUR. J. BIOCHEM. 192:741-751(1990).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   EMBL; S64695; G408241; -.
DR   EMBL; X52408; G1320; -.
DR   PIR; A01500; UTSHB.
DR   PIR; S09232; S09232.
DR   HSSP; P01233; 1HCN.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   HORMONE; SIGNAL; GLYCOPROTEIN.
FT   SIGNAL        1     20
FT   CHAIN        21    141       LUTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   CARBOHYD     33     33       BY SIMILARITY.
FT   MOD_RES      21     21       BLOCKED.
FT   VARIANT     138    141       MISSING (IN SOME MOLECULES).
FT   CONFLICT     30     30       Q -> E (IN REF. 4).
FT   CONFLICT     59     59       L -> P (IN REF. 1).
FT   CONFLICT     63     63       R -> P (IN REF. 2).
FT   CONFLICT     71     72       PM -> PPM (IN REF. 4).
FT   CONFLICT     81     81       E -> Q (IN REF. 4).
FT   CONFLICT    122    123       GP -> PG (IN REF. 3 AND 4).
FT   CONFLICT    126    126       Q -> E (IN REF. 3 AND 4).
SQ   SEQUENCE   141 AA;  15184 MW;  BA2C0204 CRC32;

Query Match     25.7%;  Score 602;  DB 1;  Length 141;
Best Local Similarity   64.0%;
Matches  71;  Conservative  22;  Mismatches  18;  Indels   0;  Gaps   0;

Db    27 PLCQPINATLAAEKEACPVCITFTTSICAGYCLSMKRVLPVILPMPQRVCTYHELRFAS 86
          |||:||||||||||||||:||||||||||||| ::|||::| ||:|| || |||:||||
Qy   169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228
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Db    87  VRLPGCPPGVDPMYSFPVALSCHCGPCRLSSTDCGGPRTOPLACHPPLPD 137
          ||||||| ||:|||:|:|:|:||::||||:|:: || :|||||||: :|||||:|||| ||
Qy   229  IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQD 279
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RESULT  13
ID      LSHB_PIG                    STANDARD;        PRT;    141 AA.
AC      P01232;
DT      21-JUL-1986 (REL. 01, CREATED)
DT      01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT      01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE      LUTROPIN BETA CHAIN PRECURSOR (LUTEINIZING HORMONE) (LSH-B) (LH-B).
GN      LHB.
OS      SUS SCROFA (PIG).
OC      EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC      EUTHERIA; ARTIODACTYLA.
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE; 91063934.
RA      EZASHI T., HIRAI T., KATO T., WAKABAYASHI K., KATO Y.;
RL      J. MOL. ENDOCRINOL. 5:137-146(1990).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE; 89306142.
RA      KATO Y., HIRAI T.;
RL      MOL. CELL. ENDOCRINOL. 62:47-53(1989).
RN      [3]
RP      SEQUENCE OF 21-139.
RX      MEDLINE; 74075724.
RA      MAGHUIN-ROGISTER G., HENNEN G.;
RL      EUR. J. BIOCHEM. 39:235-253(1973).
CC      -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC          THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC      -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC          CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC          LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR      EMBL; D00579; G217694; -.
DR      PIR; A30322; UTPGB.
DR      PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR      PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW      HORMONE; SIGNAL; GLYCOPROTEIN.
FT      SIGNAL        1     20
FT      CHAIN        21    141       LUTROPIN BETA CHAIN.
FT      DISULFID     29     77       BY SIMILARITY.
FT      DISULFID     43     92       BY SIMILARITY.
FT      DISULFID     46    130       BY SIMILARITY.
FT      DISULFID     54    108       BY SIMILARITY.
FT      DISULFID     58    110       BY SIMILARITY.
FT      DISULFID    113    120       BY SIMILARITY.
FT      CARBOHYD     33              BY SIMILARITY.
FT      CONFLICT     40     40       N -> Z.
FT      CONFLICT     30     30       R -> Z.
FT      VARIANT      21     21       BLOCKED.
FT      CONFLICT     62     62       N -> D (IN REF. 3).
FT      CONFLICT     62     62       V -> R (IN REF. 3).
FT      CONFLICT     83     83       S -> I (IN REF. 3).
FT      CONFLICT     87     87       I -> S (IN REF. 3).
FT      CONFLICT    122    123       GP -> PG (IN REF. 3).
SQ      SEQUENCE    141 AA;   14889 MW;  DA2EF539 CRC32;
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Query Match             25.5%;       Score 598;  DB 1;  Length 141;
Best Local Similarity   66.4%;       Pred. No. 2.19e-112;
          Matches  71;  Conservative  19;  Mismatches 17;  Indels  0;  Gaps  0;
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Db    27  PLCRPINATLAAAENEACPVCITFTTSICAGYCPSMVRVLPAALPPVPQPVCTYRELSFAS 86
          ||||||| |:|||||||:||||||||||||||||||||| || :||||:|||||| || |||
Qy   169  PRCRPINATLAVEKEGCPVCITVNTICAGYCPTMRVLQGVLPALPQVVCNYRDVRFES 228
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Db    87  IRLPGCPPGVDPTVSFPPVALSCHCGPCRLSSSDCGGPRAQPLACDRP 133
          |||||| ||:||||:|||:|||||||||||||||||||||||:|||||:|
Qy   229  IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDP 275
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RESULT  14
ID      LSHB_RAT                    STANDARD;        PRT;    141 AA.
AC      P01230;
DT      21-JUL-1986 (REL. 01, CREATED)
DT      21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT      01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE      LUTROPIN BETA CHAIN PRECURSOR (LUTEINIZING HORMONE) (LSH-B) (LH-B).
GN      LHB.
OS      RATTUS NORVEGICUS (RAT).
OC      EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC      EUTHERIA; RODENTIA.
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE; 85080043.
RA      JAMESON L., CHIN W.W., HOLLENBERG A.N., CHANG A.S., HABENER J.F.;
RL      J. BIOL. CHEM. 259:15474-15480(1984).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE; 83273673.
RA      CHIN W.W., GODINE J.E., KLEIN D.R., CHANG A.S., TAN L.K.,
RA      HABENER J.F.;
RL      PROC. NATL. ACAD. SCI. U.S.A. 80:4649-4653(1983).
RN      [3]
RP      SEQUENCE OF 4-141 FROM N.A.
RA      KATO Y., EZASHI T., HIRAI T., KATO T.;
RL      ZOOL. SCI. 7:877-885(1990).
RC      STRAIN=WISTAR-IMAMICHI; TISSUE=ANTERIOR PITUITARY;
CC      -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC          THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC      -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC          CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC          LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR      EMBL; V01542; G758262; -.
DR      EMBL; J00749; G205176; -.
DR      EMBL; D00576; G220808; -.
DR      PIR; A01498; UTRTB.
DR      HSSP; P01233; 1HCN.
DR      PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR      PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW      HORMONE; SIGNAL; GLYCOPROTEIN.
FT      SIGNAL        1     20
FT      CHAIN        21    141       LUTROPIN BETA CHAIN.
FT      DISULFID     29     77       BY SIMILARITY.
FT      DISULFID     43     92       BY SIMILARITY.
FT      DISULFID     46    130       BY SIMILARITY.
FT      DISULFID     54    108       BY SIMILARITY.
FT      DISULFID     58    110       BY SIMILARITY.
FT      DISULFID    113    120       BY SIMILARITY.
FT      CARBOHYD     33              PROBABLE.
SQ      SEQUENCE    141 AA;   15177 MW;  6E0C19BA CRC32;
```

```
Query Match             25.5%;       Score 597;  DB 1;  Length 141;
Best Local Similarity   64.2%;       Pred. No. 3.82e-112;
          Matches  70;  Conservative  23;  Mismatches 16;  Indels  0;  Gaps  0;
```

```
Db    27  PLCRPVNATLAAAENECFCPVCITFFTSICAGYCPSMVRVLPAALPPPVPQPVCTYRELRFAS 86
          ||||| |:||||||:| ||||||:||||||||||||| |||: :||||||||:|||||| ||
Qy   169  PRCRPINATLAVEKEGCPVCITVNTICAGYCPTMRVLQGVLPALPQVVCNYRDVRFES 228
```

```
Db    87  VRLPGCPPGVDPIVSFPVALSCRCGPCRLSSSDCGGPRTOPMTCDLPHL 135
          |||||| |||:||||:|||||||:|||||||||||||||||||:||||:||
Qy   229  IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRF 277
```

```
RESULT  15
ID      LSHB_BALAC                  STANDARD;        PRT;    118 AA.
AC      P33088;
DT      01-OCT-1993 (REL. 27, CREATED)
DT      01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
DT      01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
```

```
DE   LUTROPIN BETA CHAIN (LUTEINIZING HORMONE) (LSH-B) (LH-B).
GN   LHB.
OS   BALAENOPTERA ACUTOROSTRATA (MINKE WHALE) (LESSER RORQUAL).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; CETACEA.
RN   [1]
RP   SEQUENCE.
RA   KARASEV V.S., PANKOV Y.A.;
RL   BIOKHIMIIA 50:1972-1986(1985).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   PIR; PN0139; PN0139.
DR   HSSP; P01233; 1HCN.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; FALSE_NEG.
KW   HORMONE; GLYCOPROTEIN.
FT   DISULFID      9     57       BY SIMILARITY.
FT   DISULFID     23     72       BY SIMILARITY.
FT   DISULFID     26    110       BY SIMILARITY.
FT   DISULFID     34     88       BY SIMILARITY.
FT   DISULFID     38     90       BY SIMILARITY.
FT   DISULFID     93    100       BY SIMILARITY.
FT   CARBOHYD     13             BY SIMILARITY.
SQ   SEQUENCE    118 AA;  12414 MW;  DE251ECF CRC32;
```

Query Match   25.4%;   Score 595; DB 1; Length 118;
Best Local Similarity   60.6%;   Pred. No. 1.16e-111;
Matches   66;   Conservative   25;   Mismatches   17;   Indels   1;   Gaps   1;

```
Db      7  PLCRPINATLAAZBZACPVCITFTTSICAGYCPSMVRVLPAALPPVPZPVCTYRZLRFAS  66
           | ||||||||     | :::::||||||    | ::| ||| :||:  || | ||::||
Qy    169  PRCRPINATLAVEKEGCPVCITVNTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

Db     67  IRLPGCPPGVBPMVSFPVALSCHCGPCRLSSSBCGPGRAZPLACBRSPR 115
           |||||||||  ||:||:||::||:||||| || |::::||  :|||||:| ||
Qy    229  IRLPGCPRGVNPVVSYAVALSCQCALCRSTTDCGGPKDHPLTCD-DPR 276
```

Search completed: Wed May 6 08:53:30 1998
Job time : 19 secs.

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*****************************************************
*****************************************************
**                                                 **
**   M  M  PPPP   SSSS  RRRR    CCC  H   H         **
**   MM MM  P   P  S     R   R  C     H   H        **
**   M M M  PPPP   SSSS  RRRR   C     HHHHH   (TM) **
**   M   M  P         S  R  R   C     H   H        **
**   M   M  P     SSSS   R   R   CCC  H   H        **
**                                                 **
*****************************************************
*****************************************************
```

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MPsrch_pp   protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 6 08:53:48 1998;   MasPar time 15.81 Seconds
                                               817,861 Million cell updates/sec
Tabular output not generated.

Title: >US-08-804-166-4
Description: (1-307) from US08804166.pep
Perfect Score: 2341
Sequence: 1 SRTSLLLAFGLLCLPWLQEG..........PSLPSPSRLPGPSDTPILPQ 307

Scoring table: PAM 150
                 Gap 11

Searched: 140555 seqs, 4210429 residues

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database: sptrembl5
                 1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
                 5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
                 9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
                 13:sp_unclassified

Statistics: Mean 42.863; Variance 77.650; scale 0.552

                 Pred. No. is the number of results predicted by chance to have a
                 score greater than or equal to the score of the result being printed,
                 and is derived by analysis of the total score distribution.

                              SUMMARIES

```
Result              %    Query
No.   Score  Match  Length  DB  ID        Description                        Pred. No.
----  -----  -----  ------  --  --         -----------                        --------
  1   1024   43.7    145     2  Q13991     BETA-GONADOTROPIN.                  1.26e-200
  2   1024   43.7    165     2  Q14000     CHORIONIC GONADOTROPIN              1.26e-200
  3    945   40.2    180     4  Q95185     CHORIONIC GONADOTROPIN              1.78e-182
  4    895   38.2    471     4  Q19131     TUMOUR NECROSIS FACTOR-             5.05e-171
  5    596   25.5    135     4  Q19102     LUTEINIZING HORMONE BE             2.46e-103
  6    595   25.5    139    10  Q62778     TESTICULAR LUTEINIZING             4.12e-103
  7    582   24.9    141    10  Q60844     LUTEINIZING HORMONE BE             3.27e-100
  8    430   18.4    140    12  Q98849     GONADOTROPIN II BETA S             9.70e-67
  9    391   16.7    80     10  Q63013     TESTICULAR LUTEINIZING             2.54e-58
 10    361   15.4    147    12  Q91121     GONADOTROPIN II BETA S             6.54e-58
 11    353   15.1    137    12  Q90225     GONADOTROPIN BETA-SUBU             3.27e-50
 12    321   13.7    130    12  Q13050     GONADOTROPIN I BETA SU             1.80e-43
 13    314   13.4    138     4  P79357     GONADOTROPIN I BETA CHAIN          5.23e-42
 14    312   13.3    130    12  Q98848     GONADOTROPIN I BETA SU             1.37e-41
 15    311   13.3    138     2  Q16163     TESTICULAR LUTEINIZING             2.21e-41
 16    310   13.2    150    12  Q13051     THYROID-STIMULATING HO             2.21e-41
 17    301   12.9    150    12  Q13052     THYROTROPIN BETA SUBUN             7.41e-39
 18    294   12.5    147    12  Q28376     THYROTROPIN BETA CHAIN             3.57e-41
 19    289   12.3    150    12  Q13049     THYROTROPIN BETA SUBUN             7.96e-37
 20    271   11.6    101    10  Q62590     BETA-THYROTROPIN (FRAG             3.87e-33
 21    253   10.8    163     2  O14866     SOLUBLE DEATH RECEPTOR             1.71e-29
 22    253   10.8    163     2  O14865     DEATH RECEPTOR 3 BETA.             1.71e-29
 23    253   10.8    180     2  O00276     LYMPHOCYTE ASSOCIATED              1.72e-28
 24    248   10.6    253     2  O00280     LYMPHOCYTE ASSOCIATED              1.72e-28
 25    248   10.6    418     2  O00275     LYMPHOCYTE ASSOCIATED              1.72e-28
 26    248   9.1     348    11  O85407     HOMOLOG OF VACINIA VI              8.90e-22
 27    214   9.1     349    11  O89098     GARCIA-1966 RIGHT NEAR             8.90e-22
 28    214   9.1     349    11  O89118     SOMALIA-1977 RIGHT NEA             8.90e-22
 29    210   9.0     87      2  Q15962     THYROTROPIN BETA SUBUN             5.30e-21
 30    210   9.0     355    11  O85308     SECRETED RECEPTOR BIND             5.30e-21
 31    205   8.8     61     10  O63012     TESTICULAR LUTEINIZING             4.88e-20
 32    205   8.8     267     4  O62327     TUMOR NECROSIS FACTOR              3.13e-20
 33    187   8.0     459    10  O14755     OX40 PRECURSOR (FRAGME             1.29e-16
 34    182   7.8     283     2  O02764     TRAIL RECEPTOR 3.                  1.11e-15
 35    180   7.7     283     2  O02956     HERPESVIRUS ENTRY MEDI             2.61e-15
 36    180   7.7     299     2  O14798     CYTOTOXIC TRAIL RECEPT             2.61e-15
 37    178   7.6     324    10  O63199     FAS ANTIGEN PRECURSOR.             4.00e-15
 38    179   7.6     425     2  O16042     TUMOR NECROSIS FACTOR              4.00e-15
 39    167   7.1     202     2  O14405     SOMATOTROPIN PRECURSOR             6.39e-13
 40    167   7.1     217     2  O16631     SOMATOTROPIN PRECURSOR             6.39e-13
 41    163   7.0     411     2  O14720     DEATH RECEPTOR 5.                  3.38e-12
 42    163   7.0     411     2  O15508     P53-REGULATED DNA DAMA             3.38e-12
 43    163   7.0     411    10  O15517     CYTOTOXIC TRAIL RECEPT             3.38e-12
 44    163   7.0     440     2  O15531     APOPTOSIS INDUCING PRO             3.38e-12
 45    163   7.0     440     2  O14763     APOPTOSIS INDUCING REC             3.38e-12
```

                              ALIGNMENTS

```
RESULT  1
ID       Q13991       PRELIMINARY;    PRT;    145 AA.
AC       Q13991;
DT       01-NOV-1996 (TREMBLREL. 01, CREATED)
DT       01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT       01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE       BETA-GONADOTROPIN.
OS       HOMO SAPIENS (HUMAN).
OC       EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC       EUTHERIA; PRIMATES.
RN       [1]
RP       SEQUENCE FROM N.A.
RX       MEDLINE; 84093590.
RA       TALMADGE K., VAMVAKOPOULOS N.C., FIDDES J.C.;
RL       NATURE 307:37-40(1984).
DR       EMBL; X00266; E27486; -.
KW       SIGNAL.
SQ       SEQUENCE   145 AA;  15488 MW;  AC321C60 CRC32;
```

```
Query Match             43.7%;  Score 1024;  DB 2;  Length 145;
Best Local Similarity   99.3%;
Matches  138;  Conservative   0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy         7 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 66
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         7 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 66

Qy       169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        67 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQASSSKAPP 126

Qy       229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRRQDSSSSKAPPP 288
             |||||||||||||||||||||||||||||||| ||||||||||||||| |||||||||||
Db       127 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQASSSSKAPP 145

Qy       289 SLPSPSRLPGPSDTPILPQ 307
             |||||||||||||||||||
Db       163 SLPSPSRLPGPSDTPILPQ 181
```

```
RESULT  2
ID       Q14000       PRELIMINARY;    PRT;    165 AA.
AC       Q14000;
DT       01-NOV-1996 (TREMBLREL. 01, CREATED)
DT       01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT       01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
```

```
DE   CHORIONIC GONADOTROPIN BETA SUBUNIT.
GN   CGB.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 84008141.
RA   POLICASTRO P., OVITT C.E., HOSHINA M., FUKUOKA H., BOOTHBY M.R.,
RA   BOIME I.;
RL   J. BIOL. CHEM. 258:11492-11499(1983).
DR   EMBL; K03183; G180444; -.
DR   EMBL; K00092; G180444; JOINED.
DR   EMBL; K03182; G180444; JOINED.
SQ   SEQUENCE   165 AA;  17729 MW;  B1CAA0B1 CRC32;

Query Match             43.7%;  Score 1024;  DB 2;  Length 165;
Best Local Similarity   99.3%;
Matches  138;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Qy   27 PRCRPINATLAVEKEGCPVCITVNTIICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 86
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  169 PRCRPINATLAVEKEGCPVCITVNTIICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

Db   87 IRLPGCPRGVNPVVSYAVALSCQOALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 146
         |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Qy  229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 288

Db  147 SLPSPSRLPGPSDTPILPQ 165
         |||||||||||||||||||
Qy  289 SLPSPSRLPGPSDTPILPQ 307
```

RESULT 3
```
ID   Q95185      PRELIMINARY;  PRT;  180 AA.

AC   Q95185;
DT   01-FEB-1997 (TREMBLREL. 02, CREATED)
DT   01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   TUMOUR NECROSIS FACTOR RECEPTOR P60 (FRAGMENT).
OS   FELIS SILVESTRIS CATUS (CAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; CARNIVORA.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   DUTHIE S., NASIR L., ECKERSALL P.D.;
RL   SUBMITTED (OCT-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U72344; G1613880; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
FT   NON_TER        1       1
FT   NON_TER      180     180
SQ   SEQUENCE   180 AA;  20399 MW;  5452A6B2 CRC32;

Query Match             40.4%;  Score 945;  DB 4;  Length 180;
Best Local Similarity   86.0%;
Matches  117;  Conservative   9;  Mismatches  10;  Indels   0;  Gaps   0;

Qy   45 CPQGKYIHPQDNSICCTKCHKGTYLYNDCAGPGLDTDCRECENGTFTASENYLRQCLSCS 104
         |||||||||| |||||||||||||||||||  || | |||||||||||||||| || |||
Db   26 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDDDCRECESGSFTASENHLRHCLSCS 85

Db  105 KCRKEMYQVEISPCTYVRDTVCGCRKNQYRYWSETHFQCLNCSLCLNGTVYQISCKETQN 164
         |||||| |||||||||||||||||||||||||||||:  :||:|||||||||| ::|:|
Qy   86 KCRKEMQVEISPCTYVRDTVCGCRKNQYRYWSENLFQCFNCSLCLNGTVHLSCQEKQN 145

Db  165 TVCTCHAGFFLRGNEC 180
         |||||||||||| |||
Qy  146 TVCTCHAGFFLRENEC 161
```

RESULT 4
```
ID   O19131      PRELIMINARY;  PRT;  471 AA.

AC   O19131;
DT   01-JAN-1998 (TREMBLREL. 05, CREATED)
DT   01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   TUMOUR NECROSIS FACTOR-RECEPTOR I.
GN   TNF-RI.
OS   BOS TAURUS (BOVINE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; ARTIODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=AORTA;
RA   LEE E.-K., TALYOR M.J., KEHRLI M.E.;
RL   SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U90937; G2290398; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
SQ   SEQUENCE   471 AA;  51368 MW;  1D60FF4A CRC32;

Query Match             38.2%;  Score 895;  DB 4;  Length 471;
Best Local Similarity   73.2%;
Matches  104;  Conservative  21;  Mismatches  17;  Indels   0;  Gaps   0;

Qy   41 ESPCPQGKYIHPQDNSICCTKCHKGTYLYNDCPGPGPRDTTDCRVCAPGTYTALENHLRRCL 100
         : |||||||||| |||||||||||||||||: ::|| ||:|||||||||||||::|:|||:||
Db   23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDDDCRECESGSFTASENHLRHCL 82

Db  101 SCSRCRDEMFQVEISPCVVDRDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQE 160
         |||:||::| :||||:|:||||||||||||||||: ||| | |||||||||:|||| :||
Qy   83 SCSKCRKEMQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142
```

RESULT 5
```
ID   O19102      PRELIMINARY;  PRT;  135 AA.

AC   O19102;
DT   01-JAN-1998 (TREMBLREL. 05, CREATED)
DT   01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   LUTEINIZING HORMONE BETA SUBUNIT (FRAGMENT).
OS   CERATOTHERIUM SIMUM (WHITE RHINOCEROS) (SQUARE-LIPPED RHINOCEROS).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PERISSODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PITUITARY GLAND;
RA   SHERMAN G.B., LUND L.A.;
RL   MEDLINE; 97449288.
RA   SHERMAN G.B., LUND L.A., BUNICK D., WINN R.J.;
RN   [2]
RL   GENE 195:131-139(1997).
RC   TISSUE=PITUITARY GLAND;
RA   SHERMAN G.B., LUND L.A.;
RL   SUBMITTED (SEP-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U72659; G2462779; -.
FT   NON_TER        1       1
SQ   SEQUENCE   135 AA;  14212 MW;  F4F196D2 CRC32;

Query Match             25.5%;  Score 596;  DB 4;  Length 135;
Best Local Similarity   66.4%;
Matches   71;  Conservative  20;  Mismatches  16;  Indels   0;  Gaps   0;

Qy   21 PLCRPINATLAAENEACPVCIIFFTTSICCAGYCPSMVRVLPAALPPARQPVCITYHELRFAS 80
         | |||||||| ::||:|||||::    :||||||||:||||:  ||| || ||| : ||:||
Db  169 PRCRPINATLAVEKEGCPVCITVNTIICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

Qy   81 IRLPGCPPGVDPMVSFPVALSCRCGPCRLSSSDCGGPRAQPLACDRP 127
         |||||||  || || |:|||||:|| ||  |::|||||  | ||:
Db   81 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPP 
```

Qy 229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDP 275

RESULT 6
ID   Q62778   PRELIMINARY;   PRT;   139 AA.
AC   Q62778;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE   TESTICULAR LUTEINIZING HORMONE BETA-SUBUNIT.
GN   TLHB1.
OS   RATTUS NORVEGICUS (RAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE DAWLEY;
RX   MEDLINE; 95283549.
RA   ZHANG F.P., RANNIKKO A., HUHTANIEMI I.;
RL   BIOCHEM. BIOPHYS. RES. COMMUN. 210:858-865(1995).
DR   EMBL; U25653; G915217; -.
SQ   SEQUENCE 139 AA; 14880 MW; 5B2E7DBF CRC32;

Query Match   25.4%; Score 595; DB 10; Length 139;
Best Local Similarity   63.3%;
Matches   69; Conservative 24; Mismatches 16; Indels   0; Gaps   0;

Qy 229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDP 277
            |||||| |||::|:||||||:|:||:|||||||||| ||:|| |:
Db   85 VRLPGPPGVDPIVSFPVALSCRCGPCRLSSSDCGGPRTQPMTCDLPHL 133

RESULT 7
ID   Q60844   PRELIMINARY;   PRT;   141 AA.
AC   Q60844;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   LUTEINIZING HORMONE BETA (LUTEINIZING HORMONE BETA-SUBUNIT).
GN   LHB.
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129 SVEV;
RA   KAPUR V., MATZUK M.M.;
RL   SUBMITTED (AUG-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U25145; G9303045; -.
DR   MGD; MGI:96782; LHB.
SQ   SEQUENCE 141 AA; 15028 MW; BE50AB2B CRC32;

Query Match   24.9%; Score 582; DB 10; Length 141;
Best Local Similarity   62.4%; Pred. No. 3.27e-100;
Matches   68; Conservative 24; Mismatches 17; Indels   0; Gaps   0;

Qy   27 PLCRPVNATLAAENEFCPVCITFTTSICAGYCPSMVRVLPAALPPVPQPVCTYRELAFAS 86
            ||:||||:|| ::|:|||||||||||||:|::|| | |:||||:|| ||:|| |||| |
Db   25 PLCRPVNATLAAENEFCPVCITFTTSICAGYCPSMVRILPAALPPVPQPVCTYRELAFAS 84

Qy 169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228
            |::|||||:|:||:|:|||||||::|||||||:|:||||||:|:||||||||||||||
Db 169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

Qy 229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRF 277
            ||||| |||:|:|||||||:|:||:|||||||||||| ||:|| |::
Db   85 VRLPGPPGVDPIVSFPVALSCRCGPCRLSSSDCGGPRTQPMTCDLPHL 135

RESULT 8
ID   Q98849   PRELIMINARY;   PRT;   140 AA.
AC   Q98849;
DT   01-FEB-1997 (TREMBLREL. 02, CREATED)
DT   01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
DT   01-FEB-1997 (TREMBLREL. 02, LAST ANNOTATION UPDATE)
DE   GONADOTROPIN II BETA SUBUNIT PRECURSOR.
OS   CARASSIUS AURATUS (GOLDFISH).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OC   OSTEICHTHYES; ACTINOPTERYGII; CYPRINIFORMES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PITUITARY GLAND;
RA   YOSHIURA Y., KOBAYASHI M., KATO Y., AIDA K.;
RL   SUBMITTED (OCT-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; D88024; G1644243; -.
KW   SIGNAL.
FT   SIGNAL   1   23
FT   CHAIN   24   140   GONADOTROPIN II BETA SUBUNIT.
SQ   SEQUENCE 140 AA; 15533 MW; 7205FD03 CRC32;

Query Match   18.4%; Score 430; DB 12; Length 140;
Best Local Similarity   50.0%; Pred. No. 9.70e-67;
Matches   54; Conservative 22; Mismatches 32; Indels   0; Gaps   0;

Qy   27 PPCEPVNETVAVEKEGCPKCLVLQTTICSGHCLTKEPVYKSPFSTVYQHVCTYRDVRYET 86
            | ||||| :|||::|| ||:| |||:|: |:| ||:::|||:|::|::|| |||||| |
Db   87 VRLPDCPGVDPHITYPVALSCDCGSLCTMDTSDCTIESLQPDFCMSQR 134

Qy 169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228
            |::|||||:|:||:|:|||||||::|||||||:|:|||||||:||||||||||||||||
Db 169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

RESULT 9
ID   Q63013   PRELIMINARY;   PRT;   80 AA.
AC   Q63013;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE   TESTICULAR LUTEINIZING HORMONE BETA SUBUNIT.
GN   TLHB3.
OS   RATTUS NORVEGICUS (RAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE DAWLEY;
RX   MEDLINE; 95283549.
RA   ZHANG F.P., RANNIKKO A., HUHTANIEMI I.;
RL   BIOCHEM. BIOPHYS. RES. COMMUN. 210:858-865(1995).
DR   EMBL; U25803; G904026; -.
SQ   SEQUENCE 80 AA; 8515 MW; 74FA772D CRC32;

Query Match   16.7%; Score 391; DB 10; Length 80;
Best Local Similarity   60.0%; Pred. No. 2.54e-58;
Matches   45; Conservative 18; Mismatches 11; Indels   0; Gaps   1;

Qy   1 MVRVLPAALPPVPQPVCTYRE-RFASVRLPGCPPGVDPIVSFPVALSCRCGPCRLSSSDC 59
            |:|| ||::||| || |:||: ||:::::||||:|||||||||||||||||||||||||
Db 203 MTRVLQGVLPALPQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDC 262

RESULT 10
ID   Q91121   PRELIMINARY;   PRT;   147 AA.
AC   Q91121;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)

Qy 203 MTRVLQGVLPALPQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDC 262

Db   60 GGPRTQPMTCDLPHL 74
            ||| :|:|||| |:
Qy 263 GGPRKDHPLTCDDPRF 277

Left column

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DT   01-NOV-1996 (TREMBLREL, 01, LAST ANNOTATION UPDATE)
DE   GONADOTROPIN II BETA SUBUNIT PRECURSOR.
OS   MORONE SAXATILIS (STRIPED BASS).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; ACTINOPTERYGII;
OC   OSTEICHTHYES; ACTINOPTERYGII; PERCIFORMES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PITUITARY GLAND;
RX   MEDLINE; 96020549.
RA   HASSIN S., ELIZUR A., ZOHAR Y.;
RL   J. MOL. ENDOCRINOL. 15:23-35(1995).
DR   EMBL; L35096; G598255; -.
KW   SIGNAL.
FT   SIGNAL          1     32
FT   CHAIN          33    147
SQ   SEQUENCE      147 AA;  16398 MW;  292F2F62 CRC32;
                                                           POTENTIAL.
                                                           GONADOTROPIN II BETA SUBUNIT.

Db    36 PPCQLINQTVSLEKEGCPRCHPVETTICSGHCITKDPVIKIPFSNVYQHVCTYRDLHYKT 95
Qy   169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

Db    96 FELPDCPPGVDPTVTYPVAQSCHCGRCAMDISDCTFESLQPNFCMNDIPF 145
Qy   229 IRLPGCPRGVNPVVSYAVALSCCQALCRRSTTDCGGPKDHPLTC-DDPRF 277
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RESULT 11
ID   Q90225      PRELIMINARY;   PRT;  137 AA.
DT   01-NOV-1996 (TREMBLREL, 01, CREATED)
DT   01-NOV-1996 (TREMBLREL, 01, LAST SEQUENCE UPDATE)
DT   01-NOV-1996 (TREMBLREL, 01, LAST ANNOTATION UPDATE)
DE   GONADOTROPIN BETA-SUBUNIT.
OS   ACANTHOPAGRUS LATUS.
OC   EUKARYOTA; ANIMALIA; METAZOA; CHORDATA; VERTEBRATA; OSTEICHTHYES;
OC   ACTINOPTERYGII; PERCIFORMES; PERCOIDEI; SPARIDAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   TSAI H.J., YANG L.T.;
RL   SUBMITTED (JAN-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
SQ   SEQUENCE     137 AA;  15330 MW;  F87577B5 CRC32;

Query Match             15.1%;  Score 353;  DB 12;  Length 137;
Best Local Similarity   44.5%;
Matches    49;  Conservative   22;  Mismatches   36;  Indels   3;  Gaps   3;

Qy   169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228
Db    28 PPCQLINQTVSLEKEGCPRCHPVETTICSGHCITKDPVMKTRY-VYQHV-CTYRDLHYKT 85

Qy   229 IRLPGCPRGVNPVVSYAVALSCCQALCRRSTTDCGGPKDHPLTC-DDPRF 277
Db    86 FELPDCPPGVDPTVTYPVAQSCHCGRCAMDISDCTFESLQPNFCMNDIPF 135
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RESULT 12
ID   O13050      PRELIMINARY;   PRT;  130 AA.
DT   01-JUL-1997 (TREMBLREL, 04, CREATED)
DT   01-JUL-1997 (TREMBLREL, 04, LAST SEQUENCE UPDATE)
DT   01-JUL-1997 (TREMBLREL, 04, LAST ANNOTATION UPDATE)
DE   GONADOTROPIN I BETA SUBUNIT PRECURSOR.
OS   CYPRINUS CARPIO (COMMON CARP).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; ACTINOPTERYGII;
OC   OSTEICHTHYES; ACTINOPTERYGII; CYPRINIFORMES.

Db    86 FELPDCPLGVDPTVTYPYPVAVSVSCNGLCAMDTSDCTFESLQPNFCMNDIPF 135
Qy   169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

Qy   229 IRLPGCPRGVNPVVSYAVALSCCQALCRRSTTDCGGPKDHPLTC-DDRF 277
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Right column

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RP   SEQUENCE FROM N.A.
RA   KOBAYASHI M., IWASAKI M., KONDO H., YOSHIURA Y., WATABE S.;
RL   SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; AB003583; D1020895; -.
KW   SIGNAL.
FT   SIGNAL          1     18
FT   CHAIN          19    130                               POTENTIAL.
SQ   SEQUENCE      130 AA;  14393 MW;  3D37E6B1 CRC32;       GONADOTROPIN I BETA SUBUNIT.

Query Match             13.7%;  Score 321;  DB 12;  Length 130;
Best Local Similarity   41.3%;
Matches    43;  Conservative   24;  Mismatches   35;  Indels   2;  Gaps   2;

Qy   171 CRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALP-QVVCNYRDVRFESI 229
Db    26 CRLTNISITVESEECGSCIIIDTTACAGLCKTQESVYRSPL-MLSYQMTCNFREWTYETY 84

Qy   230 RLPGCPRGVNPVVSYAVALSCCQALCRRSTTDCGGPKDHPLTCD 273
Db    85 EFKGCPARADSVFTIPVALSCECSRKCNSDITDCGALSQQTLSCN 128
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RESULT 13
ID   P79357      PRELIMINARY;   PRT;  138 AA.
DT   01-MAY-1997 (TREMBLREL, 03, CREATED)
DT   01-MAY-1997 (TREMBLREL, 03, LAST SEQUENCE UPDATE)
DT   01-MAY-1997 (TREMBLREL, 03, LAST ANNOTATION UPDATE)
DE   THYROTROPIN BETA CHAIN.
OS   LAMA GLAMA (LLAMA).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; ARTIODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PITUITARY;
RA   KANIA S.A., FRANK L.A., ODOM T.F.;
RL   SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U89294; G1872550; -.
SQ   SEQUENCE     138 AA;  15571 MW;  33284E82 CRC32;

Query Match             13.4%;  Score 314;  DB 4;  Length 138;
Best Local Similarity   45.7%;
Matches    48;  Conservative   22;  Mismatches   29;  Indels   6;  Gaps   4;

Qy   162 VSCAGAGPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQG-V-LP--ALPQV 217
Db    71 VCTIYRDFMYKIVEIPGCPHHVTPYFSYPVAVSCKCKGKCDIDYSDC 115

Qy   218 VCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCCQALCRRSTTDC 262
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RESULT 14
ID   Q98848      PRELIMINARY;   PRT;  130 AA.
DT   01-FEB-1997 (TREMBLREL, 02, CREATED)
DT   01-FEB-1997 (TREMBLREL, 02, LAST SEQUENCE UPDATE)
DT   01-FEB-1997 (TREMBLREL, 02, LAST ANNOTATION UPDATE)
DE   GONADOTROPIN I BETA SUBUNIT PRECURSOR.
OS   CARASSIUS AURATUS (GOLDFISH).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; ACTINOPTERYGII;
OC   OSTEICHTHYES; ACTINOPTERYGII; CYPRINIFORMES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PITUITARY GLAND;
RA   YOSHIURA Y., KOBAYASHI M., KATO Y., AIDA K.;
RL   SUBMITTED (OCT-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; D88023; G1644241; -.
KW   SIGNAL.
FT   SIGNAL          1     18                                POTENTIAL.
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FT    CHAIN          19        130
SQ    SEQUENCE      130 AA;   14422 MW;  3C222BFD CRC32;
                         GONADOTROPIN I BETA SUBUNIT.

Query Match            13.3%;  Score 312;  DB 12;  Length 130;
Best Local Similarity  40.4%;  Pred. No. 1.37e-41;
Matches    42;  Conservative   23;  Mismatches  37;  Indels   2;  Gaps   2;

Db   26  CRLTNISITVESEECGSCITIDTTACAGLCKTQESYVRSPL-MLSYQNTCNFREWTYETY  84
            | ::||| | ||::|| | :|||||| | |||||  | | : |:||||: :|:
Qy  171  CRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALP-QVVCNYRDVRFESI  229

Db   85  EFKGCPARADSIFTYPVALSCECSKCNSDITDCGVLSQQTLGCN  128
            | ||| | ::|:| ||:|||||::|| :| |||| :|||:
Qy  230  RLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCD  273


RESULT  15
ID   Q16163              PRELIMINARY;   PRT;   138 AA.
AC   Q16163;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE   THYROID-STIMULATING HORMONE BETA SUBUNIT (FRAGMENT).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 94254248.
RA   MIYOSHI I., KASAI N., HAYASHIZAKI Y.;
RL   NIPPON RINSHO 52:940-947(1994).
DR   EMBL; S70587; G546849; -.
FT   NON_TER         138       138
SQ   SEQUENCE      138 AA;   15627 MW;  0539646F CRC32;

Query Match            13.3%;  Score 311;  DB 2;  Length 138;
Best Local Similarity  45.7%;  Pred. No. 2.21e-41;
Matches    48;  Conservative   22;  Mismatches  29;  Indels   6;  Gaps   4;

Db   13  LACGQAMSFCIPTEYTMHIERRECAYCLTINTTMCAGYC--MTRDINGKLFLPKYALSQD   70
            ::|:|: | | |: |:.| |: : ||:|:||||||||| ||| : |:: ||:|
Qy  162  VSCAGAGPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQG-V-LP--ALPQV  217

Db   71  VCTYRDFIYRTVEIPGCPLHVAPYFSYPVALSCKCKCGKCNTDYSDC  115
            ||| ||| : .::||||| | ||||  |  |||||||::| ::||   :||
Qy  218  VCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDC  262

Search completed: Wed May  6 08:55:06 1998
Job time : 78 secs.
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**********************************************************
                    MPSRCH
                                        (TM)
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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed May 6 13:40:53 1998; MasPar time 1173.41 Seconds
                                             1494.904 Million cell updates/sec

Title: >US-08-804-166-5
Description: (1-1147) from US08804166.seq
Perfect Score: 1147
N.A. Sequence: 1 TCGAGATGGCTACAGGTAAG.................AACTTAGGATCCTCGAG 1147
Comp: AGCTCTACCGATGTCCATTC.................TTAGAATTCCTAGGAGCTC

Scoring table: TABLE default
                 Gap 6

Match STD :   Dbase 0; Query 0

Nmatch   n.a.

Searched: 436399 seqs, 764661465 bases x 2

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database: emb153
                 1:em_in 2:em_or 3:em_om 4:em_ov 5:em_pl 6:em_htg
                 7:em_hum1 8:em_hum2 9:em_ba 10:em_ro 11:em_un 12:em_vi
                 13:em_pat
Database: genbank105
Database: .   14:gb_om 15:gb_ov 16:gb_ov 17:gb_in 18:gb_pl 19:gb_ba
                 20:gb_st 21:gb_vi 22:gb_ph 23:gb_sy 24:gb_un 25:gb_pat
                 26:gb_htg 27:gb_pr1 28:gb_pr2

Statistics: Mean 11.072; Variance 4.877; scale 2.270

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES

Result   Query
No. Score Match Length DB ID   Description   Pred. No.
--- ----- ----- ------ -- --   -----------   ---------
  1 506   44.1 1331   25 A29103   H.saplens mRNA for TNF   0.00e+00
  2 506   44.1 1368   25 A29098   Synthetic DNA for TNF-   0.00e+00
  3 506   44.1 2050   27 HUMTNFRP Human tumor necrosis f   0.00e+00
  4 506   44.1 2062   25 A21522   TNF alpha gene.   0.00e+00
  5 506   44.1 2062   25 I43805   Sequence 24 from paten   0.00e+00
  6 506   44.1 2087   27 HUMTNFR Human tumor necrosis f   0.00e+00
  7 506   44.1 2111   25 HUMTNFRB Homo sapiens tumor nec   0.00e+00
  8 506   44.1 2111   25 A26412   cDNA for (55kD TNF-BP)   0.00e+00
  9 506   44.1 2112   27 HUMTNFRC Human tumor necrosis f   0.00e+00
 10 506   44.1 2161   25 HSTNFR1A H.sapiens TNF-R mRNA f   0.00e+00
 11 506   44.1 2175   25 I64751   Sequence 1 from patent   0.00e+00
 12 506   44.1 2175   25 A43873   Sequence 1 from Patent   0.00e+00
 13 506   44.1 2176   25 A19907   Synthetic nucleotide s   0.00e+00
 14 504   43.9 6889   25 I26928   Sequence 2 from patent   0.00e+00
 15 499   43.5 2061   25 A20255   55kD receptor gene for   0.00e+00
 16 473   41.2 483   25 A29099   Synthetic DNA for TNF-   0.00e+00
 17 468   40.8 600   25 A20257   Synthetic nucleotide s   0.00e+00
 18 467   40.7 510   25 A21525   oligonucleotide probe.   0.00e+00
 19 464   40.5 600   25 I43808   Synthetic nucleotide s   0.00e+00
 20 375   32.7 504   25 A20713   Sequence 47 from paten   0.00e+00
 21 375   32.7 501   25 I43813   Synthetic nucleotide s   0.00e+00
 22 373   32.5 501   25 I43786   Sequence 56 from patent   0.00e+00
 23 366   31.9 500   25 A20254   Sequence 1 from patent   0.00e+00
 24 364   31.7 372   25 I43787   Sequence 3 from patent   0.00e+00
 25 345   30.1 474   25 A20253   Synthetic nucleotide s   0.00e+00
 26 345   30.1 474   25 A20259   Synthetic nucleotide 5   0.00e+00
 27 316   27.6 66495 27 I43809   Sequence 49 from paten   4.80e-289
 28 307   26.8 581   15 HUMGHCSA Human growth hormone (2.66e-261
 29 301   26.2 2004   15 FCU72344 Fells catus tumour nec   8.40e-254
 30 289   25.2 1826   25 SSU19994 Sus scrofa p55 TNF rec   3.00e-247
 31 289   25.2 1826   25 I02855   Sequence 3 from patent   1.09e-245
 32 288   25.1 1964   27 HSGROW2 Human germ line gene f   9.72e-235
 33 288   25.1 1964   27 HUMGH   Human growth hormone (9.72e-235
 34 288   25.1 2771   25 I41411   Human growth hormone g   9.72e-235
 35 287   25.0 2657   27 HUMGHN   Human growth hormone g   8.66e-234
 36 287   25.0 4283   25 I63120   Sequence 3 from patent   8.66e-234
 37 263   22.9 2130   14 RATTNFR Rat tumor necrosis fac   4.84e-211
 38 262   22.8 621   27 HSGROA   Human messenger RNA (f   4.28e-210
 39 255   22.2 477   25 A20263   Synthetic nucleotide s   1.77e-203
 40 255   22.2 477   25 I43811   Sequence 53 from patent   1.77e-203
 41 252   22.0 1956   14 MUSTNFR2 Murine tumor necrosis f   1.21e-200
 42 252   22.0 2048   14 MUSMTNFR1 Mouse tumor necrosis f   1.21e-200
 43 252   22.0 2063   14 MMP55R   Mouse mRNA for p55 tu   1.21e-200
 44 252   22.0 2154   14 MUSTNFX Murine mRNA for p55 tu   1.21e-200
 45 252   22.0 2179   14 MMTNFRE5 Mouse mRNA for 55-kDa   1.21e-200
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                              ALIGNMENTS

RESULT   1

LOCUS   A29103   1331 bp   DNA   PAT   03-JUL-1995
DEFINITION   H.sapiens mRNA for TNF-binding polypeptide from patent EP0393438.
ACCESSION   A29103
NID   g1247517
KEYWORDS   .
SOURCE   human.
  ORGANISM   Homo sapiens
                 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
                 Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1331)
  AUTHORS   Hauptmann,R., Himmler,A., Maurer-Fogy,I. and Stratowa,C.
  TITLE   TNF-receptor, TNF-binding protein and DNA coding therefor
  JOURNAL   Patent: EP 0393438-A 53 24-OCT-1990;
                 BOEHRINGER INGELHEIM INTERNATIONAL G.M.B.H
FEATURES   Location/Qualifiers
     source   1..1331
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT   298 a   407 c   343 g   283 t
ORIGIN

Query Match   44.1%; Score 506; DB 25; Length 1331;
Best Local Similarity 98.1%; Pred. No. 0.00e+00;
Matches 521; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

```
Db    333 GATAGTGTGTCGTGTCCCCAAGGAAAATAATATCCACCCTCAAATAATTCGATTTGCTGTACC 392
          |||||||||||||||||||||||||||||||||| || |||||||||||||||||||||||
Qy    344 GATAGTGTGTGTGTCCCCAAGGAAAATAATATCCACCCTCAAATAATTCGATTTGCTGTACC 403

Db    393 AAGTGCCACAAAAGGAAACCTACTTGTATACAATGACTGTCCAGGCCCGGCAGGAGATACGGAC 452
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    404 AAGTGCCACAAAAGGAAACCTACTTGTATACAATGACTGTCCAGGCCCGGCAGGAGATACGGAC 463

Db    453 TGCAGGGAGAGTGTGAGAGCGGGCGGCCTCCTTCACCGCTTCAGAAAAACCACCTCAGACACTGCCTC 512
          |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Qy    464 TGCAGGGAGAGTGTGAGAGCGGGCGGCCTCCTTCACCGCTTCAGAAAAACCACCTCAGACACTGCCTC 523
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Db  513  AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGAGATCTCTTCTTTTGCACAGTGGAC  572
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  524  AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTTTGCACAGTGGAC    583

Db  573  CGGGACACCGTGTGTGGGCTGCGAGGAAGAACCAGCGTACCGGCGCATTATTGGAGTGAAAACCTT  632
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  584  CGGGACACCGTGTGTGGGCTGCGAGGAAGAACCAGCGTACCGGCGCATTATTGGAGTGAAAACCTT  643

Db  633  TTCCAGTGCTTGCTTCAATTGCAGCGTGTTCAAATGGGACCGTGCCACCTCTTCCTGCCAGGAG   692
         |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Qy  644  TTCCAGTGCTTCAATTGCACCCTCTCAAATGGGACCGTGCCACCTCTTCCTGCCAGGAG         703

Db  693  AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTCTTAAGAGAAAACGAGTGTGTC       752
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  704  AAACAGAACACCGTCTGCACGTGCCATGCAGGTTTCTTCTTAAGAGAAAACGAGTGTGTC       763

Db  753  TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGCTGTGTCCTACCCCAGATTGAG     812
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  764  TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGCTGTGTCCTACCCCAGATTGAG     823

Db  813  AATGTTAAGGGCACTGAGGACTCAGGCACACCAGT-GCTGTTGCCCTGGT                862
         ||||||||||||||||||||||||||||||||||| |||||||||||||||
Qy  824  AATGTTAAGGGCACTGAGGACTCAGGCACCACCAGT-GCTGTTGCCCCTGGT              874
```

RESULT 2

```
LOCUS       A29098     1368 bp    DNA            PAT    03-JUL-1995
DEFINITION  Synthetic DNA for TNF-receptor from patent EP0393438.
ACCESSION   A29098
NID         g1248892
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1368)
  AUTHORS   Hauptmann,R., Himmler,A., Maurer-Fogy,I. and Stratowa,C.
  TITLE     TNF-receptor, TNF-binding protein and DNA coding therefor
  JOURNAL   Patent: EP 0393438-A 48 24-OCT-1990;
            BOEHRINGER INGELHEIM INTERNATIONAL G.M.B.H
FEATURES             Location/Qualifiers
     source          1..1368
                     /organism="unidentified"
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     source          1..1368
                     /organism="artificial sequence"
                     /db_xref="taxon:29278"
BASE COUNT      293 a    424 c    375 g    276 t
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Query Match        44.1%;  Score 506;  DB 25;  Length 1368;
Best Local Similarity 98.1%;
Matches  521;  Conservative 0;  Mismatches 9;  Indels 1;  Gaps 1;
                   Pred. No. 0.00e+00;
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Qy  121  GATAGTGTGTGTCCCCAAGGAGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGGTACC       180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  GATAGTGTGTGTCCCCAAGGAGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGGTACC       240

Qy  344  GATAGTGTGTCCCCAAGGAGAAAATATATCCACCCTCAAAAATAATTCGATTTGCTGGTACC       403
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Db  404  AAGTGCCCACAAAAGGAAACCTACTTGTTACAAGACTCTCCAGGCCCCCGGGGCAGGATACGGAC  463

Qy  404  AAGTGCCCACAAAAGGAAACCTACTTGTTACAAGACTCTCCAGGCCCCCGGGGCAGGATACGGAC  463
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Db  241  TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCACCGCCTCAGAAAACCTCAGACACTGCCTC  300

Qy  464  TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACTCAGACACTGCCTC       523
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Db  301  AGCTGCTCCAAATGCCGAAAATGGGTCAGGTGGAGATCTCTTCTTCTTGCACAGTGGAC       360

Qy  524  AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTTTGCACAGTGGAC     583
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Db  361  CGGGACACCGTGTGTGGGCTGCGAGGAAGAACCAGCGCATTATTGGAGTGAAAACCTT         420
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RESULT 3

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LOCUS       HUMTNFRP     2050 bp    mRNA            PRI    11-OCT-1991
DEFINITION  Human tumor necrosis factor receptor (TNF) mRNA, complete cds.
ACCESSION   M60275 M37764
NID         g339759
KEYWORDS    TNF receptor; transmembrane receptor; tumor necrosis factor
            receptor.
SOURCE      Human placenta, cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2050)
  AUTHORS   Gray,P.W., Barrett,K.J., Chantry,D., Turner,M. and Feldman,M.
  TITLE     Cloning of human tumor necrosis factor (TNF) receptor cDNA and
            expression of recombinant soluble TNF-binding protein
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384 (1990)
  MEDLINE   91017509
COMMENT     Draft entry and computer-readable sequence for [Proc. Natl. Acad.
            Sci. U.S.A. (1990) In press] kindly submitted
            by P.W.Gray, 13-AUG-1990.
FEATURES             Location/Qualifiers
     source          1..2050
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                     /db_xref="taxon:9606"
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     sig_peptide     155..274
                     /gene="TNF receptor"
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                     KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVI
                     FFGLCLLSLLFIGLMYRYQRWKSKLYSIVCGKKSTPEKEGELEGTTTKPLAPNPSFSPT
                     PGFTPTLGFSPVPSSTFTSSSTYTPGDCPNFAAPRREVAPPYQGADPILATALASDPI
                     PNPLQKWEDSAHKPQSLDTDDPATLYAVVENVPPLRWKEEVRRGLSDHEIDRLELQN
                     GRCLREAQYSMLATWRRRTPREATLELLGRVLRDMDLLGCLEDIEEALCAPPLPPAPS
                     LLR"
     gene            155..274
                     /gene="TNF receptor"
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                     /product="TNF receptor"
BASE COUNT      429 a    611 c    566 g    444 t
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Qy  584  CGGGACACCGTGTGTGGGCTGCGAGGAAGAACCAGCGTACCGGCGCATTATTGGAGTGAAAACCTT  643
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Db  421  TTCCAGTGCTTGCTTCAATTGCAGCGTGTTCTGCTTCCTCAATGGGACCGTGCCAGGAG         480

Qy  644  TTCCAGTGCTTGCTTCAATTGCAGCGTGTTCTGCTTCCTCAATGGGACCGTGCCAGGAG         703
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481  AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTCTTAAGAGAAAACGAGTGTGTC       540

Qy  704  AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTCTTAAGAGAAAACGAGTGTGTC       763
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541  TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGCTGTGTCCTACCCCAGATTGAG     600

Qy  764  TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGCTGTGTCCTACCCCAGATTGAG     823
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Db  601  AATGTTAAGGGCACTGAGGACTCAGGCACCACCAGT-GCTGTTGCCCCTGGT             650

Qy  824  AATGTTAAGGGCACTGAGGACTCAGGCACCACCAGCAGCGCGGTGCTGCCCCCAGGT        874
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Db  764  TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGCTGTGTCCTACCCCAGATTGAG     823
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Query Match        44.1%;  Score 506;  DB 27;  Length 2050;
Best Local Similarity 98.1%;
Matches  521;  Conservative 0;  Mismatches 9;  Indels 1;  Gaps 1;
                   Pred. No. 0.00e+00;
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Db  275  GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGGTACC       334
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```
RESULT 4

LOCUS       A21522       2062 bp    RNA        PAT       26-JUL-1994
DEFINITION  TNF alpha gene.
ACCESSION   A21522
NID         g579599
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2062)
  AUTHORS
  JOURNAL   Patent: GB 2246569-A 1 05-FEB-1992;
FEATURES             Location/Qualifiers
     source          1..2062
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                     /db_xref="taxon:9606"
     gene            155..1522
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     CDS             155..1522
                     /gene="TNF alpha gene"
                     /codon_start=1
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                     /db_xref="SWISS-PROT:P19438"
                     /translation="MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVC
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                     SKCREMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE
                     KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPVI
                     FFGLCLLSLLFIGLMYRYQRWKSKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPT
                     PGFFTPLGESPVPSSTFTSSSYTPGDCPNFAAPRREVAPPYQGADPILATALASDPI
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BASE COUNT      429 a    617 c    573 g    443 t
ORIGIN

Query Match             44.1%;  Score 506;  DB 25;  Length 2062;

Qy    344 GATAGTGTGTGTCCCCAAGGAAAAATATATCCACCCTCAAAATAATTAATTCGATTTGCTGTACC 403
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Db    335 AAGTGCCACAAAGGAACCTACTTGTTACAATGACTTGTTTCCAGGCCCGGGGCAGGATACCGAC 394

Qy    404 AAGTGCCACAAAGGAACCTACTTGTTACAATGACTTGTTTCCAGGCCCGGGGCAGGATACCGAC 463
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Db    395 TGCAGGGAGTGTGAGAGCGCGGCTCCTTCACCGCTCAGAAAACCACCTCAGACACTGCCTC 454

Qy    464 TGCAGGGAGTGTGAGAGCGCGGCTCCTTCACCGCTCAGAAAACCACCTCAGACACTGCCTC 523
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Db    455 AGCTGCTCCAAATGCCGAAAGGAAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 514

Qy    524 AGCTGCTCCAAATGCCGAAAGGAAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583
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Db    515 CGGGACACCCGTGTGTGGGCTGTCAGGAAGAACCAGTTATTGGGACTGGAAAAACCTT 574

Qy    584 CGGGACACCCGTGTGTGGGCTGTCAGGAAGAACCAGTTATTGGGACTGGAAAAACCTT 643
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Db    575 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTGTCCCAGGAG 634

Qy    644 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTGTCCCAGGAG 703
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    635 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 694

Qy    704 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 763
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Db    695 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 754

Qy    764 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 823
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    755 AATGTTAAGGGCACTGAGGACTCAGGCACCACACAGCCGGTGCTGCTGCCCCAGGT 804

Qy    824 AATGTTAAGGGCACTGAGGACTCAGGCACCACACAGT-GCTGTTGCCCCTGGT 874

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RESULT 5

Best Local Similarity   98.1%;
Matches   521;   Conservative   0;   Pred. No. 0.00e+00;   Mismatches   9;   Indels   1;   Gaps   1;

Qy    824 AATGTTAAGGGCACTGAGGACTCAGGCACCACCACAGT-GCTGTTGCCCCTGGT 874
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Db    824 AATGTTAAGGGCACTGAGGACTCAGGCACCACCACAGCCGGTGCTGCTGCCCCAGGT 874

LOCUS       I43805       2062 bp    DNA        PAT       10-JUL-1997
DEFINITION  Sequence 24 from patent US 5633145.
ACCESSION   I43805
NID         g2468903
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2062)
  AUTHORS   Feldmann,M., Gray,P.W., Turner,M.J.C. and Brennan,F.M.
  TITLE     TNF.alpha. receptor-derived binding protein
  JOURNAL   Patent: US 5633145-A 24 27-MAY-1997;
FEATURES             Location/Qualifiers
     source          1..2062
                     /organism="unknown"
BASE COUNT      429 a    617 c    573 g    443 t
ORIGIN

Query Match             44.1%;  Score 506;  DB 25;  Length 2062;
Best Local Similarity   98.1%;  Pred. No. 0.00e+00;
Matches   521;   Conservative   0;   Mismatches   9;   Indels   1;   Gaps   1;

Db    275 GATAGTGTGTGTCCCCAAGGAAAAATATATCCACCCTCAAAATAATTAATTCGATTTGCTGTACC 334
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Qy    344 GATAGTGTGTGTCCCCAAGGAAAAATATATCCACCCTCAAAATAATTAATTCGATTTGCTGTACC 403

Db    335 AAGTGCCACAAAGGAACCTACTTGTTACAATGACTTGTTTCCAGGCCCGGGGCAGGATACCGAC 394
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    404 AAGTGCCACAAAGGAACCTACTTGTTACAATGACTTGTTTCCAGGCCCGGGGCAGGATACCGAC 463

Db    395 TGCAGGGAGTGTGAGAGCGGGCTCCTTCAGAAAACCACCTCAGACACTGCCTC 454
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Qy    464
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RESULT 6

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LOCUS       HUMTNFR        2087 bp    mRNA            PRI       10-NOV-1993
DEFINITION  Human tumor necrosis factor receptor mRNA, complete cds.
ACCESSION   M33294
NID         g339744
KEYWORDS    cell surface receptor; tumor necrosis factor receptor.
SOURCE      Human placenta, cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2087)
  AUTHORS   Schall,T.J., Lewis,M., Koller,K.J., Lee,A.L., Rice,G.C., Wong,G.H.,
            Gatanaga,T., Granger,G.A., Lentz,R., Raab,H., Kohr,W.J. and
            Goeddel,D.V.
  TITLE     Molecular cloning and expression of a receptor for human tumor
            necrosis factor
  JOURNAL   Cell 61, 361-370 (1990)
  MEDLINE   90235285
COMMENT     Draft entry and computer-readable sequence for [1] kindly submitted
            by T.Schall, 26-MAR-1990.
FEATURES             Location/Qualifiers
     source          1..2087
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     CDS             182..1549
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BASE COUNT     433 a     624 c     581 g     449 t
ORIGIN
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Best Local Similarity   98.1%;
Query Match   44.1%;

Matches 521;   Conservative 0;   Mismatches 9;   Indels 1;   Gaps 1;

Score 506;   DB 27;   Length 2087;
Pred. No. 0.00e+00;

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Qy    464 TGCAGGGAGAGTGGAGAGCGGCGGCTCCTTCACCGCTTCACGCACCTGAGAACACTGCCTC 523
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Db    455 AGCTGCTCCAAATGCCGAAATGGGTGCAGGTGGAGATCTCTTCTTGCACAGTGGAC 514
Qy    524 AGCTGCTCCAAATGCCGAAATGGGTGCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    515 CGGGACACCGTGTGTGGGCTGCAGGAAGAACCAGTACCGGCCATTATTGGACTGAAAACT 574
Qy    584 CGGGACACCGTGTGTGGGCTGCAGGAAGAACCAGTACCGGCCATTATTGGAGTGAAAACTT 643
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Db    575 TTCCAGTGCTTCAATTGCAGCCTTCGCTGCCTCAATGGGACGGTGCACCTGTCAGGAG 634
Qy    644 TTCCAGTGCTTCAATTGCACCCTTCGCTGCCTCAATGGGACCGTGCACCTGTCAGGAG 703
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Db    635 AAACAGAACACCGTTGCACCTGCCATGCCATGCCTGCCACCCACCCAGATTGAG 694
Qy    704 AAACAGAACACCGTCTGCACCTGCCACCTGCCTGGACGGTTCTTTCTGAGAGAAAACG 763
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    695 TCCTGTGTAGTAACTGTAAGAAAAAGCCTGAGTGCAGTTGTTGTCCTACCCCAGATTGAG 754
Qy    704 AAACAGAACACCGTCTGCACCTGCCACCTGCCTGGACGGTTCTTTCTGAGAGAAAACG 763
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Db    764 TCCTGTGTAGTAACTGTAAGAAAAAGCCTGAGTGCAGTTGTTGTCCTACCCCAGATTGAG 823
Qy    755 AATGTTAAGGGCACTGAGGAGCTCAGGCAACCACCAGT-GCTGTTGCCCCTGGT 804
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Db    764 TCCTGTGTAGTAACTGTAAGAAAAAGCCTGAGTGCAGTTGTTGTCCTACCCCAGATTGAG 823
Qy    824 AATGTTAAGGGCACTGAGGAGCTCAGGCAACCACCAGCCGGTGCTCCCCCAGGT 874
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Db    755 AATGTTAAGGGCACTGAGGAGCTCAGGCAACCACCAGT-GCTGTTGCCCCTGGT 804
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RESULT 7

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LOCUS       HUMTNFRB       2111 bp    mRNA            PRI       14-NOV-1990
DEFINITION  Homo sapiens tumor necrosis factor receptor mRNA, complete cds.
ACCESSION   M58286 M33480
NID         g339753
KEYWORDS    tumor necrosis factor receptor.
SOURCE      Human cell line HL60, cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2111)
  AUTHORS   Loetscher,H., Pan,Y.-C.E., Lahm,H.-W., Gentz,R., Brockhaus,M.,
            Tabuchi,H. and Lesslauer,W.
  TITLE     Molecular cloning and expression of the human 55 kd tumor necrosis
            factor receptor
  JOURNAL   Cell 61, 351-359 (1990)
  MEDLINE   90235284
FEATURES             Location/Qualifiers
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Qy    302 GATAGTGTGTGTCCCCAAGGAAAAATATCCACCCTCAAAATAATAATTCGATTTGCTGTACC 361
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    344 GATAGTGTGTGTGTCCCCAAGGAAAAATATCCACCCTCAAAATAATAATTCGATTTGCTGTACC 403
Qy    362 AAGTGCCACAAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 421
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    404 AAGTGCCACAAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 463
Qy    422 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTGAGACACTGCCTC 481
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Db    464 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTGAGACACTGCCTC 523
Qy    482 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 541
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583
Qy    542 CGGGACACCGTGTGTGGGCTGCAGGAAGAACCAGTACCGGCCATTATTGGAGTGAAAACCTT 601
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Db    584 CGGGACACCGTGTGTGGGCTGCAGGAAGAACCAGTACCGGCCATTATTGGAGTGAAAACCTT 643
Qy    602 TTCCAGTGCTTCAATTGCAGCCTTCGCTGCCTCAATGGGACCGTGCACCTCTCCGTGCCAG 661
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Db    644 TTCCAGTGCTTCAATTGCACCCTTCGCTGCCTCAATGGGACCGTGCACCTCTCCTGTCCAG 703
Qy    662 AAACAGAACACCGTGTGCACCTGCCATGCAGGGTTCTTTCTAAGAGAAAACGAGTGTGTC 721
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Db    704 AAACAGAACACCGTCTGCACCTGCCATGCAGGGTTCTTTCTAAGAGAAAACGAGTGTGTC 763
Qy    722 TCCTGTAGTAACTGTAAGAAAAAGCCTGGAGTGCACGAAGTTGTGCTTCACCCCAGATTGAG 781
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Db    764 TCCTGTAGTAACTGTAAGAAAAAGCCTGGAGTGCACGAAGTTGTGCTTCACCCCAGATTGAG 823
Qy    782 AATGTTAAGGGCACTGAGGAGCTCAGGCAACCACCAGCCGGTGCTCCCCCAGGT 831
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Db    824 AATGTTAAGGGCACTGAGGAGCTCAGGCAACCACCAGCCGGTGCTCCCCCAGGT 874
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BASE COUNT      445 a      629 c      587 g      450 t
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Query Match     44.1%;     Score 506;  DB 27;     Length 2111;
Best Local Similarity  98.1%;  Pred. No. 0.00e+00;
Matches   521;  Conservative  0;  Mismatches  9;  Indels  1;  Gaps  1;
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Qy  344 GATAGTGTGTGTCCCCAAGGAAAAATAATATATCCACCCTCAAAATAATTGCTGTACC 403
Db  367 AAGTGCCACAAAAGGAACCTACTTGTACAATGACTGTCCAGCCCGGGGCCCGGGCAGGATACGGAC 426
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Qy  404 AAGTGCCACAAAAGGAACCTACTTGTACAATGACTGTCCAGGCCGGGGCCCGGGCAGGATACCGAC 463
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Qy  464 TGCAGGGAGTGTGAGAGCGGCGGCTCCTTCACCCGCCTTCAGAAAACCACCTCAGACACTGCCTC 523
Db  487 AGCTGCTCCAAAATGCCGAAAAGGATCAGGGTGGAGATCTCTTCTTCTTGCACAGTGGAC 546
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Db  547 CGGGACACCGTGTGTGGCTGCAGGAAGAACACCAGTACCGGCCATTATTGGAGTGAAAACCTT 606
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Db  607 TTCCAGTGCTTCAATTGCACGCCTCTGCCTCAATGGGACCGTGCACCCTCTCCTGTCCAGGAG 666
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Db  667 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTTCTTTAAGAGAAAACAGAGTGTGTC 726
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RESULT  8
LOCUS        A26412          2111 bp   DNA           PAT        26-APR-1995
DEFINITION   cDNA for (55kD TNF-BP) tumor necrosis factor binding protein from
             patent EP0417563.
ACCESSION    A26412
NID          g904968
KEYWORDS
SOURCE       unidentified.
  ORGANISM   unidentified
             unclassified.
REFERENCE    1  (bases 1 to 2111)
  AUTHORS    Brockhaus,M., Dembic,Z., Gentz,R., Lesslauer,W., Loetscher,H. and
             Schlaeger,E.J.
  TITLE      TNF-binding proteins
  JOURNAL    Patent: EP 0417563-A 24 20-MAR-1991;
             F. HOFFMANN-LA ROCHE AG
FEATURES             Location/Qualifiers
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CDS             187..1554
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                /db_xref="PID:g904969"
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BASE COUNT      445 a      629 c      587 g      450 t
ORIGIN
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Query Match     44.1%;     Score 506;  DB 25;     Length 2111;
Best Local Similarity  98.1%;  Pred. No. 0.00e+00;
Matches   521;  Conservative  0;  Mismatches  9;  Indels  1;  Gaps  1;
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Qy  307 GATAGTGTGTGTCCCCAAGGAAAAATAATATATCCACCCTCAAAATAATTAATTGCTGTACC 366
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Db  344 GATAGTGTGTGTCCCCAAGGAAAAATAATATATCCACCCTCAAAATAATTGCTGTACC 403
Qy  367 AAGTGCCACAAAAGGAACCTACTTGTACAATGACTGTCCAGCCCGGGGCCCGGGCAGGATACGGAC 426
        |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db  404 AAGTGCCACAAAAGGAACCTACTTGTACAATGACTGTCCAGGCCGGGGCCCGGGCAGGATACCGAC 463
Qy  427 TGCAGGGAGTGTGAGAGCGGCGGCTCCTTCACCCGCCTTCAGAAAACCACCTCAGACACTGCCTC 486
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Db  464 TGCAGGGAGTGTGAGAGCGGCGGCTCCTTCACCCGCCTTCAGAAAACCACCTCAGACACTGCCTC 523
Qy  487 AGCTGCTCCAAAATGCCGAAAAGGATCAGGGTGGAGATCTCTTCTTCTTGCACAGTGGAC 546
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Db  524 AGCTGCTCCAAAATGCCGAAAAGGGATCAGGGTGGAGATCTCTTCTTCTTGCACAGTGGAC 583
Qy  547 CGGGACACCGTGTGTGGCTGCAGGAAGAACACCAGTACCGGCCATTATTGGAGTGAAAACCTT 606
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Qy  607 TTCCAGTGCTTCAATTGCACGCCTCTGCCTCAATGGGACCGTGCACCCTCTCCTGTCCAGGAG 666
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Qy  667 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTTCTTTAAGAGAAAACAGAGTGTGTC 726
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Db  704 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTTCTTTAAGAGAAAACAGAGTGTGTC 763
Qy  727 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTCCTACCCCAGATTGAG 786
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Db  764 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTCCTACCCCAGATTGAG 823
Qy  787 AATGTTAAGGGCACTGAGGACTCAGGCACCACCACAGT-GCTGTTGCCCCTGGT 836
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Db  824 AATGTTAAGGGCACTGAGGACTCAGGCACCACCACAGTCGCTGTTGCCCCTGGT 874
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RESULT  9
LOCUS        HUMTNFRC        2112 bp   mRNA          PRI        30-SEP-1991
DEFINITION   Human tumor necrosis factor receptor (TNF receptor) mRNA, complete
             cds.
ACCESSION    M63121 M75861
NID          g339755
KEYWORDS     tumor necrosis factor receptor.
SOURCE       Human cDNA to mRNA.
  ORGANISM   Homo sapiens
             Eukaryota; mitochondrial eukaryotes; Metazoa; Choordata;
             Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 2112)
  AUTHORS    Himmler,A., Maurer-Fogy,I., Kroenke,M., Scheurich,P.,
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TITLE       Pfizenmaier,K., Lantz,M., Olsson,I., Hauptmann,R., Stratowa,C. and
               Adolf,G.R.
            Molecular cloning and expression of human and rat tumor
               necrosis factor receptor chain (p60) and its soluble derivative, tumor
               necrosis factor-binding protein
JOURNAL     DNA Cell Biol. 9, 705-715 (1990)
MEDLINE     91090841
FEATURES             Location/Qualifiers
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                /gene="TNF receptor"
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BASE COUNT     435 a    632 c    589 g    456 t
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Query Match      44.1%;  Score 506;  DB 27;  Length 2112;
Best Local Similarity   98.1%;  Pred. No. 0.00e+00;
Matches  521;  Conservative   0;  Mismatches   9;  Indels  1;  Gaps  1;

Qy  327 GATAGTGTGTGTCCCAAGGAAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 386
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Db  344 GATAGTGTGTGTCCCCAAGGAAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403

Qy  387 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 446
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Qy  447 TGCAGGGAGAGTGTGAGAGACCGGCGCTCCTTCACCGCTTCAGAAAACCACCTCAGAACTC 506
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Qy  507 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 566
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Db  584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCACTACCGGCATTATTGGTGAGAAAACCTT 643

Qy  627 TTCCAGTGCTTCAAATTGCAGCCTTCAATGGGACCGTGCACCCTCCTGCCACGGAG 686
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Qy  807 AATGTTAAGGCACTGAGGACTCAGGCACCACACAGT-GCTGTTGCCCCTGGT 856
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Right column:

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LOCUS       HSTNFR1A     2161 bp     RNA          PRI       18-JAN-1993
DEFINITION  H.sapiens TNF-R mRNA for tumor necrosis factor receptor type 1.
ACCESSION   X55313
NID         g37223
KEYWORDS    TNF-R gene; tumor necrosis factor receptor type 1.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 2161)
AUTHORS     Nophar,Y., Kemper,O., Brakebusch,C., Englemann,H., Zwang,R.,
               Aderka,D., Holtmann,H. and Wallach,D.
TITLE       Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA
               for the type I TNF-R, cloned using amino acid sequence data of its
               soluble form, encodes both the cell surface and a soluble form of
               the receptor
JOURNAL     EMBO J. 9 (10), 3269-3278 (1990)
MEDLINE     91006021
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                PNPLQKWEDSAHKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQN
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BASE COUNT     459 a    642 c    604 g    456 t
ORIGIN

Query Match      44.1%;  Score 506;  DB 27;  Length 2161;
Best Local Similarity   98.1%;  Pred. No. 0.00e+00;
Matches  521;  Conservative   0;  Mismatches   9;  Indels  1;  Gaps  1;

Qy  376 GATAGTGTGTGTCCCAAGGAAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 435
        ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db  344 GATAGTGTGTGTCCCCAAGGAAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403

Qy  436 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 495
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Db  436 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 495

Qy  404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 463
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Qy 464 TGCAGGGAGTGTGAGAGCGGCGCTCCTTCACCGGTTCAGAAAACCACCTCAGACACTGCCTC 523
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Qy 524 AGCTGCTCCAAATGCCGAAAAGGGTCAGGTGGAGAGATCTCTTCTTGCACAGTGGAC 583
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RESULT 11

LOCUS   I6475I   2175 bp   DNA   PAT   26-SEP-1997
DEFINITION Sequence 1 from patent US 5665859.
ACCESSION   I6475I
NID   g2481645
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 2175)
  AUTHORS   Wallach,D., Brakebusch,C., Varfolomeev,E. and Batkin,M.
  TITLE   Molecules influencing the shedding of the TNF receptor, their
            preparation and their use
            Patent: US 5665859-A 1 09-SEP-1997;
  JOURNAL
FEATURES   Location/Qualifiers
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BASE COUNT   474 a   641 c   604 g   456 t
ORIGIN

Query Match   44.1%; Score 506; DB 25; Length 2175;
  Best Local Similarity   98.1%;
  Matches   521; Conservative   0; Pred. No. 0.00e+00; Mismatches   9; Indels   1; Gaps   1;

Qy 376 GATAGTGTGTGTCCCAAGGAAAATATATCACCCTCAAAATAATTGGATTGTTCCTGTACC 435
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Qy 436 AAGTGCCACAAAGGAACCTACTTGTACAAATGACTGTCCAGGCCCGCAGGCCAGGATACGGAC 495
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Qy 556 AGCTGCTCCAAATGCCGAAAAGGGAAATGGGTCAGGTGGAGAGATCTCTTCTTGCACAGTGGAC 615
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Qy 824 AATGTTAAGGGCCACTGAGGACTCAGGCGCCACCACAGCCGCGGTGCTGCCCCCAGGT 874

RESULT 12

LOCUS   A43873   2175 bp   DNA   PAT   06-MAR-1997
DEFINITION Sequence 1 from Patent EP0657536.
ACCESSION   A43873
NID   g2299022
KEYWORDS   .
SOURCE   unidentified.
  ORGANISM unidentified
            unclassified.
REFERENCE   1 (bases 1 to 2175)
  AUTHORS   Wallach,D., Brakebusch,C., Varfolomeev,E. and Batkin,M.
  TITLE   Proteases capable of shedding the soluble TNF-receptor and TNF-R
            derived peptides and antibodies against the proteases inhibiting
            the shedding
  JOURNAL   Patent: EP 0657536-A 1 14-JUN-1995;
COMMENT   YEDA RES & DEV (IL)
            Other publication 2A 9407962 951121
            Other publication JP 7194376 950801
            Other publication AU 7574294 950504
            Other publication CA 2133872 950413.
FEATURES   Location/Qualifiers
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                     PQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC
                     SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHVWSENLFQCFNCSLCLNGTVHLSCQE
                     KQNTVCTCHAGFFLRENCVSCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPVI
                     FFGLCLLSLLFIGLMYRQRWKSKLYSIVCGKSTPEKEGELEGTTIKPLAPNPSFSPT
                     PGFTPTLGFSPVPSSTFTSSSTYTPGDCPENFAAPRREVAPYQGADPILATALASDPI
                     PNPLQKWEDSAHKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQN
                     GRCLREAQYSMLATWRRRTPRREATLELIGRVLRDMDLLGCLEDIEEALCGPAALPPA
                     PSLLR"
BASE COUNT   474 a   641 c   604 g   456 t
ORIGIN

Query Match   44.1%; Score 506; DB 25; Length 2175;
  Best Local Similarity   98.1%;
  Matches   521; Conservative   0; Pred. No. 0.00e+00; Mismatches   9; Indels   1; Gaps   1;

Db 376 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTGGATTGTTCCTGTACC 435
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 344 GATAGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATATATCCACCCTCAAAATAATTGCTGTACC 403

Db 436 AAGTGCCACAAAGGAACCTACTTGTACAAATGACTGTCCAGGCCCGGGGCCAGGATACGGAC 495
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Qy 404 AAGTGCCACAAAGGAACCTACTTGTACAAATGACTGTCCAGGCCCGGGGCCAGGATACCGGAC 463

Db 496 TGCAGGGAGTGTGAGAGCGGCGCTCCTTCACCGGTTCAGAAAACCACCTCAGACACTGCCTC 555
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 13

```
LOCUS       A19907          2176 bp    DNA        PAT         04-OCT-1994
DEFINITION  Synthetic nucleotide sequence Type I TNF receptor gene.
ACCESSION   A19907
NID         g641222
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 2176)
  AUTHORS   Wallach,D., Nophar,Y., Kemper,O., Engelmann,H., Brakebusch,C. and
            Aderka,D.
  TITLE     Expression of the recombinant tumor necrosis factor binding protein
            I (TBP-I)
  JOURNAL   Patent: EP 0433900-A 28 26-JUN-1991;
            YEDA RESEARCH AND DEVELOPMENT COMPANY LIMITED
FEATURES             Location/Qualifiers
     source          1..2176
                     /organism="Artificial sequences"
BASE COUNT      474 a    642 c    604 g    456 t
ORIGIN
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Query Match   44.1%; Score 506; DB 25; Length 2176;
Best Local Similarity   98.1%; Pred. No. 0.00e+00;
Matches 521; Conservative   0; Mismatches   9; Indels   1; Gaps   1;

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Qy        464 TGCAGGGAGTGTGAGAGCGGCGGCTCCTTCAGAAAACCACCTCAGACACTGCCCTC 523
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 AGCTGCTCCAAAATGCCGAAAGGAAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 615
Qy        524 AGCTGCTCCAAAATGCCGAAAGGAAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 CGGGACACCCGTGTGTTGGCTGCAGGAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 675
Qy        584 CGGGACACCCGTGTGTTGGCTGCAGGAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        676 TTCCAGTGCTTCAATTGCACCCTCTGCCTCAATGGACCGTCACCTCTTGCCAGGAG 735
Qy        644 TTCCAGTGCTTCAATTGCACCCTCTGCCTCAATGGACCGTCACCTCTTGCCAGGAG 703
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        736 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTTCTAAGAGAAAACGAGTGTGTC 795
Qy        704 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTTCTAAGAGAAAACGAGTGTGTC 763
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Db        796 TCCTGTAGTAACTGTAAGAAGAGCCTGGAGTGCACGAAGTTGTCCCCTACCCCAGATTGAG 855
Qy        764 TCCTGTAGTAACTGTAAGAAGAGCCTGGAGTGCACGAAGTTGTCCCCTACCCCAGATTGAG 823
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        856 AATGTTAAGGGCCACTGAGGACTCAGGCACCACCAGCAGT-GCTGTTGCCCCTGGT 905
Qy        824 AATGTTAAGGGCACTGAGGACTCAGGCACCACCAGCCGGTGCTGTTGCCCCAGGT 874
              ||||||||||| ||||||||||||||||||||||||||||  || |||||||||| |||
```

RESULT 14

```
LOCUS       I26928          6889 bp    DNA        PAT         01-OCT-1996
DEFINITION  Sequence 2 from patent US 5561053.
ACCESSION   I26928
NID         g1606798
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 6889)
  AUTHORS   Crowley,C.W.
  TITLE     Method for selecting high-expressing host cells
  JOURNAL   Patent: US 5561053-A 2 01-OCT-1996;
FEATURES             Location/Qualifiers
     source          1..6889
                     /organism="unknown"
BASE COUNT     1729 a   1826 c   1681 g   1653 t
ORIGIN
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Query Match   43.9%; Score 504; DB 25; Length 6889;
Best Local Similarity   99.0%; Pred. No. 0.00e+00;
Matches 509; Conservative   0; Mismatches   5; Indels   0; Gaps   0;

```
Qy        464 TGCAGGGAGTGTGAGAGCGGCGGCTCCTTCAGAAAACCACCTCAGACACTGCCCTC 523
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1845 TGCAGGGAGTGTGAGAGGCGGCGGCTCCTTCACCGCTGCTTCAGAAAACCACCTCAGACACTGCCCTC 1904
Qy        524 AGCTGCTCCAAAATGCCGAAAGGAAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1905 AGCTGCTCCAAAATGCCGAAAGGAAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 1964
Qy        584 CGGGACACCCGTGTGTTGGCTGCAGGAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1965 CGGGACACCCGTGTGTTGGCTGCAGGAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 2024
Qy        644 TTCCAGTGCTTCAATTGCACCCTCTGCCTCAATGGACCGTCACCTCTTGCCAGGAG 703
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2025 TTCCAGTGCTTCAATTGCACCCTCTGCCTCAATGGACCGTCACCTCTTGCCAGGAG 2084
Qy        704 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTTCTAAGAGAAAACGAGTGTGTC 763
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2085 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTTCTAAGAGAAAACGAGTGTGTC 2144
Qy        764 TCCTGTAGTAACTGTAAGAAGAGCCTGGAGTGCACGAAGTTGTCCCCTACCCCAGATTGAG 823
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2145 TCCTGTAGTAACTGTAAGAAGAGCCTGGAGTGCACGAAGTTGTCCCCTACCCCAGATTGAG 2204
Qy        824 AATGTTAAGGGCCACTGAGGACTCAGGCACCACCAGCCGGTGCTGTTGCCCCAGGT 874
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Query Match   ...
Best Local Similarity   ...
Matches 509; Conservative   0; Mismatches   ...

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Db       1725 GATAGTGTGTGTCCCCAAGGAGAAAATATATCCACCCTCAAAAATAATAATTGATTTGTGTACC 1784
Qy        344 GATAGTGTGTGTCCCCAAGGAGAAAATATATCCACCCTCAAAAATAATTGATTTGCTGTACC 403
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||| |||||
Db       1785 AAGTGCCACAAAGGAACCTACTTGTACAAATGACTGTCCAGGCCCGGGGGCAGGATACCGAC 1844
Qy        404 AAGTGCCACAAAGGAACCTACTTGTACAAATGACTGTCCAGGCCCGGGGGCAGGATACCGAC 463
```

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Db    2205  AATGTTAAGGGCACTGAGGAGACTCAGGCACCACAG  2238
            |||||||||||||||||||||||||||||||||||
Qy     824  AATGTTAAGGGCACTGAGGACTCAGGCACCACAG  857
```

```
RESULT  15

LOCUS        A20255          2061 bp    DNA              PAT       20-SEP-1995
DEFINITION   55kd receptor gene for human TNF-alpha.
ACCESSION    A20255
NID          g1247401
KEYWORDS     .
SOURCE       human.
  ORGANISM   Homo sapiens
             Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
             Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 2061)
  AUTHORS
  TITLE      MODIFIED HUMAN TNFALPHA (TUMOR NECROSIS FACTOR ALPHA) RECEPTOR
  JOURNAL    Patent: WO 9207076-A 23 30-APR-1992;
FEATURES             Location/Qualifiers
  source       1..2061
             /organism="Homo sapiens"
             /db_xref="taxon:9606"
BASE COUNT    429 a   616 c   573 g   443 t
ORIGIN

Query Match     43.5%;  Score 499;  DB 25;  Length 2061;
Best Local Similarity   97.9%;  Pred. No. 0.00e+00;
Matches    520;  Conservative    0;  Mismatches    9;  Indels   2;  Gaps   2;

Db     275  GATAGTGTGTGTCCCAAGGAAAAAATATATCCACCCTCAAAATAAATTAAATTCGATTTGCTGTACC  334
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Qy     344  GATAGTGTGTGTCCCAAGGAAAAATATATCCACCCTCAAAATAAATTCGAATTTGCTGTACC  403

Db     335  AAGTGCCACAAAAGGAACCTACTTGTACAATGACTGTCCAGCCCCGGGGCAGGATACGGAC  394
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     404  AAGTGCCACAAAAGGAACCTACTTGTACAATGACTGTCCAGCCCCGGGGCAGGATACGGAC  463

Db     395  TGCAGGGAGTGTGAGAGCGGGCCTCCTTCACCGCCTTCAGAAAACCACCTCAGACACTGCCTC  454
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     464  TGCAGGGAGTGTGAGAGCGGGCCTCCTTCACCGCCTTCAGAAAACCACCTCAGACACTGCCTC  523

Db     455  AGCTGCTCCAAAATGCCGAAAGGAAAATGGGTCAGGTGGAGATCTCTTCTTCTTGCACAGTGGAC  514
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     524  AGCTGCTCCAAAATGCCGAAAGGAAAATGGGTCAGGTGGAGATCTCTTCTTCTTGCACAGTGGAC  583

Db     515  CGGGGACACCCGTGTGTGGGCTGCAGGAAGAAACCAGTACCGGCCATTATTGGAGTGAAAACCTT  574
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     584  CGGGGACACCCGTGTGTGGGCTGCAGGAAGAAACCAGTACCGGCCATTATTGGAGTGAAAACCTT  643

Db     575  TTCCAGTGCTTCAATTGCAGCCTTCGCCTCAATGGGACCGGTGCAC-TCTCCTGCCAGGAG  633
            ||||||||||||||||||||||||||| |||||||||||||||||  ||||||||||
Qy     644  TTCCAGTGCTTCAATTGCACCCTTCGCCTCAATGGGACCGGTGCACCTCACCTCCTGTCAGGAG  703

Db     634  AAACAGAAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC  693
            ||||||||||||||||| ||||||||||||||||| || |||||||||||||||||||||
Qy     704  AAACAGAAACACCGTCTGCACCTGCCATGCAGGTTTCTTTTAAGAGAAAACGAGTGTGTC  763

Db     694  TCCTGTGAGTAACTGTAAGAAAAAGCCTGGAGTGCACGGAAGTTGTGCCTACCCCAGATTGAG  753
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     764  TCCTGTAGTAACTGTAAGAAAAAGCCTGGAGTGCACGGAAGTTGTCCCTACCCCAGATTGAG  823

Db     754  AATGTTAAGGGCACTGAGGAGACTCAGGCACCACAGT-GCTGTTGCCCCTGGT  803
            |||||||||||||||||||||||||||||||||||| |||||| |||
Qy     824  AATGTTAAGGGCACTGAGGACTCAGGCACCACCACGCCGGTGCTGCTGCCCCCAGGT  874
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**************************************
           M P S R C H  (TM)
**************************************

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**************************************

MPsrch.nn   n.a. - n.a. database search, using Smith-Waterman algorithm

Run on:        Wed May 6 14:19:06 1998;   MasPar time 149.10 Seconds
                                          887.730 Million cell updates/sec

Tabular output not generated.

Title:         >US-08-804-166-5
Description:   (1-1147) from US08804166.seq
Perfect Score: 1147
N.A. Sequence: 1  TCGAGATGGCTACAGGTAAG.........AATCTTAAGGATCCCTCGAG 1147
Comp:             AGCTCTACCGATGTCCATTC.........TTAGAATTCCTAGGGAGCTC

Scoring table: TABLE default
               Gap 6

Nmatch  STD :  Dbase 0; Query 0
Searched:      159651 seqs, 57698962 bases x 2
Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database:      n-geneseq30
               1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
               8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
               14:part14 15:part15 16:part16 17:part17 18:part18
               19:part19 20:part20 21:part21 22:part22 23:part23
               24:part24 25:part25 26:part26 27:part27 28:part28
               29:part29 30:part30 31:part31 32:part32 33:part33

Statistics:    Mean 9.143;  Variance 4.888;  scale 1.870

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	506	44.1	1334	1	Q06282	Plasmid Tumour Necros	0.00e+00
2	506	44.1	1368	3	Q49932	Lambda-derived TNF-R	0.00e+00
3	506	44.1	2062	3	Q20973	TNF-alpha binding pro	0.00e+00
4	506	44.1	2062	4	Q24440	Encodes TNF-alpha 55k	0.00e+00
5	506	44.1	2088	2	Q10883	30kD TNF inhibitor pr	0.00e+00
6	506	44.1	2111	2	Q10955	Encodes human 55kD TN	0.00e+00
7	506	44.1	2175	15	Q90513	p55 TNF-R gene.	0.00e+00
8	504	43.9	2141	1	Q06285	Human Tumour Necrosis	0.00e+00
9	504	43.9	2176	2	Q12215	Type I TNF receptor.	0.00e+00
10	504	43.8	6889	18	T15931	DHFR/intron (WTrasSD)	0.00e+00
11	502	43.8	2170	9	Q50870	p55 Tumour necrosis f	0.00e+00
12	468	40.8	608	4	Q24441	Encodes truncated TNF	0.00e+00
13	375	32.7	504	4	Q24445	Encodes truncated TNF	1.89e-267
14	345	30.1	474	4	Q24442	Encodes truncated TNF	1.16e-243
15	288	25.1	2771	31	T76770	Rat Fabp1 gut-specifi	1.27e-198
16	287	25.0	2160	33	T62826	Human growth hormone	7.82e-198
17	280	24.4	336	6	Q41459	Human growth hormone	2.55e-192
18	264	23.0	707	17	T03236	Single chain gonadotr	9.85e-180
19	264	23.0	719	17	T03235	Single chain gonadotr	9.85e-180
20	264	23.0	728	17	T03224	Single chain gonadotr	9.85e-180
21	264	23.0	743	17	T03219	Single chain gonadotr	9.85e-180
22	264	23.0	743	17	T03233	Single chain gonadotr	9.85e-180
23	264	23.0	743	17	T03231	Single chain gonadotr	9.85e-180
24	264	23.0	744	17	T03221	Single chain gonadotr	9.85e-180
25	264	23.0	752	17	T03229	Single chain gonadotr	9.85e-180
26	264	23.0	752	17	T03227	Single chain gonadotr	9.85e-180
27	264	23.0	836	17	T03212	Single chain gonadotr	9.85e-180
28	264	22.8	592	24	T41695	Dimeric glycoprotein	3.67e-178
29	264	22.8	312	17	T03237	Gonadotropin alpha su	1.89e-173
30	264	22.3	836	17	T03243	Single chain gonadotr	1.89e-173
31	264	22.2	256	17	T03243	Single chain gonadotr	1.89e-173
32	255	22.2	477	4	Q24444	Encodes truncated TNF	1.15e-172
33	255	22.2	2173	1	Q06284	Rat Tumour Necrosis F	1.15e-172
34	255	18.6	462	4	N30032	Sequence of gene for	5.08e-125
35	255	16.9	2660	3	N30032	Porcine alpha subunit	1.27e-112
36	255	15.5	608	2	003846	Ovine FSH alpha subun	2.31e-103
37	178	14.5	716	2	010059	Encodes truncated TNF	1.15e-103
38	166	14.3	731	1	003843	Bovine alpha subunit	4.03e-102
39	164	13.1	480	1	003849	Equine alpha subunit	4.52e-91
40	150	12.5	482	1	003820	Gene encoding equine	1.76e-86
41	144	11.3	1027	2	010878	Partial sequence of c	8.03e-76
42	130	8.8	345	11	065374	Fish gonadotropic hor	5.08e-54
43	101	8.8	340	2	N91174	Gene encoding of c	1.55e-52
44	99	8.6	360	11	065373	Fish gonadotropic hor	1.40e-38
45	80	7.0	267	3	N50521	Sequence encoding sal	7.41e-38

ALIGNMENTS

```
RESULT

                    1
AC  Q06282  standard; DNA; 1334 BP.
    Q06282;
DT  29-JAN-1991 (first entry)
DE  Plasmid Tumour necrosis Factor-Binding Protein 15 cDNA insert.
KW  Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
OS  Homo sapiens.
FH  Key              Location/Qualifiers
FT  CDS              213..1325
FT  /*tag= a
FT  /product=TNF-BP
PN  PTNF-BP15; ss.
PN  24-OCT-1990.
PR  06-APR-1990; 106624.
PR  21-APR-1989; DE-913101.
PR  21-JUN-1989; DE-920282.
PA  (BOEH ) BOEHRINGER INGELHEIMINT.
PA  (BOEH ) BOEHRINGER INGELHEIM.
PI  Hauptmann R, Himmler A, Maurer-Fogy I, Stratowa C;
DR  WPI; 90-321987/43.
DR  P-PSDB; R07449.
PT  DNA encoding TNF binding protein and TNF- receptor - used in
PT  tumour treatment and to understand mechanisnsm to TNF action
PS  Disclosure; Fig 1(1-3); 51PP; German.
CC  PTNF-BP15 is one of 30 positives clones in a screened cDNA library
CC  from induced TNF-induced fibrosarcoma cells. A TNF-BP had been
CC  isolated from the urine of patients with uraemia and probes/primers
CC  were constructed from the determined amino acid sequence.
CC  To produce a vector expressing a soluble form of TNF-binding
CC  protein, this plasmid was cut with XmnI, amplified by PCR and the
CC  amplified DNA cut with BamHI and EcoRI.
CC  The resulting 0.75 kb DNA fragment was inserted into pT7/T3 alpha-19
CC  (BRL) cut with the same enzymes to recover pTNF-BP. This was cut
CC  with BamHI and EcoRI, and the recovered fragment inserted into
CC  pAD-CMVl (Q06283) to give the required plasmid pADTNF-BP.
CC  See also Q06282-Q06285.
SQ  Sequence  1334 BP;   299 A;   409 C;   342 G;   284 T;

Query Match      44.18;   Score 506;   DB 1;   Length 1334;
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Left column

```
RESULT 2
ID   Q49932 standard; cDNA to mRNA; 1368 BP.
AC   Q49932;
DT   29-APR-1994 (first entry)
DE   Lambda-derived TNF-R cDNA.
KW   Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;
KW   IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;
KW   rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;
KW   pulmonary fibrosis; silicosis; allograft; xenograft; rejection;
KW   graft verses host disease; sepsis; Inflammation; allergy;
KW   autoimmune dysfunction; ss.
OS   Homo sapiens.
OS   Lambda-gt10-7-ctnfbp.
FH   Key              Location/Qualifiers
FT   CDS              1..1366
FT                    /tag= a
FT                    /product= hTNF-R
FT   sig_peptide      1..120
FT                    /tag= b
FT   mat_peptide      121..1363
FT                    /tag= c
PN   WO9319777-A.
PD   14-OCT-1993
PF   26-MAR-1993; U02938.
PR   30-MAR-1992; US-860710.
PA   (IMMV ) IMMUNEX CORP.
PI   Smith CA;
DR   WPI; 93-336592/42.
DR   P-PSDB; R42059.
PT   New fusion protein tumour necrosis factor and human interleukin-1
PT   receptor - useful in therapy, diagnosis and assays of e.g.
PT   rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.
PS   Disclosure; Page 57-59; 85pp; English.
```

```
Best Local Similarity 98.18; Conservative  0;  Pred. No. 0.00e+00;  Mismatches 9;  Indels 1;  Gaps 1;
Matches 521;

Qy   344 GATAGTGTGTGTCCCCAAGGAAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403
         |||||||||||| |||||||||||||||||||||||||| ||||||||||||| |||||
Db   333 gatagtgtgtgtcccaaggaaaatatatcccaccctcaaaaataattcgatttgtgtacc 392

Qy   404 AAGTGCCACAAAGGAACCTACTTGTACAAATGACACTGTCCAGGCGCCGGGGCAGGATACCGAC 463
         ||||||||||| ||||| ||||||||||| ||| ||||||||||||||||||||||||||| |||
Db   393 aagtgccacaaggaaccactacttgtacaatgactgtccaggcgccggggcaggatacggac 452

Qy   464 TGCAGGGAGTGTGAGAGCGCGGCTCCTTCACCGCTTCAGAAAAACCACCTCAGACACTGCCTC 523
         |||||||  ||||| |||| |||| |||||| | | ||| |||||||||||||||||||||||||
Db   453 tgcaggggagtgtgtgagcggggctcctccagcaaccacctcagacactgcctc 512

Qy   524 AGCTGGCTCCAAATGCCGGAAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583
         ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db   513 agctggctccaaatgcccgaaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 572

Qy   584 CGGGACACCGTGTGTGGGCTGCAGGAAGAACCAGTACCGCGGCCATTATTGGAGTGAAAAACCTT 643
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db   573 cgggacaccgtgtgtgggctgcaggaagaaccagtaccgcggccattattggagtgaaaacctt 632

Qy   644 TTCCAGTGCTTCAATTGCAGCCCTCTCCAATGGGACCTGCACCTCTCCTGTCCAGGAG 703
         |||||||||||||||||||||||||||||||||||| ||||| |||||||| |||||
Db   633 ttccagtgcttcaattgcagccctctccaatgggacgtgcacctctcctgcccaggag 692

Qy   704 AAACAGAACACCGTGTGTGCCTGCAGGTTTCTTCTTCTCTAAGAGAAAACGAGTGTGTC 763
         ||||||| ||| ||||||| ||||||||| |||||||||||||||||||||||||||
Db   693 aaacagagaaacacgtgtgtcacctgcaggttcttcttctctaagagaaaacgagtgtgtgtc 752

Qy   764 TCCTGTGTAGTTAACTGTTAAGAAAAAGCCTGGAGTGCACGAAGTTGTCCCGTACCCCAGATTGAG 823
         |||||||||||||||||||||||||| |||||||||||||
Db   753 tcctgtgtagttaactgttaagaaaagcctgggagtgcacctctccctgcccagag 812

Qy   824 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGCCGGTGCTGCCCAGGT 874
         |||||||||||||||||||||||||||||||||||||  | |||| ||||
Db   813 aatgttaaggggcactgaggactcaggcaccacagt-gctgttgccctggt 862
```

Right column

```
CC   The sequences given in Q49931-32 encode human tumour necrosis factor
CC   receptor (TNF-R) and the sequences in Q49933-34 encode human
CC   interleukin-1 receptor (IL-1R). These sequences were used in the
CC   production of a fusion protein which conformed to one of the
CC   formulae:
CC      TNF-R-linker-TNF-R-linker-IL-1R
CC      IL-1R-linker-TNF-R-linker-TNF-R or
CC      TNF-R-linker-TNF-R-linker-IL-1R
CC   The linker may comprise 5-100 amino acids selected from Gly, Asp,
CC   Ser, Thr and Ala. These linkers separate the individual moieties
CC   by such a distance that each component of the fusion protein is
CC   capable of folding into the secondary or tertiary structure required
CC   for its biological activity. These fusion proteins may be used in
CC   therapy, diagnosis and assays for conditions mediated by TNF or IL-1,
CC   particularly in conditions in which both TNF and IL-1 play a causative
CC   role. They may be used to treat cachexia, rheumatoid arthritis,
CC   diabetes, multiple sclerosis, pulmonary fibrosis and silicosis,
CC   cerebral malaria, allograft and xenograft rejection in graft verses
CC   host disease, sepsis, septic shock, Inflammation, allergies and
CC   autoimmune dysfunctions.
SQ   Sequence 1368 BP;   292 A;   424 C;   376 G;   276 T;

Query Match 44.1%;  Score 506;  DB 8;  Length 1368;
Best Local Similarity 98.1%;  Pred. No. 0.00e+00;  Mismatches 9;  Indels 1;  Gaps 1;
Matches 521;  Conservative

Qy   344 GATAGTGTGTGTCCCCAAGGAAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403
         |||||||||||| |||||||||||||||||||||||||| ||||||||||||| |||||
Db   121 gatagtgtgtgtcccaaggaaaatatatcccaccctcaaaaataattcgatttgtgtacc 180

Qy   404 AAGTGCCACAAAGGAACCTACTTGTACAAATGACACTGTCCAGGCGCCGGGGCAGGATACCGAC 463
         ||||||||||| ||||| ||||||||||| ||| ||||||||||||||||||||||||||| |||
Db   181 aagtgccacaaggaaccactacttgtacaatgactgtccaggcgccggggcaggatacggac 240

Qy   464 TGCAGGGAGTGTGAGAGCGCGGCTCCTTCACCGCTTCAGAAAAACCACCTCAGACACTGCCTC 523
         |||||||  ||||| |||| |||| |||||| | | ||| |||||||||||||||||||||||||
Db   241 tgcaggggagtgtgtgagcggggctcctccagcaaccacctcagacactgcctc 300

Qy   524 AGCTGGCTCCAAATGCCGGAAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583
         ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db   301 agctggctccaaatgcccgaaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 360

Qy   584 CGGGACACCGTGTGTGGGCTGCAGGAAGAACCAGTACCGCGGCCATTATTGGAGTGAAAAACCTT 643
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db   361 cgggacaccgtgtgtgggctgcaggaagaaccagtaccgcggccattattggagtgaaaacctt 420

Qy   644 TTCCAGTGCTTCAATTGCAGCCCTCTCCAATGGGACCTGCACCTCTCCTGTCCAGGAG 703
         |||||||||||||||||||||||||||||||||||| ||||| |||||||| |||||
Db   421 ttccagtgcttcaattgcagccctctccaatgggacgtgcacctctcctgcccaggag 480

Qy   704 AAACAGAACACCGTGTGTGCCTGCAGGTTTCTTCTTCTCTAAGAGAAAACGAGTGTGTC 763
         ||||||| ||| ||||||| ||||||||| |||||||||||||||||||||||||||
Db   481 aaacagaaaacacgtgtgtcacctgcaggttcttcttctctaagagaaaacgagtgtgtgtc 540

Qy   764 TCCTGTGTAGTTAACTGTTAAGAAAAAGCCTGGAGTGCACGAAGTTGTCCCGTACCCCAGATTGAG 823
         |||||||||||||||||||||||||| |||||||||||||
Db   541 tcctgtgtagttaactgttaagaaaagcctgggagtgcacctctccctgcccagag 600

Qy   824 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGCCGGTGCTGCCCAGGT 874
         |||||||||||||||||||||||||||||||||||||  | |||| ||||
Db   601 aatgttaaggggcactgaggactcaggcaccacagt-gctgttgccctggt 650
```

```
RESULT 3
ID   Q20973 standard; DNA; 2062 BP.
AC   Q20973;
DT   11-MAY-1992 (first entry)
DE   TNF-alpha binding protein gene.
KW   Tumour necrosis factor alpha; autoimmune diseases; cachectin; ss;
KW   extracellular domain.
OS   Homo sapiens.
FH   Key              Location/Qualifiers
FT   CDS              155..1522
```

Left column

```
FT                  /*tag- a
FT                  /*tag- b
FT   mat_peptide    155..274
FT                  /*tag- c
FT   mat_peptide    275..1522
FT   misc_feature   473..532
FT                  /*tag- d
FT   misc_feature
FT                  /note= "homologous to probe Q20974"
FT   misc_feature   242..751
FT                  /*tag- e
FT                  /note= "encodes the extracellular domain of human
FT                  TNF alpha receptor"
PN   GB2246569-A.
PD   05-FEB-1992.
PF   15-JUN-1990; 013410.
PR   15-JUN-1990; GB-013410.
PA   (CHAR-) CHARING CROSS SUNLE.
PI   Feldman M, Gray P, Turner M, Brennan F;
DR   WPI; 92-043613/05.
DR   P-PSDB; R20787.
PT   New tumour necrosis factor alpha binding protein and polypeptide
PT   - useful in treating cachexia, sepsis and auto immune diseases
PT   e.g. rheumatoid arthritis
PS   Disclosure; Fig 1; 25pp; English.
CC   The sequence is that of DNA encoding tumour necrosis factor alpha
CC   binding protein which was obtd. from a human placental cDNA library
CC   in lambda gt11 using a probe (Q20974). The DNA also encodes the
CC   extracellular domain of human TNF alpha receptor and as such it is
CC   useful for treating diseases where TNF alpha is involved as a
CC   causative agent, e.g. cachexia, sepsis and autoimmune diseases,
CC   specifically rheumatoid arthritis. See also Q20974.
SQ   Sequence   2062 BP;   429 A;   616 C;   573 G;   444 T;

Query Match         44.1%;   Score 506;   DB 3;   Length 2062;
Best Local Similarity  98.1%;
Matches   521;   Conservative   0;   Pred. No. 0.00e+00;   Mismatches   9;   Indels   1;   Gaps   1;

Db  275 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 334
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403

Db  335 aagtgccacaaaggaacctacttgtacaatgactgtccaggcgcccgggcaggatacggac 394
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCGCCCGGGCAGGATACGGAC 463

Db  395 tgcaggggagtgtgagacggcgtcctccaccgcttcagaaaaccacctcagacactgcctc 454
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  464 TGCAGGGAGTGTGAGACGGCGTCCTCCACCGCTTCAGAAAAACCACCTCAGACACTGCCTC 523

Db  455 agctgctcccaaatgccgaaaaggaaatgggtcagttggagatctcttgtcacagtggac 514
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  524 AGCTGCTCCCAAATGCCGAAAAGGAAATGGGTCAGTTGGAGATCTCTTGTCACAGTGGAC 583

Db  515 cgggacaccgtgtgtcggctgcaggaagaaccagtaccggccattattggagtgaaaactt 574
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  584 CGGGACACCGTGTGTCGGCTGCAGGAAGAACCAGTACCGGCCATTATTGGAGTGAAAACTT 643

Db  575 ttccagtgcttcaattggcagcctctgctcaattggaccgtgcaacctctcctgccoaggag 634
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Qy  644 TTCCAGTGCTTCAATTGGCAGCCTCTGCTCAATTGGACCGTGCAACCTCTCCTGCCGGAG 703

Db  635 aaacagaaacacgtgtgcacctgccatgcagtgtttttctttaagagaaaacgagtgtgtc 694
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  704 AAACAGAAACACGTGTGCACCTGCCATGCAGTTTCTTTCTTAAGAGAAAACGAGTGTGTC 763

Db  695 tcctgtagtaactgtaagaaaagcctgcacagtgtcctacccccagatgag 754
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  764 TCCTGTAGTAACTGTAAGAAAAGCCTGCACAGTGTCCTACCCCCAGATTGAG 823

Db  755 aatgttaagggcactgaggactcaggcacccacagt-gctgttgccccctggt 804
        ||||||||||||||||||||||||||||||||||||| |||||||||||||||
Qy  824 AATGTTAAGGGCACTGAGGACTCAGGCACCCACAGCCGGTGCTGCCCCCAGGT 874
```

Right column

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RESULT 4

ID   Q24440 standard; DNA; 2062 BP.
AC   Q24440;
DT   05-NOV-1992 (first entry)
DE   Encodes TNF-alpha 55kD receptor.
KW   tumour necrosis factor alpha; extracellular binding domain;
KW   treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
KW   malaria; viral meningitis; graft versus host disease;
KW   autoimmune disease; rheumatoid arthritis.
OS   Homo sapiens.
FH   Key               Location/Qualifiers
FH
FT   CDS               156..1517
FT                     /*tag- a
FT                     /product= human TNF-alpha
FT   mat_peptide       1265..1267
FT                     /*tag- b
FT   mat_peptide       1265..1267
FT                     /*tag- c
FT                     /note= "3"
FT                     /codon- Seq:"AAG", aa:Leu
FT   mat_peptide       1433..1435
FT                     /*tag- e
FT                     /codon- Seq:"GAC", aa:Asn
FT   sig_peptide       156..274
FT                     /*tag- f
FT                     /codon- Seq:"TCG", aa:Thr
FT   mat_peptide       1258..1260
PN   WO9207076-A.
PD   30-APR-1992;
PN   18-OCT-1991; G01826.
PF   18-OCT-1990; GB-022648.
PA   (CHAR-) CHARING CROSS SUNLEY RES CENT.
PI   Brennan FM, Feldmann M, Gray PW, Turner MJC;
DR   WPI; 92-167156/20.
DR   P-PSDB; R24000
PT   New polypeptide capable of binding human TNF alpha - comprises
PT   first three cysteine-rich subdomains of TNF alpha receptor for
PT   treating autoimmune disease, septic shock, HIV etc.
PS   Claim 4; Fig 1; 43pp; English.
CC   This sequence encodes human TNF-alpha 55kD receptor . A placenta cDNA
CC   library in gt10 was screened with probe Q29236. Ten hybridising clones
CC   were plaque purified and cDNA size determined by PAGE against an
CC   Eco RI digested phage DNA. The inserts of two cDNA clones were then
CC   sequenced. The coding region of the majority of the human TNF-alpha
CC   55kD receptor was isolated as an EcoRI fragment encoding 374 amino
CC   acids, and cloned into a mammalian cell expression vector, resulting
CC   in pTNFR. A derivative of the TNF-alpha receptor was produced by
CC   engineering a termination codon just prior to the transmembrane
CC   domain. PCR with primers Q29237,8 generated a 300bp
CC   restriction fragment which was cloned into prTNFR, giving pTNFRed.
CC   DNA sequencing confirmed the designed DNA sequence.
CC   The TNF-alpha receptor expression plasmids were then transfected
CC   into monkey COS-7 cells.
CC   See also Q24440-51, R24000, R24080-84, R27585, Q29236-8
SQ   Sequence   2062 BP;   429 A;   618 C;   572 G;   443 T;

Query Match         44.1%;   Score 506;   DB 4;   Length 2062;
Best Local Similarity  98.1%;
Matches   521;   Conservative   0;   Pred. No. 0.00e+00;   Mismatches   9;   Indels   1;   Gaps   1;

Db  275 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 334
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403

Db  335 aagtgccacaaaggaacctacttgtacaatgactgtccaggcgcccgggcaggatacggac 394
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCGCCCGGGCAGGATACGGAC 463

Db  395 tgcaggggagtgtgagagggcgctcctccaccgcttcacccgcttcagaaaaacacctcagacaactgcctc 454
        |||||||||||||||| ||||||||||||||||||||||            |||||||||||||||||||||
Qy  464 TGCAGGGAGTGTGAGACGGCGTCCTCCACCGCTTCAGAAAAACCACCTCAGACACTGCCTC 523
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Db   455 agctgctccaaatgccgaaaggaaatggggtcaggtggaagatctcttcttcttgcacagtggac 514
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   524 AGCTGCTCCAAATGCCGAAAGGAAATGGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db   515 cgggacaccgtgtgtggctcaggaggaagacccagtaccggccattattgggtgaaaccctt 574
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   584 CGGGACACCGTGTGTGGCTCCAGGAAGAACCAGTACCGGCCATTATTGGAGTGAAAACCTT 643

Db   575 ttccagtgcttcaattgcagcctctgcctcaagtgggacgtgcaccctctcctgcaaggag 634
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   644 TTCCAGTGCTTCAATTGCACCCTCTGCCTCAAATGGGACGTGCACCCTCTCCTGTCAGGAG 703

Db   635 aacacagaccgtgtgcacctgccatgcagcgttcttcttctaagagaaaaacgagtgtgtc 694
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   704 AAACAGAACACCGTCTGCCACCTGCCACGGTTTCTTCTTTCTAAGAGAAAAACGAGTGTGTC 763

Db   695 tcctgtgtaactgtaagaaaagcctggagtcagcaagttgtgcctaccccagagtgag 754
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   764 TCCTGTGTAACTGTAAGAAAAGCCTGGAGTCAGCAAGTTGTGCCTACCCCAGAGTTGAG 823

Db   755 aatgttaagggcactgaggactcaggcaccacaagt-gctgttgccctggt 804
         ||||||||||||||||||||||||||||||||||| ||||||||||| |||
Qy   824 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGCCGCGGTGCTGCCCCAGGT 874
```

RESULT 5

```
ID   Q10083  standard; cDNA; 2088 BP.
AC   Q10083;
DT   13-MAY-1991  (first entry)
DT   24-JAN-1991.
PN   AU9058976-A.
PF   16-JUL-1990;  058976.
PF   18-JUL-1989;  US-381080.
PR   11-DEC-1989;  US-450329.
PR   07-FEB-1990;  US-479661.
PA   (SYNE-) SYNERGEN INC.
WPI; 91-073847/11.
DR   P-PSDB; R10986.
CC   Tumour necrosis factor inhibitor - for suppression of TNF-alpha
CC   and -beta, useful as therapeutic agent.
CC   Disclosure; Fig 21; 142pp; English.
CC   The sequence encodes the entire 30 kD TNF inhibitor. The clone from
CC   which the sequence was obtd. was isolated from a cDNA library
CC   prepd. from RNA form U937 cells treated with PMA/PHA.  The whole
CC   gene can be inserted into expression vectors for prepn. of TNF
CC   inhibitor for use in the treatment of inflammatory and degenerative
CC   diseases.
CC   See also Q10878, Q10884 and Q10907.
SQ   Sequence 2088 BP;  626 C;  578 G;  445 T;

FH   Key            Location/Qualifiers
FT   CDS            171..1536
FT   /*tag= a

KW   Tumour necrosis factor; inhibitor; ss.
OS   Homo sapiens.
DE   30kD TNF inhibitor precursor gene in lambda-gt10-7ctnfbp.
```

```
Query Match     44.1%;  Score 506;  DB 2;  Length 2088;
Best Local Similarity  98.1%;
Matches  521;  Conservative  0;  Mismatches  9;  Indels  1;  Gaps  1;

Db   289 gatagtgtgtgtcccaaggaaaatatatccaccctcaaatattcgatttgctgtacc 348
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   344 GATAGTGTGTGTCCCAAGGAAAATATATCCACCCTCAAATAATTCGATTTGCTGTACC 403

Db   349 aagtgtcacacaaggaacctacctcgtacaatgactgtcaggagtcaggadatacggac 408
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   404 AAGTGTCACAAAGGAACCTACTACCTTGTACAATGACTGTCCAGGCCGGGACACCGGAC 463

Db   409 tgcaggggagtgtgagagcggacactcctcttccacgg... 468
         ||||||||||||||||||||||||||||||||||||
Qy   464 TGCAGGGAGTGTGAGAGCGGGCTCCTCACGCCTTCAGAAAAAACCACTCAGACACTGCCTC 523
```

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Db   469 agctgctccaaatgccgaaaggaaatggggtcaggtggaagatctcttcttcttgcacagtggac 528
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   524 AGCTGCTCCAAATGCCGAAAGGAAATGGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db   529 cgggacaccgtgtgtggctcaggaggaagacccagtaccggccattattgggtgaaaccctt 588
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   584 CGGGACACCGTGTGTGGCTCCAGGAAGAACCAGTACCGGCCATTATTGGAGTGAAAACCTT 643

Db   589 ttccagtgcttcaattgcagcctctgcctcaagtgggacgtgcaccctctcctgcaaggag 648
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   644 TTCCAGTGCTTCAATTGCACCCTCTGCCTCAAATGGGACGTGCACCCTCTCCTGTCAGGAG 703

Db   649 aacacagaccgtgtgcacctgccatgcagcgttcttcttctaagagaaaaacgagtgtgtc 708
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   704 AAACAGAACACCGTCTGCCACCTGCCACGGTTTCTTCTTTCTAAGAGAAAAACGAGTGTGTC 763

Db   709 tcctgtgtaactgtaagaaaagcctggagtcagcaagttgtgcctaccccagagtgag 768
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Qy   764 TCCTGTGTAACTGTAAGAAAAGCCTGGAGTCAGCAAGTTGTGCCTACCCCAGAGTTGAG 823

Db   769 aatgttaagggcactgaggactcaggcaccacaagt-gctgttgccctggt 818
         ||||||||||||||||||||||||||||||||||| ||||||||||| |||
Qy   824 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGCCGCGGTGCTGCCCCAGGT 874
```

RESULT 6

```
ID   Q10955  standard; cDNA; 2111 BP.
AC   Q10955;
DT   24-MAY-1991  (first entry)
DT   20-MAR-1991.
PN   EP-417563-A.
PD   20-MAR-1991.
PF   31-AUG-1990;  116707.
PR   12-SEP-1989;  CH-003319.
PR   08-MAR-1990;  CH-000746.
PR   20-APR-1990;  CH-001347.
PA   (HOFF ) HOFFMANN-LA ROCHE AG.
PI   Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;
PI   Schlaeger EJ;
WPI; 91-081851/12.
DR   P-PSDB; R11082.
CC   Insoluble tumour necrosis factor binding proteins - and DNA
CC   encoding them, useful in pharmaceutical prods. and for antibody
CC   prodn.
CC   Claim 4; Fig 1; 26pp; German.
CC   Partial amino acid sequences were determined for the 55 and 75kD
CC   TNF-BPs (see R11072,R11081) and oligonucleotide primers were
CC   synthesised based on these partial sequences. The primers were used
CC   to produce a cDNA fragment for use as aprobe to screen a human
CC   placental cDNA bank constructed in lambda gt11. Positive clones were
CC   identified and sequenced. DNA constructs comprising the TNF-BP coding
CC   sequence may also contain a fragment encoding a human Ig domain.
CC   Recombinant constructs are used to transform cells to confer
CC   improved TNF-binding properties.
CC   See also Q10956.
SQ   Sequence 2111 BP;  628 C;  588 G;  450 T;

FH   Key            Location/Qualifiers
FT   sig_peptide    187..273
FT   /*tag= a
FT   mat_peptide    274..1551
FT   /*tag= b

KW   Tumour Necrosis Factor; binding protein; septic shock;
KW   autoimmune glomerulonephritis; lymphokine; cytokine.
DE   Encodes human 55kD TNF-binding protein.
/product= 55kD TNF-BP
```

```
Query Match     44.1%;  Score 506;  DB 2;  Length 2111;
Best Local Similarity  98.1%;
Matches  521;  Conservative  0;  Mismatches  9;  Indels  1;  Gaps  1;

Db   307 gatagtgtgtgtcccaaggaaaatatatccaccctcaaatattcgatttgctgtacc 366
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   344 GATAGTGTGTGTCCCAAGGAAAATATATCCACCCTCAAATAATTCGATTTGCTGTACC 403
```

Left column

Db 367 aagtgcacaaggaacttacttgtacaatgactgtgtcaggagccccgggggcaggagatacggac 426
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCAGGAGCCCGGGGCAGGAGATACGGAC 463

Db 427 tgcaggggagtgtcgaggacgggcggctcccttcaccgcttcagaaaaccaacttagacactgcctc 486
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 464 TGCAGGGAGTGTGAGACGGGCGGCTTCAGAAAACCACCTCAGACACTGCCTC 523

Db 487 agctgctccaaatgccgaaagtgggtcaggtggagatcctcttctgcacagtggac 546
   |||||||||||||||||||||||||||||||||||||||||||||||||
Qy 524 AGTGCTCCAAATGCCGAAAGTGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583

Db 547 cgggaaccgtgtgtgctgcaggagaagaaccagtaccggcattattggagtgaaaaacctt 606
   |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 584 CGGGACACCGTGTGTGGCTGCAGGAGAAGAACCAGTACCGGCATTATTGGAGTGAAAAACCTT 643

Db 607 ttccagtgctccaattgagccctctcctgccaggag 666
   |||||||||||||||||||||||||||||||||
Qy 644 TTCCAGTGCTTCAATTGCAGCCTCTCCTGCCAGGAG 703

Db 667 aaacagaacaccgtgtgcacctgccatgcaggttcttctctaagagaaacgagtgtgtc 726
   ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 704 AAACAGAACACCGTGTGCCACCTGCCATGCAGGTTTCTTCTTAAGAGAAAACGAGTGTGTC 763

Db 727 tcctgtagtaactgtaagaaaagcctggagtgcacgaagttgtgcctaccccagattgag 786
   ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 764 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTCCCTACCCCAGATTGAG 823

Db 787 aatgttaaggcactgaggactcaggaccaccacagt-gctgttgccctggt 836
   |||||||||||||||||||||||||||||||| |||||||||||||
Qy 824 AATGTTAAGGCACTGAGGACTCAGGACCACCAGCCGGTGCTGCCCCCAGGT 874

RESULT 7
ID Q90513 standard; DNA; 2175 BP.
AC Q90513;
DT 19-JAN-1996 (first entry)
DE p55 TNF-R gene.
KW p55; tumour necrosis factor receptor; TNF-R; human; chimera;
KW epidermal growth factor receptor; EGF-R; protease; inhibitor;
KW phorbol myristate acetate; PMA; ss.
OS Homo sapiens.
FH Key   Location/Qualifiers
FT CDS   256.1623
FT /tag= a
FT /product= p55 TNF-R
FT misc_signal 2143..2149
FT /tag= b
FT /note= "possible poly-A signal"
PR 12-OCT-1993; IL-107268.
PF 11-OCT-1994; 075742.
PD 04-MAY-1995.
PN AU9475742-A.
PS Disclosure: Fig 1; 40pp; English
PT antagonising deleterious effects of TNF.
PT (TNF) receptor - from cell-bound TNF- receptor, useful for
PT New protease capable of cleaving soluble tumour necrosis factor
P-PSDB; R75084.
DR WPI; 95-19432/26.
PI Batkin M, Brakebusch C, Varfolomeev E, Wallach D;
PA (YEDA) YEDA RES & DEV CO LTD.

CC This sequence represents human p55 tumour necrosis factor (TNF-R) DNA.
CC Expression of this receptor is regulated by shedding of the extracellular
CC receptor fragment. The p55 TNF-R can be shed in response to different
CC inducing agents, e.g. phorbol myristate acetate (PMA), depending on cell
CC type. The only region of the receptor whose structure affects the
CC shedding response is the spacer region (see R75012) in the extracellular
CC domain. This region is located close to a site of cleavage of the
CC molecule, and links the Cys rich module to the transmembrane domain. The
CC spacer region of the encoded protein was used to create the chimeras
CC between human p55 TNF-R and murine epidermal growth factor receptor
CC (EGF-R) that are represented by deletion mutations (R75013-25) and substitutions
CC subjected to deletion mutations (R75013-25) and substitutions

Right column

CC (R75026-47). Of the spacer region, the most important residues are
CC Asn 172, Val 173, Lys 174 and Gly 175, with Val 173 being the most
CC important of these. The shedding of the receptor is independent of the
CC side chain identity of these residues. Mutations which alter the
CC dependence on the identity of Val 173. Mutations which alter the
CC conformation of the protein adversely effect the shedding process. The
CC mutations shown in R75013-47 were introduced in order to create an
CC inhibitor of a protease that is capable of cleaving the soluble TNF-R
CC from the cell bound TNF-R. Fragments of these inhibitors can be seen in
CC R75017-9, R75025, R75033-5 and R75042-3. These protease inhibitors can
CC be used for enhancing TNF function.

SQ Sequence 2175 BP; 474 A; 642 C; 603 G; 456 T;

Query Match 44.18; Score 506; DB 15; Length 2175;
Best Local Similarity 98.18;
Matches 521; Conservative 0; Mismatches 9; Indels 1; Gaps 1;
          Pred. No. 0.00e+00;

Db 376 gatagtgtgtgtcccaagaggaaaatatatacccacccctcaaaataattcgatttgtgtacc 435
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 344 GATAGTGTGTGTCCCAAGAGGAAAAATATATCCCACCCCTCAAAATAATTAATTCGATTTGTGTACC 403

Db 436 aagtgccacaaaggaacctacttgtacaatgactgtcaggagcccggggcaggagatacggac 495
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGAGCCCGGGGCAGGAGATACGGAC 463

Db 496 tgcagggagtgtgagacggctcccgctccagaaaaccaacctcagactgcctc 555
   |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 464 TGCAGGGAGTGTGAGACGGGCGGCTTCCTTCAGAAAAACCACCTCAGACTGCCTC 523

Db 556 agctgctccaaatcgccgaaaaatggtcaggttcttcttctaagagaaaacgagtgtgtc 615
   ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 524 AGCTGCTCCAAATGCCGAAAGGGTCAGGTGGAGATCTCTTCTTGCACACAGTGGAC 583

Db 616 cgggacaccgtgtgtggctgcaggagaagaaccagtaccggcattattggagtgaaaaacctt 675
   |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 584 CGGGACACCGTGTGTGGCTGCAGGAGAAGAACCAGTACCGGCATTATTGGAGTGAAAAACCTT 643

Db 676 ttccagtgcttcaattgcagcctctcctgccaggag 735
   |||||||||||||||||||||||||||||||||||
Qy 644 TTCCAGTGCTTCAATTGCAGCCTCTCCTGCCAGGAG 703

Db 736 aaacagaacaccgtgtgccacctgccatgcaggtttcttcttaagagaaaacgagtgtgtc 795
   ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 704 AAACAGAACACCGTGTGCCACCTGCCATGCAGGTTTCTTCTTAAGAGAAAACGAGTGTGTC 763

Db 796 tcctgtagtaactgtaagaaaagcctggagtgcacgaagttgtcctaccccagattgag 855
   ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 764 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTCCCTACCCCAGATTGAG 823

Db 856 aatgttaaggcactgaggactcaggaccaccacagt-gctgttgccctggt 905
   |||||||||||||||||||||||||||||||||| ||||||||||||||
Qy 824 AATGTTAAGGCACTGAGGACTCAGGACCACCAGCCGGTGCTGCCCCCAGGT 874

RESULT 8
ID Q06285 standard; DNA; 2141 BP.
AC Q06285;
DT 29-JAN-1991 (first entry)
DE Human Tumour Necrosis Factor-Receptor cDNA insert.
KW Tumour necrosis factor binding protein; TNF BP; TNF-receptor;
KW lambdaTNF-R2; raTNF-R8; ss.
OS Homo sapiens.
FH Key   Location/Qualifiers
FT CDS   213..1577
FT /tag= a
FT /label= huTNF-R
PN EP-393438-A.
PD 24-OCT-1990.
PF 06-APR-1990; 106624.
PR 21-APR-1989; DE-913101.
PR 21-JUN-1989; DE-920282.
PA (BOEH) BOEHRINGER INGELHEIMINT.
PI Hauptmann R, Himmler A, Maurer-Fogy I, Stratowa C;

DR   WPI; 90-321987/43.
DR   P-PSDB; R07451.
PT   DNA encoding TNF binding protein and TNF- receptor - used in
PT   tumour treatment and to understand mechanism to TNF action
PS   Disclosure; Fig 91(1-2); 51pp; German.
CC   raTNF-R8 (Q06284) was used to screen the HS913T cDNA library.
CC   LambdaTNF-R2 encodes the complete human TNF-R2 and was used to
CC   construct a plasmid (pADTNF-R) expressing the product the same way
CC   as pADTNF-BP (see Q06282).
CC   See also Q06282-Q06285.
SQ   Sequence 2141 BP; 455 A; 633 C; 593 G; 460 T;

Query Match   43.9%; Score 504; DB 1; Length 2141;
Best Local Similarity   97.9%; Pred. No. 0.00e+00;
Matches 520; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy   333 gatagtgtgtccccaaggaaaatatatcccaccctcaaaataattcgattgctgtacc 392
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403

Qy   393 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccgggagatacggac 452
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGAGATACGGAC 463

Qy   453 tgcaggggagtgtgagagcggctcctctt caccgcttcagagaaacacctcagacacactgcctc 512
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   464 TGCAGGGGAGTGTGAGAGCGGCTCCTCTTCACCGCTTCAGAAAACACCTCAGACACTGCCTC 523

Qy   513 agctgctccaaatgccgaaagggaaatgggtcaggtggagatctctcttcttgcacagtggac 572
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   524 AGCTGCTCCAAATGCCGAAAGGGAAATGGGTCAGGTGGAGATCTCTTCTTTGCACAGTGGAC 583

Qy   573 cgggacaccgtgtgtggctgcaggaagaaccatacggcacttattggagtgaaaacctt 632
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Qy   633 ttccagtgcttcaattgcagccctctgcctcaaatgggacaccgtgcacctctcctgcaggag 692
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   693 TTCCAGTGCTTCAATTGCACCCCTCTGCCTCAAATGGGACACCGTGCACCTCTCGTCAGGAG 703

Qy   644 ... 644
              ...
Db   644 ...

Qy   693 aaacagaacaccgtgtcacctgccatgcaggtttcttcttcttaagagaaacgagtgtgttc 752
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   704 AAACAGAACACCGTGTCACCTGCCATGCAGGTTTCTTCTTCTTAAGAGAAACGAGTGTGTC 763

Qy   753 tcctgtgtagtaactgtaagaaagccctggagtgcagtggtgtgtcctaccccagagattcag 812
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db   764 TCCTGTGTAGTAACTGTAAGAAAGCCTGGAGTGCAGTGGTGTCCTACCCCAGATTGAG 823

Qy   813 aatgttaagggcactgaggactcaaggcacacagt-gctgttgccctggt 862
              ||||||||||||||||||||||||||||||| ||||| |||
Db   824 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGCCGGTTGCCCCCAGGT 874

RESULT 9
ID   Q12215 standard; DNA; 2176 BP.
AC   Q12215;
DT   12-SEP-1991 (first entry)
DE   Type I TNF receptor.
KW   Tumour Necrosis Factor; TNF; binding protein; TBP-I; ss.
OS   Homo sapiens.
FH   Key   Location/Qualifiers
FH
FT   terminator   244..246
FT   /*tag= a
FT   /note= "in-frame termination codon"
FT   CDS   256..1620
FT   /*tag= a
FT   /product= type I TNF receptor
FT   sig_peptide   256..318
FT   /*tag= b
FT   mat_peptide   319..1620
FT   /*tag= c
FT   misc_RNA   319..864
FT   /*tag= d

FT   /label= soluble_domain
FT   /note= "may be 2 codons shorter or a few codons
FT   longer"
FT   misc_feature   376..414
FT   /*tag= e
FT   /note= "TBP-I derived sequence"
FT   misc_feature   583..627
FT   /*tag= f
FT   /note= "TBP-I derived sequence"
FT   misc_feature   850..858
FT   /*tag= g
FT   /note= "TBP-I derived sequence"
FT   misc_feature   889..957
FT   /*tag= h
FT   /note= "TBP-I derived sequence"
FT   misc_RNA
FT   /*tag= i
FT   /label= transmembrane_domain
FT   repeat_unit   385..504
FT   /*tag= m
FT   /number= 1
FT   repeat_unit   505..633
FT   /*tag= j
FT   /number= 2
FT   repeat_unit   634..756
FT   /*tag= k
FT   /number= 3
FT   repeat_unit   757..858
FT   /*tag= l
FT   /number= 4
FT   polyA_signal   2145..2150
FT   /*tag= m
PN   EP-433900-A.
PD   26-JUN-1991.
PF   13-DEC-1990; 124133.
PR   13-DEC-1989; IL-0926697.
PR   12-JUL-1990; IL-095064.
PA   (YEDA) YEDA RES & DEV CO LTD.
PI   Wallach D, Nophar Y, Kemper O, Engelmann H, Brakebush C;
PI   Aderka D;
DR   WPI; 91-186774/26.
DR   P-PSDB; R12550.
PT   Recombinant tumour necrosis factor binding protein I - prepd. by
PT   transfecting eukaryotic cells with vector contg. deoxyribonucleic
PT   acid encoding human type I TNF receptor or soluble domain
PS   Disclosure; Fig 1(D); 30pp; English.
CC   The Tumour Necrosis Factor Binding Protein I is the soluble form of
CC   type I TNF-receptor and constitutes a fragment of the cell surface
CC   form of this receptor, corresp. to its extracellular domain.
CC   There is no characteristic poly(A) addition signal near the 3' end
CC   of the cDNA. The sequence ACTAAA (tag m) may serve as an
CC   alternative to this signal, but with low efficiency.
CC   See also Q12212-15.
SQ   Sequence 2176 BP; 475 A; 644 C; 602 G; 455 T;

Query Match   43.9%; Score 504; DB 2; Length 2176;
Best Local Similarity   97.9%; Pred. No. 0.00e+00;
Matches 520; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy   376 gatagtgtgtccccaaggaaaatatatcccaccctcaaaataattcgattgctgtacc 435
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 403

Qy   436 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccgggagatacggac 495
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGAGATACGGAC 463

Qy   496 tgcaggggagtgtgagagcggctcctcttcaccgcttcagagaaacacctcagacacactgcctc 555
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   464 TGCAGGGGAGTGTGAGAGCGGCTCCTCTTCACCGCTTCAGAAAACACCTCAGACACTGCCTC 523

Qy   556 agctgctccaaatgccgaaagggaaatgggtcaggtggagatctctcttcttgcacagtggac 615
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   524 AGCTGCTCCAAATGCCGAAAGGGAAATGGGTCAGGTGGAGATCTCTTCTTTGCACAGTGGAC 583

Qy   616 cgggacaccgtgtgtggctgcaggaagaaccagtacggcattattggagtgaaaacctt 675
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   584 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 643

Left column — RESULT 10

```
Qy   584  CGGGACACCGTGTGTGGGCTGCAGGAAGAAACCAGTACCGGCGCATTATTGGAGTGTGAAAACCTT  643
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   676  ttccagtgcttcaattgcagcctctgcctcaatgggacgtgcacctctcctgccaggag        735

Qy   644  TTCCAGTGCTTCAATTGCACCCTTCCTGCCTCAATGGGACGTGCACCTCTCCTGTCAGGAG       703
          ||||||||||||||||||||||||
Db   736  aaacagaacacacgtgtgcacctgccaatgcaggatttcttcttctaagagaaaagagtgtgtc   795

Qy   704  AAACAGAACACACGTGTGCACCTGCCAATGCAGGATTTCTTCTTCTAAGAGAAAAGAGTGTGTC    763
          ||||||||||||||||||||||
Db   796  tcctgtagtaactgtaagaaaagcctggagtgtgacgaagttgtgctcacccagattgag       855

Qy   764  TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGTGACGAAGTTGTGCTCACCCAGATTGAG       823
          ||||||||||||||||
Db   856  aatgttaaggcgcactgaggactcaggcgcaccacag                              905

Qy   824  AATGTTAAGGGCCACTGAGGACTCAGGCGCACCACAG                              874
```

```
RESULT 10
ID   T15931 standard; DNA; 6889 BP.
AC   T15931;
DT   20-JUN-1996  (first entry)
DE   DHFR/Intron (WTrasSD)-TnFr-IgG dicistronic vector.
KW   Recombinant host cell; dihydrofolate reductase; selectable marker;
KW   DHFR; ras splice donor; dicistronic vector; gene expression;
KW   immunoadhesin; TnFr-IgG; tumour necrosis factor; ds.
OS   Synthetic.
PN   WO9604391-A1.
PD   15-FEB-1996;
PF   28-JUL-1995; U05576.
PR   05-AUG-1994; US-286740.
PA   (GETH ) GENENTECH INC.
PI   Crowley CW;
DR   WPI; 96-129407/13.
PT   A dicistronic vector (T15930) comprises a regulatory region
PT   derived from the cytomegalovirus immediate-early gene, a
PT   selectable dihydrofolate reductase gene positioned within an
PT   intron having a 5' wild-type ras splice donor site, a downstream
PT   sequence coding for an immunoadhesin, TnFr-IgG, capable of binding
PT   tumour necrosis factor, and a poly-A sequence.  Transfection of CHO
CC   DHFR- cells and subsequent methotrexate amplification and growth of
CC   the cells in nutrient-rich medium gave TnFr-IgG in yields of 9.5
CC   ug/ml (15-fold higher compared to conventional vector amplified
CC   pools).
SQ   Sequence   6889 BP;   1729 A;   1826 C;   1681 G;   1653 T;

Query Match    43.9%;   Score 504;   DB 18;   Length 6889;
Best Local Similarity   99.0%;
Matches   509;   Conservative   0;   Mismatches   5;   Indels   0;   Gaps   0;
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Db  1725  gatagtgtgtgtcccaaggagaaatatatccaccctcaaaataattcgatttgctgtacc      1784
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   344  GATAGTGTGTGTCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC       403

Db  1785  aagtgccacaaaggaacctactctgtacaatgactgtccaggccgggggcaggataccggac    1844
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   404  AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGGAC    463

Db  1845  tgcaggggagtgtgagagcggtcctcttcaggagaaaaccaccagacaactgcctc         1904
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   464  TGCAGGGGAGTGTGAGAGCGGTCCTCTTCAGGAGAAAAACCACCTCAGACAACTGCCTC     523

Db  1905  agctgctcccaaaatgcccagaaatgggtcaggtgtggagatctcctccttgcacagtggac   1964
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   524  AGCTGCTCCCAAAATGCCCAAAGTGGGTCAGGTGTGGAGATCTCCTTGCACAGTGGAC      583

Db  1965  cgggacaccgtgtggtggctgcaggaggaagaaccagtaccggcattattggagtgaaaacctt  2024
```

Right column — RESULT 11

```
Qy   584  CGGGACACCGTGTGTGGGCTGCAGGAAGAAACCAGTACCGGCGCATTATTGGAGTGTGAAAACCTT  643
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2025  ttccagtgcttcaattgcagcctctgcctcaatgggacgtgcacctctcctgccaggag       2084

Qy   644  TTCCAGTGCTTCAATTGCACCCTTCCTGCCTCAATGGGACGTGCACCTCTCCTGTCAGGAG      703
          ||||||||||||||||||||||||
Db  2085  aaacagaacacacgtgtgcacctgccaatgcaggatttcttcttctaagagaaaagagtgtgtc  2144

Qy   704  AAACAGAACACACGTGTGCACCTGCCAATGCAGGATTTCTTCTTCTAAGAGAAAAGAGTGTGTC   763
          ||||||||||||||||||||||
Db  2145  tcctgtagtaactgtaagaaaagcctggagtgtgacgaagttgtgctcacccagattgag      2204

Qy   764  TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGTGACGAAGTTGTGCTCACCCAGATTGAG      823
          ||||||||||||||||
Db  2205  aatgttaaggcgcactgaggactcaggcgcaccacag                             2238

Qy   824  AATGTTAAGGGCCACTGAGGACTCAGGCGCACCACAG                             857
```

```
RESULT 11
ID   Q50870 standard; DNA; 2170 BP.
AC   Q50870;
DT   13-MAY-1994  (first entry)
DE   p55 Tumour necrosis factor receptor coding sequence.
KW   TNF; tumour necrosis factor; receptor; disease; autoimmunity;
KW   rheumatoid arthritis; graft rejection; graft vs. host; septic shock;
KW   effector protein; ss.
OS   Homo sapiens.
FH   Key                 Location/Qualifiers
FT   CDS                 256..1623
FT   /*tag=  a
FT   /product= p55 Tumour necrosis factor receptor.
PN   EP-568925-A.
PD   10-NOV-1993;
PF   29-APR-1993; 106981.
PR   03-MAY-1992; IL-101769.
PA   (YEDA ) YEDA RES & DEV CO LTD.
PI   Brakebusch C, Wallach D;
DR   WPI; 93-353057/45.
DR   P-PSDB; R42197.
PT   Modulating activity of tumour necrosis factor receptor - using
PT   peptide(s), antibodies, etc. which interact with critical regions
PT   of receptor or effector protein, for controlling auto-immune
PT   disease; septic shock, etc.
PS   Claim 2; Figure 1; 17pp; English.
CC   Modification of the tumour necrosis factor receptor by mutation or
CC   deletion modulates signal transduction and/or cleavage effected by
CC   the receptor.  This modulation of activity can also be achieved
CC   using effector proteins which interact with the TNF receptor.
CC   Molecules which interact with the TNF receptor or the effector
CC   proteins can be used to treat or prevent diseases associated with
CC   TNF activity e.g. autoimmune disease; rheumatoid arthritis; graft
CC   rejection; graft vs. host disease or septic shock. They can also
CC   be used to treat overdoses of exogenous TNF.
SQ   Sequence   2170 BP;   474 A;   657 C;   584 G;   455 T;

Query Match    43.8%;   Score 502;   DB 9;   Length 2170;
Best Local Similarity   97.7%;
Matches   519;   Conservative   0;   Mismatches   11;   Indels   1;   Gaps   1;
```

```
Db   376  gatagtgtgtgtcccaaggagaaatatatccaccctcaaaataattcgatttgctgtacc      435
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   344  GATAGTGTGTGTCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC       403

Db   436  aagtgccacaaaggaacctactctgtacaatgactgtccaggccgggggccaggatacggac    495
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   404  AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACCGGAC    463

Db   496  tgcaggggagtgtgagagcggtctcctttcaccgcttcaccgacacctgcctc            555
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   464  TGCAGGGGAGTGTGAGAGCGGTCCTCTTCAGGAGAAAAACCACCTCAGACAACTGCCTC     523
```

RESULT 12

```
ID    Q24441 standard; DNA; 608 BP.
AC    Q24441;
DT    05-NOV-1992 (first entry)
DE    Encodes truncated TNF-alpha 55kD receptor (197 amino acids).
KW    tumour necrosis factor alpha; extracellular binding domain;
KW    treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
KW    malaria; viral meningitis; graft versus host disease;
OS    Homo sapiens.
PN    WO9207076-A.
PN    30-APR-1992.
PF    18-OCT-1991;
PR    18-OCT-1990; GB-022648.
PA    (CHAR-) CHARING CROSS SUNLEY RES CENT.
DR    Brennan FM, Feldmann M, Gray PW, Turner MJC;
PI    WPI; 92-167156/20.
PT    P-PSDB; R24080.
PT    New polypeptide capable of binding human TNF alpha - comprises
PT    first three cysteine-rich subdomains of TNF alpha receptor for
PS    treating autoimmune disease, septic shock, HIV etc.
CC    Example; Fig 7; 43bp; English.
CC    This sequence encodes the designed TNF-alpha 55kD receptor
CC    derivative, as present in PTNFRecd. This was produced as described in
CC    Q24441. This derivative lacks the 81 carboxyl terminal residues of
CC    the cytoplasmic domain. The derivative could be used in the
CC    regulation of TNF-alpha mediated responses by binding and
CC    sequestering human TNF-alpha e.g. in the treatment of pulmonary
CC    diseases, septic shock, HIV infection, malaria, viral meningitis,
CC    graft versus host disease and autoimmune diseases, esp. rheumatoid
CC    arthritis.
CC    See also Q24440-51, R24000, R24080-84, R27585, Q29236-8
SQ    Sequence 608 BP; 148 A; 159 C; 165 G; 136 T;
```

Query Match 40.8%; Score 468; DB 4; Length 608;
Best Local Similarity 98.8%; Pred. No. 0.00e+00;
Matches 474; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
Qy    556 agctgctccaaatgccgaaaggaaatggggtcaaggtcaggtcaagatctcttcttgcacagtgac 615
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGGTCAAGGTCAGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583
Qy    616 cgggacaccgtgtgtggctgcaggaagaagaaccagtaccggcattattggagtgaaaacctt 675
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    584 CGGGACACCGTGTGTGGCTGCAGGAAGAAGAACCAGTACCGGCATTATTGGAGTGAAAAACCTT 643
Qy    676 ttccagtgcttcaattgcagcctctgcctgcacctctcctgcaggag 735
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    644 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCTCAATGGGACCGTGCACCTCGTCCTGCAGGAG 703
Qy    736 aaacagaacacgtgcacctgccatgcaggttcttcttctaagagaaaacgagtgtgtc 795
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    704 AAACAGAACACGTGCACCTGCCATGCAGGTTCTTCTTCTAAGAGAAAACGAGTGTGTC 763
Qy    796 tcctgtagtaactgtaagaaaagcctgcacgaagttgtgcctacccccagattgag 855
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    764 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGAGTGTGCAGGAGTTGTGCCTACCCCAGATTGAG 823
Qy    856 aatgttaagggcactgaggactcaggcaccacagt-gctgttgccctggt 905
          ||||||||||||||||||||||||||||||||||| |||||||||||||
Db    824 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGCCGGGTGCTGCCCCAGT 874
```

RESULT 13

```
ID    Q24445 standard; DNA; 504 BP.
AC    Q24445;
DT    05-NOV-1992 (first entry)
DE    Encodes truncated TNF-alpha 55kD receptor (165 amino acids).
KW    tumour necrosis factor alpha; extracellular binding domain;
KW    treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
KW    autoimmune disease; rheumatoid arthritis.
OS    Homo sapiens.
PN    WO9207076-A.
PN    30-APR-1992.
PF    18-OCT-1991;
PR    18-OCT-1990; GB-022648.
PA    (CHAR-) CHARING CROSS SUNLEY RES CENT.
DR    Brennan FM, Feldmann M, Gray PW, Turner MJC;
PI    WPI; 92-167156/20.
PT    P-PSDB; R24084.
PT    New polypeptide capable of binding human TNF alpha - comprises
PT    first three cysteine-rich subdomains of TNF alpha receptor for
PS    treating autoimmune disease, septic shock, HIV etc.
CC    Example; Fig 11; 43bp; English.
CC    This sequence encodes the designed TNF-alpha 55kD receptor
CC    derivative, as present in pdeltaIV. This construct was generated by
CC    cloning of the BglII/HindIII digested product of a PCR using
CC    primers 5A and 4D into BglII/HindIII 5'deltaC1a. This introduced
CC    a termination codon after amino acid 167, to yield pdeltaIV.
CC    This derivative lacks the membrane proximal 4th subdomain, yet
CC    retains the ability to bind TNF-alpha with high affinity
CC    (10power8 - 10power9 Mpower-1) The deriv. can be used in the
CC    regulation of TNF-alpha mediated responses by binding and
CC    sequestering human TNF-alpha e.g. in the treatment of pulmonary
CC    diseases, septic shock, HIV infection, malaria, viral meningitis,
CC    graft versus host disease and autoimmune diseases, esp. rheumatoid
CC    arthritis. The deriv. is given at 10-100ug/dose.
CC    See also Q24440-51, R24000, R24080-84, R27585, Q29236-8
SQ    Sequence 504 BP; 137 A; 138 G; 107 T;
```

Query Match 32.7%; Score 375; DB 4; Length 504;
Best Local Similarity 99.0%; Pred. No. 1.89e-267;
Matches 379; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy    464 TGCAGGGAGAGTGTGAGAGCGGCGGCTCCTTCACCGGCTTCAGAAAACCACCTCAGACACTGCCTC 523
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    309 agctgctccaaatgccgaaaggaaatggggtcaaggtcaggtggagatctcttcttgcacagtggac 368
Qy    524 AGCTGCTCCAAATGCCGAAAGGAAATGGGGTCAAGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 583
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    369 cgggacaccgtgtgtggctgcaggaagaagaaccagtaccggcattattggagtgaaaaacctt 428
Qy    584 CGGGACACCGTGTGTGGCTGCAGGAAGAAGAACCAGTACCGGCATTATTGGAGTGAAAAACCTT 643
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    429 ttccagtgcttcaattgcagcctctgcctctcaatgggaccgtgcacctcgtcctgcaggag 488
Qy    644 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCTCAATGGGACCGTGCACCTCGTCCTGCAGGAG 703
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    489 aaacagaacacgtgcacctgccatgcaggttcttcttctaagagaaaacgagtgtgtc 548
Qy    704 AAACAGAACACGTGCACCTGCCATGCAGGTTCTTCTTCTAAGAGAAAACGAGTGTGTC 763
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    549 tcctgtagtaactgtaagaaaagcctgggagtgtgcaggagttgtgcctaccccagattgag 608
Qy    764 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGAGTGTGCAGGAGTTGTGCCTACCCCAGATTGAG 823
```

```
Qy    129 gatagtgtgtgtccccaaggaaaatatatcccaccctcaaataatattcgatttgctgtgtacc 188
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAATAATTCGATTTGCTGTGTACC 403
Qy    189 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccgggggccgggggatacggac 248
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGGCCGGGGATACGGAC 463
Qy    249 tgcagggagtgtgagagcggagcctcctcaccgttcagaaaaccaccctcagacactgcctc 308
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Qy    121 gatagtgtgtgtccccaaggaaaatatatcccaccctcaaataattcgatttgctgtgtacc 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    344 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAATAATTCGATTTGCTGTGTACC 403
Qy    181 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccgggggccgggggatacggac 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    404 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGGCCGGGGATACCGAC 463
```

```
Qy  241 tgcgaggagtgtgagacggcgttcctcaccgttcagagaaaccaccaactgctc 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  464 TGCAGGGAGTGTGAGAGCGGCGTTCCTCAGCTTCAGAAAACCACCAGACACTGCCTC 523

Qy  301 agctgcgtccaaatgccgaaaggaaatgggtcagtgatgagatctctcttctgcacagtggac 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  524 AGCTGCGTCCAAATGCCGAAAAGGAAATGGGTCAGTGATGAGATCTCTCTTCTGCACAGTGGAC 583

Qy  361 cgggacacacgtgtgtggctgcaggagaagaacacagtaccggcacattattgggagtgaaaacctt 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  584 CGGGACACACGTGTGTGGCTGCAGGAGAAGAACACAGTACCGGCACATTATTGGGAGTGAAAACCTT 643

Qy  421 ttccagtgcttcaattgcacctctcccgtgcaccctctcccgtgccaggag 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  584 TTCCAGTGCTTCAATTGCACCTCTCCCGTGCACCCTCTCCCGTGCCAGGAG 643

Qy  704 AAACAGAACACCGTCTCCACCTG 726
        |||||||||||||||||||||||
Db  481 aaacagaacaccgtgtgaacctg 503
```

RESULT 14

```
ID    Q24442 standard; DNA; 474 BP.
AC    Q24442;
DT    05-NOV-1992 (first entry)
DE    Encodes truncated TNF-alpha 55kD receptor (155 amino acids).
KW    tumour necrosis factor alpha; extracellular binding domain;
KW    treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
KW    malaria; viral meningitis; graft versus host disease;
KW    autoimmune disease; rheumatoid arthritis.
OS    Homo sapiens.
PN    WO9207076-A.
PD    30-APR-1992.
PF    18-OCT-1991; G01826.
PR    18-OCT-1990; GB-022648.
PA    (CHAR-) CHARING CROSS SUNLEY RES CENT.
PI    Brennan FM, Feldmann M, Gray PW, Turner MJC;
PS    Example: Fig 8; 43pp; English.
CC    This sequence encodes the designed TNF-alpha 55kD receptor
CC    derivative, as present in pdelta1. This construct was generated by
CC    joining PCR fragments by means of overlaps introduced into the
CC    primers used for PCR. Gel purified products of PCR's using
CC    5'Cla, IA, IB, and 5D primers were mixed and subjected to further
CC    amplification using 5'Cla and 5D as primers. The resulting fragment
CC    was digested with ClaI and BglII and cloned into ClaI/BglII
CC    digested pTNFRecd, to yield pdelta1, containing the sequence given.
CC    This derivative could be used to regulate TNF-alpha mediated responses
CC    by binding and sequestering human TNF-alpha e.g. in the treatment of
CC    pulmonary diseases, septic shock, HIV infection, malaria, viral
CC    meningitis, graft versus host disease and autoimmune diseases, esp.
CC    rheumatoid arthritis.
DR    WPI; 92-167156/20.
DR    P-PSDB; R24081.
```

```
Qy  Query Match      30.1%;  Score 345;  DB 4;  Length 474;
    Best Local Similarity  98.3%;   Pred. No. 1.16e-243;
    Matches  351;   Conservative  0;  Mismatches  6;  Indels  0;  Gaps  0;
SQ  Sequence      474 BP;   110 A;   126 C;   132 G;   106 T;

Qy  118 agagagtgtgagacggcgtcctcacccgttcagaaaaccaccagaacactgcctcagc 177
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  118 AGAGAGTGTGAGAGCGGCGTCCTCACCCGTTCAGAAAACCACCAGACACTGCCTCAGC 177

Qy  467 AGGGAGTGTGAGAGCGGCGGTCCTTCACCCGTTCAGAAAACCACCAGACACTGCCTCAGC 526
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  178 tgctccaaatgccgaaaggaaatgggtcaggtgggagatctctcttgcacagtggaccgg 237

Qy  527 TGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGGAGATCTCTTCTTGCACAGTGGACCGG 586
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  527 TGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGGAGATCTCTTCTTGCACAGTGGACCGG 586

Db  238 gacaccgtctgggctgaggagaacaagtaccggcattattggagtgaaaacctttc 297
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

Page 9 (second column)

```
Qy  587 GACACCGTGTGTGGCTGCAGGAGGAAGAACAACCAGTACCGGCGCATTATTGGGAGTGAAAACCTTTTC 646
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  298 cagtgcttcaattgcagcctctgcctcaattggacgtgcaacctctgcctctgccaggagaaa 357

Db  647 CAGTGCTTCAAATTGCACCTCTGCCTCAAATGGGACCGTGCAACCTCTCCGTCAGGAGAAA 706
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  358 cagaacaccgtgtgcactgcatgcaggtgtttctttccttcttctaaagaaaaacgagtgtgtcc 417

Qy  707 CAGAACACCGTGTGCACCTGCCATGCAGGTTCTTTCTTCTAAGAGAAAAACGAGTGTGTCTCC 766
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  418 tgtagtaactgtaagaaaagcctggaagtgcacgaagttgtgccacccagattag 474

Db  767 TGTAGTAACTGTAAGAAAAGCCTGGAAGTGCACGAAGTTGTCCCTACCCCAGATTGAG 823
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

RESULT 15

```
ID    T76770 standard; cDNA; 2771 BP.
AC    T76770;
DT    15-SEP-1997 (first entry)
DE    Rat Fabp1 gut-specific promoter and human growth hormone exon 1.
KW    Human GDP-L-fucose:beta-D-galactoside-2-alpha-L-fucosyltransferase;
KW    GDP-L-fucose:beta-D-N-acetylglucosamide 3/4-alpha-L-fucosyltransferase;
KW    alpha 1,2 FT; alpha 1,3/4 FT; tissue-specific promoter;
KW    rat liver fatty acid binding protein; transgene; transgenic mouse;
KW    animal model; intestinal adhesion; Helicobacter pylori infection;
KW    stomach; small intestine; gut; epithelial cell; surface receptor;
KW    carbohydrate antigen; gastritis; peptic ulcer; neoplasia;
KW    gastric adenocarcinoma; Lewis antigen; fucosylation; ds.
OS    Chimeric - Homo sapiens.
OS    Chimeric - Rattus sp.
FH    Key             Location/Qualifiers
FT    promoter        1..617
FT    /*tag=          a
FT    /note=          "Corresponds to nucleotides -596 to +21 of
FT                    the rat liver fatty acid binding protein
FT    gene"
FT    exon            620..2771
FT    /*tag=          b
FT    /number=        1
FT    /note=          "Corresponds to nucleotides +3 to +2150 of
FT                    the human growth hormone (hGH) gene; it is
FT                    desirable for cDNA coding for a human
FT                    fucosyltransferase to be inserted into
FT                    exon 1 of the hGH gene"
PN    US5625124-A.
PD    29-APR-1997.
PF    11-JUL-1994; 273411.
PR    11-JUL-1994; US-273411.
PA    (UNIW ) UNIV WASHINGTON.
PI    Falk P, Gordon JI;
DR    WPI; 97-258275/23.
PT    Animal model for Helicobacter pylori infection - comprising
PT    transgenic mouse expressing human enzyme promoting intestinal
PT    adhesion
PS    Example 2; Columns 25-28; 24pp; English.
CC    A claimed transgenic mouse expresses, in its intestinal epithelial
CC    cells, the enzyme human GDP-L-fucose:beta-D-galactoside 2-alpha-L-
CC    fucosyltransferase (also called alpha 1,2 FT) or human GDP-L-fucose:
CC    beta-D-N-acetylglucosamide 3/4-alpha-L-fucosyltransferase (also
CC    called alpha 1,3/4 FT). The enzyme is expressed under the
CC    control of a gut epithelial cell-specific promoter and Helicobacter
CC    pylori adheres to the transgenic cells. The transgenic mouse and
CC    intestinal epithelial cells from it are useful as models for screening
CC    compounds for the ability to inhibit adhesion of H. pylori to gut
CC    epithelial cells. The first 617 nucleotides of the present chimeric
CC    sequence encode the promoter from rat liver fatty acid binding protein
CC    (Fabpl) which can direct foreign gene expression to the pit cell
CC    lineage of the mouse gastric epithelium, to proliferating and non-
CC    proliferating cells in intestinal crypts, as well as to the four
CC    principal differentiated cell lineages along the crypt-to-villus axis
CC    of the small intestine. The remainder of the sequence corresponds to
CC    corresponds to exon 1 of the human growth hormone (hGH) gene, into
CC    which a sequence coding for a human fucosyltransferase (hFT) can be
```

```
CC   inserted. No hGH will be produced because the initiator Met codon
CC   and the first translation stop codon will be from the hFT sequence
CC   and there is no ribosome re-entry sequence. The hGH exon 1 ensures
CC   efficient splicing of the transgene primary transcript, improves
CC   stability of the cytoplasmic hFT mRNA and allows transgene
CC   expression to be monitored by in situ hybridisation using a
CC   digoxigenin-labelled hGH oligonucleotide.
SQ   Sequence   2771 BP;    666 A;    718 C;    704 G;    683 T;

Query Match            25.1%;   Score 288;  DB 31;  Length 2771;
Best Local Similarity  95.6%;   Pred. No. 1.27e-198;
Matches  323;   Conservative   0;   Mismatches  11;   Indels  4;   Gaps  3;

Query Match

Db      680 atggctacaggtaaggcgcccctaaaaatcccttgggcacaatgtgtcctgaggggagg 739
            ||||||||||||||||||||||||||||| |||||||||||||||||||||||||| |||
Qy        6 ATGGCTACAGGTAAGGCGCCCCTAAAAATCCCTTTGGGCACAATGTGTCCTGAGGGGAGAGG 65

Db      740 cagcgaacctgtagatggggacgggggggcactaaccctcaggtttgggcttctgaatg--ag 797
            ||||| |||||||||||| |||||||| |||||||||||||||||||| ||||||||| |||
Qy       66 CAGCGACCTGTPAGATGGGACGGGGGCCACTAACCCTCAGGTTTGGGGCTTTTGAAATGTGAG 125

Db      798 tatcgccaatgtaagcccagtatg-gcc-aatctcagaaagctcctggtccctggagggat 855
            ||| |||||||||||||||||||| ||| |||||||||||||||||||||||||||||||||
Qy      126 TATGGCCATGTAAGCCCAGTATTTGCCCAATCTCAGAAAGCTCCTGGTCCCTGGAGGGAT 185

Db      856 ggagagagaaaacaaacagctcctggagacaggggaagtgctggccctcttcgtctccggc 915
            ||||||||||||||||||||||||||||| ||||| |||||||| |||||||| ||| ||||
Qy      186 GGAGAGAGAAAAACAAACAGCTCCTGGAGCAGGGGACACTCCTGGCCTCTTCGGCTCTGCCGGC 245

Db      916 tccctcttgttcgcctcctggttctcccccaggctcccgggacgtccctggcgtcctttctg 975
            ||| | |||| |||| || ||||||||||| ||||||| |||||||||||| || || | |||
Qy      246 TCCGTGTGTTGCCCGTGTGGTTTCTCCCCACGGCTCCCCGGACGTCCCTGCGCTCCTGGGCTTTTG 305

Db      976 gcctgctcctgcctgggcttcaagagaggggcagtgcc 1013
            ||||||||| || |||||||||||||||||||||||||
Qy      306 GCCTGCTCTGCCCTGCCCTGGCTTCAAGAGAGGGGCAGTGCC 343

Search completed: Wed May   6 14:21:41 1998
Job time : 155 secs.
```

```
**********************************************************
                    MPSRCH (TM)
**********************************************************
```

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****

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed May 6 14:00:59 1998; MasPar time 1055.78 Seconds
                                          1320.756 Million cell updates/sec

Tabular output not generated.

Title:
Description: >US-08-804-166-5.seq
Perfect Score: (1-1147) from US08804166.seq
N.A. Sequence: 1147
        Comp: 1 TCGAGATGGCTACAGGTAAG..................AATCTTAAGGATCCCTCGAG 1147
                AGCTCTACCGATGTCCATTC:.................TTAGAATTCCTAGGGAGCTC

Scoring table: TABLE default
        Gap 6

Nmatch STD :   Dbase 0; Query 0

Searched: 1610801 seqs, 607859669 bases x 2

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database: embl-est
                1:em_est1 2:em_est2 3:em_est3 4:em_est4 5:em_est5
                6:em_est6 7:em_est8 8:em_est9 9:em_est13

Database: genbank-est
                10:gb_est1 11:gb_est2 12:gb_est3 13:gb_est4 14:gb_est5
                15:gb_est6 16:gb_est7 17:gb_est8 18:gb_est9 19:gb_est10
                20:gb_est11 21:gb_est15 22:gb_gss 23:gb_est12 24:gb_est13
                25:gb_est14 26:gb_est15 27:gb_est16 28:gb_est17
                29:gb_est18 30:gb_est19 31:gb_est20

Statistics: Mean 11.165; Variance 1.901; scale 5.873

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

### SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description | Pred. No. |
|---|---|---|---|---|---|---|---|
| 1 | 262 | 22.8 | 373 | 23 | HUM505B08B | Human placenta cDNA 5' | 0.00e+00 |
| 2 | 262 | 22.8 | 379 | 23 | C18240 | Human placenta cDNA 5' | 0.00e+00 |
| 3 | 262 | 22.8 | 392 | 11 | R76249 | Homo sapiens | 0.00e+00 |
| 4 | 261 | 22.8 | 423 | 12 | YJ31N01.r1 Homo sapiens | | 0.00e+00 |
| 5 | 262 | 22.8 | 464 | 23 | C17209 | Human placenta cDNA 5' | 0.00e+00 |
| 6 | 262 | 22.8 | 467 | 11 | R71429 | Homo sapiens | 0.00e+00 |
| 7 | 260 | 22.7 | 433 | 11 | R23843 | yh48c04.r1 Homo sapien | 0.00e+00 |
| 8 | 260 | 22.7 | 452 | 12 | H00781 | yi51d03.r1 Homo sapien | 0.00e+00 |
| 9 | 258 | 22.5 | 478 | 23 | C17142 | yj30d01.r1 Homo sapien | 0.00e+00 |
| 10 | 255 | 22.2 | 458 | 11 | C18403 | Human placenta cDNA 5' | 0.00e+00 |
| 11 | 254 | 22.1 | 482 | 12 | R77385 | yi75d1l.r1 Homo sapien | 0.00e+00 |
| 12 | 250 | 21.8 | 336 | 23 | H03289 | yj44h10.r1 Homo sapien | 0.00e+00 |
| 13 | 249 | 21.7 |  |  | HUM530G10B | Human placenta cDNA 5' | 0.00e+00 |

### ALIGNMENTS

| RESULT | | | | | |
|---|---|---|---|---|---|
| LOCUS | 1 | HUM505B08B | 373 bp | mRNA | EST | 21-MAY-1996 |

DEFINITION  Human placenta cDNA 5'-end GEN-505B08.
ACCESSION   D58574
NID         g968208
KEYWORDS    EST; EST(expressed sequence tag); Human placenta; similar to
            known(May 29,1995).
SOURCE      Homo sapiens cDNA to mRNA, clone_lib:Clontech human placenta polyA+
            mRNA (#6518).
ORGANISM    Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
            Homo.
REFERENCE   1  (bases 1 to 373)
AUTHORS     Fujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Nagata,M.,
            Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiya,H.,
            Takaichi,A., Takeda,S., Watanabe,T., Takahashi,E., Hirai,Y.,
            Maekawa,H., Shin,S. and Nakamura,Y.
TITLE       Unpublished(004)
JOURNAL     Unpublished (1995)
REFERENCE   2  (bases 1 to 373)
AUTHORS     Fujiwara,T.
TITLE       Direct Submission
JOURNAL     Submitted (30-MAY-1995) to the DDBJ/EMBL/GenBank databases. Tsutomu
            Fujiwara, Otsuka GEN Research Institute,Otsuka Pharmaceutical
            Co.,Ltd; 463-10 kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01,
            Japan (Tel:0886-65-2888, Fax:0886-37-1035)
COMMENT     Submitted (30-May-1995) to DDBJ by:
            Tsutomu Fujiwara
            Otsuka GEN Research Institute
            Otsuka Pharmaceutical Co.,Ltd
            463-10 kagasuno Kawauchi-cho
            Tokushima, Tokushima
            771-01
            Japan
            Phone: 0886-65-2888

| c | 14 | 238 | 20.7 | 519 | 31 | AA779136 | zj46h11.s1 Soares feta | 0.00e+00 |
|---|---|---|---|---|---|---|---|---|
| | 15 | 236 | 20.6 | 423 | 23 | C17966 | Human placenta cDNA 5' | 0.00e+00 |
| | 16 | 232 | 20.2 | 519 | 23 | C18044 | Human placenta cDNA 5' | 0.00e+00 |
| | 17 | 231 | 20.1 | 386 | 17 | W86567 | zh63h08.r1 Soares feta | 0.00e+00 |
| | 18 | 231 | 20.1 | 403 | 11 | R65664 | H. sapiens partial cDN | 0.00e+00 |
| | 19 | 231 | 20.1 | 471 | 12 | H47149 | yu23f09.r1 Homo sapien | 0.00e+00 |
| | 20 | 230 | 20.0 | 430 | 12 | H00795 | yp73d07.r1 Homo sapien | 0.00e+00 |
| | 21 | 228 | 19.9 | 439 | 12 | H01069 | yj30f02.r1 Homo sapien | 0.00e+00 |
| | 22 | 223 | 19.4 | 513 | 23 | AA441787 | yj26c09.r1 Homo sapien | 0.00e+00 |
| | 23 | 221 | 19.3 | 336 | 11 | R79875 | zw62b09.s1 Soares tota | 0.00e+00 |
| c | 24 | 221 | 19.3 | 468 | 11 | R23095 | yl85a07.r1 Homo sapien | 0.00e+00 |
| | 25 | 220 | 19.2 | 526 | 31 | HUM505C02B | yh31g05.r1 Homo sapien | 0.00e+00 |
| | 26 | 220 | 19.2 | 527 | 31 | H94810 | Human placenta cDNA 5' | 0.00e+00 |
| | 27 | 219 | 19.1 | 294 | 10 | AA777267 | yu21c05.r1 Soares feta | 0.00e+00 |
| c | 28 | 218 | 19.0 | 360 | 14 | T48916 | yb07c06.r1 Homo sapien | 0.00e+00 |
| | 29 | 217 | 19.0 | 291 | 13 | HSC32B021 | yb07c06.r1 Homo sapien | 0.00e+00 |
| | 30 | 217 | 18.9 | 348 | 11 | H77743 | yu23f09.r1 Homo sapien | 0.00e+00 |
| | 31 | 216 | 18.8 | 478 | 11 | R33236 | yh84d10.r1 Homo sapien | 0.00e+00 |
| | 32 | 216 | 18.8 | 420 | 10 | AA778170 | zf45c10.s1 Soares feta | 0.00e+00 |
| c | 33 | 212 | 18.5 | 291 | 23 | T49525 | ya76f03.r1 Homo sapien | 0.00e+00 |
| | 34 | 207 | 18.0 | 465 | 29 | HUM511F08B | Human placenta cDNA 5' | 0.00e+00 |
| c | 35 | 207 | 18.0 | 291 | 23 | HUM511F08B | Human placenta cDNA 5' | 0.00e+00 |
| | 36 | 205 | 17.9 | 365 | 11 | R23453 | zj19d06.s1 Soares feta | 0.00e+00 |
| | 37 | 205 | 17.9 | 393 | 11 | R33285 | yh39b02.r1 Homo sapien | 0.00e+00 |
| | 38 | 205 | 17.9 | 438 | 14 | AA704477 | yw65f07.r1 Homo sapien | 0.00e+00 |
| | 39 | 204 | 17.8 | 261 | 23 | N57230 | Human placenta cDNA 5' | 0.00e+00 |
| | 40 | 201 | 17.5 | 465 | 14 | HUM525D05B | za35c04.r1 Soares feta | 0.00e+00 |
| | 41 | 198 | 17.3 | 450 | 12 | W01919 | yj20g12.s1 Soares feta | 0.00e+00 |
| c | 42 | 198 | 17.3 | 450 | 29 | H04324 | yj62g07.s1 Soares feta | 0.00e+00 |
| | 43 | 198 | 17.3 | 479 | 11 | R68866 | y137d02.r1 Homo sapien | 0.00e+00 |
| | 44 | 197 | 17.2 | 347 | 11 | R34458 | yh85b04.r1 Homo sapien | 0.00e+00 |
| | 45 | 193 | 16.8 | 344 | 11 | R27121 | yh52h07.r1 Homo sapien | 0.00e+00 |

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FEATURES
        source
                Fax : 0886-37-1035.
                     Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="Clontech human placenta polyA+ mRNA (#6518)"
BASE COUNT        94 a        88 c        84 g        107 t
ORIGIN

Query Match        22.8%;     Score 262;    DB 23;    Length 373;
Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
Matches 262;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    47 TTGCCCAGAATGCACGCTACAGGAAAAACCCATTCTTCTTCCCCAGCCGGGTGCCCAATACT 106
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   874 TTGCCCAGAATGCACGCTACAGGAAAAACCCATTCTTCTTCCCCAGCCGGGTGCCCAATACT 933

Qy   107 TCAGTGCAATGGGCGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCAAAGAAGAC 166
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   934 TCAGTGCAATGGGCGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCAAAGAAGAC 993

Qy   167 GATGTTGGGTCCAAAAGAACGTCACCTCACTTGCTCGTGTGTAGCTAAATCATATAA 226
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   994 GATGTTGGGTCCAAAAGAACGTCACCTCACTTGCTCGTGTGTAGCTAAATCATATAA 1053

Qy   227 CAGGGTCACAGTAATGGGGGGGGTTTCAAAGTGGAGAACCACACAGGCGGTGCCACTGCAGTAC 286
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1054 CAGGGTCACAGTAATGGGGGGGGTTTCAAAGTGGAGAACCACACAGGCGGTGCCACTGCAGTAC 1113

Qy   287 TTGTTATTATCACAAAATCTTAA 308
         |||||||||||||||||||||||
Db  1114 TTGTTATTATCACAAAATCTTAA 1135


RESULT 2
LOCUS       C18240          379 bp    mRNA            EST        09-SEP-1996
DEFINITION  Human placenta cDNA 5'-end GEN-559D08.
ACCESSION   C18240
NID         g1579842
KEYWORDS    EST; EST(expressed sequence tag); Human placenta.
SOURCE      Homo sapiens placenta cDNA to mRNA, clone:559D08.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
            Homo.
REFERENCE   1  (sites)
  AUTHORS   Fujiwara,T., Hirano,H., Hishiaki,H., Horie,M., Kawai,A., Kuga,Y.,
            Kyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y.,
            Shinomiya,H., Suzuki,M., Takaichi,A., Takeda,S., Watanabe,T.,
            Maekawa,H., Nakamura,Y. and Takahashi,E.
  TITLE     Otsuka cDNA project
  JOURNAL   Unpublished (1996)
REFERENCE   2  (bases 1 to 379)
  AUTHORS   Fujiwara,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUN-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu
            Fujiwara, Otsuka GEN Research Institute,Otsuka Pharmaceutical
            Co.,Ltd; 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01,
            Japan (Tel:+81-886-65-2888, Fax:+81-886-37-1035)
FEATURES             Location/Qualifiers
        source       1..379
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="559D08"
                     /tissue_type="placenta"
BASE COUNT        94 a        95 c        85 g        104 t
ORIGIN

Query Match        22.8%;     Score 262;    DB 23;    Length 379;
Best Local Similarity 99.6%;   Pred. No. 0.00e+00;
Matches 261;  Conservative   1;  Mismatches   0;  Indels   0;  Gaps   0;
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Db    67 TTGCCCAGAATGCACGCTACAGGAAAAACCCATTCTTCTTCCCCAGCCGGGTGCCCAATACT 126
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Qy   874 TTGCCCAGAATGCACGCTACAGGAAAAACCCATTCTTCTTCCCCAGCCGGGTGCCCAATACT 933

Db   127 TCAGTGCAATGGGCGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCAAAGAAGAC 186
         |||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Qy   934 TCAGTGCAATGGGCGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCAAAGAAGAC 993

Db   187 GATGTTGGGTCCAAAAGAACGTCACCTCACTTGCTCGTGTGTAGCTAAATCATATAA 246
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   994 GATGTTGGGTCCAAAAGAACGTCACCTCACTTGCTCGTGTGTAGCTAAATCATATAA 1053

Db   247 CAGGGTCACAGTAATGGGGGGGGTTTCAAAGTGGAGAACCACACAGGCGGTGCCACTGCAGTAC 306
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Qy  1054 CAGGGTCACAGTAATGGGGGGGGTTTCAAAGTGGAGAACCACACAGGCGGTGCCACTGCAGTAC 1113

Db   307 TTGTTATTATCACAAAATCTTAA 328
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Qy  1114 TTGTTATTATCACAAAATCTTAA 1135


RESULT 3
LOCUS       R76249          392 bp    mRNA            EST        06-JUN-1995
DEFINITION  yl72b05.r1 Homo sapiens cDNA clone 144753 3' similar to gb:V00518
            GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (HUMAN);.
ACCESSION   R76249
NID         g850931
KEYWORDS    EST.
SOURCE      human clone=144753 library=Soares placenta Nb2HP vector=pT7T3D
            (Pharmacia) with a modified polylinker host=DH10B (ampicillin
            resistant) primer=Promega -21m13 Rsite1=Not I Rsite2=Eco RI Female
            placenta obtained at birth (full term). 1st strand cDNA was primed
            with a Not I - oligo(dT) primer [5'
            AACTGGAAGAATTCGGCGCCCGAGGAATTTTTTTTTTTTTTTTT 3'], double-stranded
            cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
            I and cloned into the Not I and Eco RI sites of the modified pT7T3
            vector. Library went through one round of normalization. Library
            constructed by Bento Soares and M.Fatima Bonaldo.
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 392)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 328
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES             Location/Qualifiers
        source       1..392
                     /organism="Homo sapiens"
                     /clone="144753"
BASE COUNT       100 a        90 c        89 g        112 t
ORIGIN

Query Match        22.8%;     Score 262;    DB 11;    Length 392;
Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
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Matches   262; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Db     35  TTGCCCAGAAATGCACGCTACAGGAAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT  94
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Qy    874  TTGCCCAGAAATGCACGCTACAGGAAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT  933

Db     95  TCAGTGCATGGGCGCTGCTGCTTCTCTAGAGCATATCCCACTCACTAAGGTCCAAGAAGAC  154
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    934  TCAGTGCATGGGCGCTGCTGCTTCTCTAGAGCATATCCCACTCACTAAGGTCCAAGAAGAC  993

Db    155  GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCAGAGTCGTGTGTAGGTAAATCATATAA  214
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    994  GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCAGAGTCGTGTGTAGGTAAATCATATAA  1053

Db    215  CAGGGTCACAGTAATGGGGGGGTTTCAAAGTGGAGAACCACACACGCGGTGCCACTGCAGTAC  274
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1054  CAGGGTCACAGTAATGGGGGGGTTTCAAAGTGGAGAACCACACACGCGGTGCCACTGCAGTAC  1113

Db    275  TTGTTATTATCACAAAATCTTAA  296
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Qy   1114  TTGTTATTATCACAAAATCTTAA  1135
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RESULT   4

LOCUS   H00861   423 bp   mRNA   EST   19-JUN-1995
DEFINITION   yj31h01.r1 Homo sapiens cDNA clone 150385 5' similar to gb:V00518
             GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (HUMAN);.
ACCESSION   H00861
NID   g863794
KEYWORDS   EST.
SOURCE   human clone-150385 library-Soares placenta Nb2HP vector-pT7T3D
             (Pharmacia) with a modified polylinker host-DH10B (ampicillin
             resistant) primer-M13RP1 Rsite1-Not I Rsite2-Eco RI Female placenta
             obtained at birth (full term). 1st strand cDNA was primed with a
             Not I - oligo(dT) primer [5'
             AACTGGAAGAAATTCGCGGCCGCGGGAATTTTTTTTTTTTTTTTTTT 3'], double-stranded
             cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
             I and cloned into the Not I and Eco RI sites of the modified pT7T3
             vector. Library went through one round of normalization. Library
             constructed by Bento Soares and M.Fatima Bonaldo.
ORGANISM   Homo sapiens
             Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
             Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
             Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
             Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 423)
AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
             Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
             Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
             Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
             Wilson,R.
TITLE   The WashU-Merck EST Project
JOURNAL   Unpublished (1995)
COMMENT   This clone is available royalty-free through LLNL ; contact the
             IMAGE Consortium (info@image.llnl.gov) for further information.
             Contact: Wilson RK
             WashU-Merck EST Project
             Washington University School of Medicine
             4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
             Tel: 314 286 1800
             Fax: 314 286 1810
             Email: est@watson.wustl.edu
             High quality sequence stops: 344
             Source: IMAGE Consortium, LLNL
             1. .423
FEATURES   Location/Qualifiers
     source   1. .423
                      /organism="Homo sapiens"
                      /clone="150385"
BASE COUNT   109 a   95 c   119 g   5 others   95 t
ORIGIN
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Query Match   22.8%; Score 261; DB 12; Length 423;
Best Local Similarity   99.6%; Pred. No. 0.00e+00;
Matches   261; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

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Db     18  TTGCCCAGAAATGCACGCTACAGGANAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT  77
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Qy    874  TTGCCCAGAAATGCACGCTACAGGAAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT  933

Db     78  TCAGTGCATGGGCGCTGCTGCTTCTCTAGAGCATATCCCACTCACTAAGGTCCAAGAAGAC  137
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    934  TCAGTGCATGGGCGCTGCTGCTTCTCTAGAGCATATCCCACTCACTAAGGTCCAAGAAGAC  993

Db    138  GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCAGAGTCGTGTGTAGGTAAATCATATAA  197
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    994  GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCAGAGTCGTGTGTAGGTAAATCATATAA  1053

Db    198  CAGGGTCACAGTAATGGGGGGGTTTCAAAGTGGAGAACCACACACGCGGTGCCACTGCAGTAC  257
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1054  CAGGGTCACAGTAATGGGGGGGTTTCAAAGTGGAGAACCACACACGCGGTGCCACTGCAGTAC  1113

Db    258  TTGTTATTATCACAAAATCTTAA  279
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Qy   1114  TTGTTATTATCACAAAATCTTAA  1135
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RESULT   5

LOCUS   C17209   464 bp   mRNA   EST   04-SEP-1996
DEFINITION   Human placenta cDNA 5'-end GEN-541F08.
ACCESSION   C17209
NID   g1571916
KEYWORDS   EST; EST(expressed sequence tag); Human placenta.
SOURCE   Homo sapiens placenta cDNA to mRNA, clone:541F08.
ORGANISM   Homo sapiens
             Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
             Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
             Homo.
REFERENCE   1 (sites)
AUTHORS   Fujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y.,
             Kyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shinizu,F., Shimada,Y.,
             Shinomiya,H., Suzuki,M., Takaichi,A., Takeda,S., Watanabe,T.,
             Maekawa,H., Nakamura,Y. and Takahashi,E.
TITLE   Otsuka cDNA project
JOURNAL   Unpublished (1996)
REFERENCE   2 (bases 1 to 464)
AUTHORS   Fujiwara,T.
TITLE   Direct Submission
JOURNAL   Submitted (13-MAY-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu
             Fujiwara, Otsuka GEN Research Institute,Otsuka Pharmaceutical
             Co.,Ltd; 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01,
             Japan (Tel:+81-886-65-2888, Fax:+81-886-37-1035)
FEATURES   Location/Qualifiers
     source   1. .464
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="541F08"
                      /tissue_type="placenta"
BASE COUNT   114 a   117 c   95 g   138 t
ORIGIN
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Query Match    22.8%;  Score 262;  DB 23;  Length 464;
Best Local Similarity    100.0%;  Pred. No. 0.00e+00;
Matches    262;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db     39  TTGCCCAGAAATGCACGCTACAGGAAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT  98
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    874  TTGCCCAGAAATGCACGCTACAGGAAAAACCCATTCTTCTCCCAGCCGGGTGCCCCAATACT  933

Db     99  TCAGTGCATGGGCGCTGCTGCTTCTCTAGAGCATATCCCACTCACTAAGGTCCAAGAAGAC  158
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    934  TCAGTGCATGGGCGCTGCTGCTTCTCTAGAGCATATCCCACTCACTAAGGTCCAAGAAGAC  993

Db    159  GATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCAGAGTCGTGTGTAGGTAAATCATATAA  218
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Qy    994 GATGTTGGTCCAAAAAGAAACGTCACCTCCAGAGTCCCACTTGCTGTGTAGCTAAATCATATAA
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Db    219 CAGGGTCACAGTAATGGGGGGGTTTCAAAAGTGGAGAACCACACGCGGGGTCCCACTGCAGTAC 278
Qy   1054 CAGGGTCACAGTAATGGGGGGGTTTCAAAAGTGGAGAACCACACGCGGGGTCCCACTGCAGTAC 1113
Db    279 TTGTTATTATCACAAATCTTAA 300
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Qy   1114 TTGTTATTATCACAAATCTTAA 1135
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RESULT 6

LOCUS   R71429   467 bp   mRNA   EST   01-JUN-1995
DEFINITION yl5ld03.r1 Homo sapiens cDNA clone 142757 5' similar to gb:V00518
            GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (HUMAN);.
ACCESSION   R71429
NID   g844946
KEYWORDS   EST.
SOURCE   human clone~142757 library~Soares placenta Nb2HP vector~pT7T3D
            (Pharmacia) with a modified polylinker host~DH10B (ampicillin
            resistant) primer~M13RP1 Rsite1~Not I Rsite2~Eco RI Female placenta
            obtained at birth (full term). 1st strand cDNA was primed with a
            Not I - oligo(dT) primer (5'
            AACTGGAAGAATTCGGCGGCGGCCGCAGGAATTTTTTTTTTTTTTTTT 3'), double-stranded
            cDNA was ligated to Eco RI and Not I adaptors (Pharmacia), digested with Not
            I and cloned into the Not I and Eco RI sites of the modified pT7T3
            vector. Library went through one round of normalization. Library
            constructed by Bento Soares and M.Fatima Bonaldo.
  ORGANISM Homo sapiens
            Eukaryotae; Metazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 467)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE   The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT   Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 386
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES   Location/Qualifiers
     source   1..467
                     /organism="Homo sapiens"
                     /clone="142757"
BASE COUNT   113 a   114 c   98 g   139 t   3 others
ORIGIN

Query Match   22.8%;   Score 262; DB 11; Length 467;
Best Local Similarity   100.0%;   Pred. No. 0.00e+00;
Matches   262; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy     50 TTGCCCAGAATGCAGCCTACAGGAAAAACCCATTCTTCTCCCAGCCGGCCCCAATACT 109
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Db    874 TTGCCCAGAATGCAGCCTACAGGAAAAACCCATTCTTCTCCCAGCCGGCCCCAATACT 933
Db    110 TCAGTGCATGGGCGTCGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAGAC 169
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    934 TCAGTGCATGGGCGTCGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAGAC 993
```

RESULT 7

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Db    170 GATGTTGGTCCAAAAAGAAACGTCACCTCCAGAGTCCCACTTGCTGTGTAGCTAAATCATATAA 229
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    994 GATGTTGGTCCAAAAAGAAACGTCACCTCCAGAGTCCCACTTGCTGTGTAGCTAAATCATATAA 1053
Db    230 CAGGGTCACAGTAATGGGGGGGTTTCAAAAGTGGAGAACCACACGCGGGGTCCCACTGCAGTAC 289
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1054 CAGGGTCACAGTAATGGGGGGGTTTCAAAAGTGGAGAACCACACGCGGGGTCCCACTGCAGTAC 1113
Db    290 TTGTTATTATCACAAATCTTAA 311
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Qy   1114 TTGTTATTATCACAAATCTTAA 1135
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LOCUS   R23843   433 bp   mRNA   EST   20-APR-1995
DEFINITION yh48c04.r1 Homo sapiens cDNA clone 132966 5' similar to gb:V00518
            GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (HUMAN);.
ACCESSION   R23843
NID   g778731
KEYWORDS   EST.
SOURCE   human clone~132966 library~Soares placenta Nb2HP vector~pT7T3D
            (Pharmacia) with a modified polylinker host~DH10B (ampicillin
            resistant) primer~M13RP1 Rsite1~Not I Rsite2~Eco RI Female placenta
            obtained at birth (full term). 1st strand cDNA was primed with a
            Not I - oligo(dT) primer (5'
            AACTGGAAGAATTCGGCGGCGGCCGCAGGAATTTTTTTTTTTTTTTTT 3'), double-stranded
            cDNA was ligated to Eco RI and Not I adaptors (Pharmacia), digested with Not
            I and cloned into the Not I and Eco RI sites of the modified pT7T3
            vector. Library went through one round of normalization. Library
            constructed by Bento Soares and M.Fatima Bonaldo.
  ORGANISM Homo sapiens
            Eukaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 433)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE   The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT   Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 334
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES   Location/Qualifiers
     source   1..433
                     /organism="Homo sapiens"
                     /clone="132966"
BASE COUNT   111 a   104 c   90 g   127 t   1 others
ORIGIN

Query Match   22.7%;   Score 260; DB 11; Length 433;
Best Local Similarity   98.9%;   Pred. No. 0.00e+00;
Matches   263; Conservative   0; Mismatches   3; Indels   0; Gaps   0;

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Qy      2 CAGGGATTGCCAGAATGCAGCCTACAGAGAAAACCATTCTTCTCCCAGCCGGCCCCAA 61
          |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    870 CAGGTTGCCCAGAATGCAGCCTACAGAGAAAACCATTCTTCTCCCAGCCGGCCCCAA 929
Db     62 TACTTCAGTGCATGCATGGGCGTCGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGA 121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    930 TACTTCAGTGCATGGGCGTCGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGA 989
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Qy      122 AGACGATAGTGTTGGTCCAAAAAGAACGTCACCTCAGAGTCCCACTTGCTCGTGTAGCTAAATCAT 181
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      990 AGACGATAGTGTTGGTCCAAAAAGAACGTCACCTCAGAGTCCCACTTGCTCGTGTAGCTAAATCAT 1049

Qy      182 ATAACAGGGGTCACAGTAATGGGGGGGGGGTTTCAAAAGTGGGAGAAC 241
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db     1050 ATAACAGGGGTCACAGTAATGGGGGGGGGGTTTCAAAAGTGGAGAAC 1109

Qy      242 GTACTTGTTATTATCACAAAATCTTAA 267
            |||||||||||||||||||||||||||
Db     1110 GTACTTGTTATTATCACAAAATCTTAA 1135
```

RESULT 8

LOCUS   H00781   452 bp   mRNA   EST   19-JUN-1995
DEFINITION yj30d01.r1 Homo sapiens cDNA clone 150241 5' similar to gb:V00518
            GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (HUMAN);.
ACCESSION   H00781
NID   g863714
KEYWORDS   EST.
SOURCE   human clone-150241 library-Soares placenta Nb2HP vector-pT7T3D
            (Pharmacia) with a modified polylinker host-DH10B (ampicillin
            resistant) primer-M13RP1 Rsite1-Not I Rsite2-Eco RI Female placenta
            obtained at birth (full term). 1st strand cDNA was primed with a
            Not I - oligo(dT) primer (5'
            AACTGGAAGAATTCGGCACGAGGAATTTTTTTTTTTTTTTTTT 3'), double-stranded
            cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
            I and cloned into the Not I and Eco RI sites of the modified pT7T3
            vector. Library went through one round of normalization. Library
            constructed by Bento Soares and M.Fatima Bonaldo.
ORGANISM   Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 452)
AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
TITLE   The Washu-Merck EST Project
JOURNAL   Unpublished (1995)
COMMENT   Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High qality sequence stops: 322
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES   Location/Qualifiers
     source   1..452
                     /organism="Homo sapiens"
                     /clone="150241"
BASE COUNT   107 a   104 c   103 g   133 t   5 others
ORIGIN

Query Match   22.7%;   Score 260; DB 12; Length 452;
Best Local Similarity 100.0%;   Pred. No. 0.00e+00;
Matches   260;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   44 TTGCCCAGAATGCACGCTACAGGAAAACCATTCTTCTTCTCCAGCGCCGGGTGCCCAATACT 103
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   104 TCAGTGCCATGGGCGGCTGCTTCTCCACTCCACTCAAGGTCCAAGAAGAC 163
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RESULT 9

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Qy      934 TCAGTGCCATGGGCGGCTGCTTCTCTAGAGCATATCCACTCCACTCAAGGTCCAAGAAGAC 993
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 CAGAATGCACGCTACAGGAAAACCATTCTTCTCTCCAGCCGGGTGCCCAATACTTCAG 60
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LOCUS   C17142   478 bp   mRNA   EST   04-SEP-1996
DEFINITION Human placenta cDNA clone 5'-end GEN-539G04.
ACCESSION   C17142
NID   g1571849
KEYWORDS   EST; EST(expressed sequence tag); Human placenta.
SOURCE   Homo sapiens placenta cDNA to mRNA, clone:539G04.
ORGANISM   Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
            Homo.
REFERENCE   1 (sites)
AUTHORS   Fujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y.,
            Kyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shinada,Y.,
            Shinomiya,H., Suzuki,M., Takaichi,A., Takeda,S., Watanabe,T.,
            Maekawa,H., Nakamura,Y. and Takahashi,E.
TITLE   Otsuka cDNA project
JOURNAL   Unpublished (1996)
REFERENCE   2 (bases 1 to 478)
AUTHORS   Fujiwara,T.
TITLE   Direct Submission
JOURNAL   Submitted (13-MAY-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu
            Fujiwara, Otsuka GEN Research Institute,Otsuka Pharmaceutical
            Co.,Ltd; 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01,
            Japan (Tel:+81-886-65-2888, Fax:+81-886-37-1035)
FEATURES   Location/Qualifiers
     source   1..478
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="539G04"
                     /tissue_type="placenta"
BASE COUNT   125 a   113 c   96 g   144 t
ORIGIN

Query Match   22.5%;   Score 258; DB 23; Length 478;
Best Local Similarity 100.0%;   Pred. No. 0.00e+00;
Matches   258;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 CAGAATGCACGCTACAGGAAAACCATTCTTCTCTCCAGCCGGGTGCCCAATACTTCAG 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   878 CCAGAATGCACGCTACAGGAAAACCATTCTTCTCTCCAGCCGGGTGCCCAATACTTCAG 937

Qy   61 TGCAATGGGCGCTGCTTCTCTAGAGCATATCCACTCCACTCAAGGTCCAAGAAGACGATG 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   938 TGCAATGGGCGCTGCTTCTCTAGAGCATATCCACTCCACTCAAGGTCCAAGAAGACGATG 997

Qy   121 TTGGTCCAAAAGAACGTCACCTCAGAGTCCCACTTGCTCGTGTAGCTAAATCATAACAGG 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   998 TTGGTCCAAAAGAACGTCACCTCAGAGTCCCACTTGCTCGTGTAGCTAAATCATAACAGG 1057

Qy   181 GTCACAGTAATGGGGGGGGGTTTCAAAAGTGGAGAACCACACACGGGCGCGTGCCCACTG 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1058 GTCACAGTAATGGGGGGGGGTTTCAAAAGTGGAGAACCACACACGGGCGCGTGCCCACTG 1117

Qy   241 TATTATCACAAAATCTTAA 258
            |||||||||||||||||||
Db   241 TATTATCACAAAATCTTAA 258
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Qy    1118 TATTATCACAAATCTTAA 1135

RESULT 10

LOCUS          C18403          330 bp      mRNA                    09-SEP-1996
DEFINITION     Human placenta cDNA 5'-end GEN-561H02.
ACCESSION      C18403
NID            C18403
KEYWORDS       EST; EST(expressed sequence tag); Human placenta.
SOURCE         Homo sapiens placenta cDNA to mRNA, clone:561H02.
ORGANISM       Homo sapiens
               Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
               Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
               Homo.
REFERENCE      1  (sites)
AUTHORS        Fujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y.,
               Kyushiki,H., Nagata,M., Okuno,S., Ozaki,R., Shimizu,F., Shimada,Y.,
               Shinomiya,H., Suzuki,M., Takaichi,A., Takeda,S., Watanabe,T.,
               Maekawa,H., Nakamura,Y. and Takahashi,E.
TITLE          Otsuka cDNA project
JOURNAL        Unpublished (1996)
REFERENCE      2  (bases 1 to 330)
AUTHORS        Fujiwara,T.
TITLE          Direct Submission
JOURNAL        Submitted (24-JUN-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu
               Fujiwara, Otsuka GEN Research Institute Otsuka Pharmaceutical
               Co.,Ltd; 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01,
               Japan (Tel:+81-886-65-2888, Fax:+81-886-37-1035)
FEATURES       Location/Qualifiers
   source      1..330
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /clone="561H02"
               /tissue_type="placenta"
BASE COUNT         82 a         87 c         73 g         88 t
ORIGIN

Query Match    22.2%;   Best Local Similarity  99.6%;  Conservative  0;  Mismatches  0;  Indels  1;  Gaps  1;
Match          261;     Score 255;   DB 23;   Length 330;

Qy       67 TTGCCCAGAAATGCACGCTACAGGAAAAACCCATTCTTCTCCCAGCCGGGGTGCCCCAATACT 126
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      874 TTGCCCAGAAATGCACGCTACAGGAAAAACCCATTCTTCTCCCAGCCGGGGTGCCCCAATACT 933

Qy      127 TCAGTGCAATGGGCGTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 186
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      934 TCAGTGCAATGGGCGTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGAC 993

Qy      187 GATGTTGGTGTCCAAAAAGAACGTCACCTCAGAGTCCCACTTGCTGTGTAGCTAAATCATATAA 246
            ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db      994 GATGTTGGTGTCCAAAAAGAACGTCACCTCAGAGTCCCACTTGCTGTGTAGCTAAATCATATAA 1053

Qy      247 CAGGGTCACAGTAATGGGGGGTTTCAAAGTGGGAGA-CCACACGGCGTGCCACTGCAGTAC 305
            |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db     1054 CAGGGTCACAGTAATGGGGGGTTTCAAAGTGGAGACCACACGGCGTGCCACTGCAGTAC 1113

Qy     1114 TTGTTATTATTCACAAATCTTAA 1135
            |||||||||||||||||||
Db      306 TTGTTATTATTCACAAATCTTAA 327

RESULT 11

LOCUS          R77385          458 bp      mRNA      EST          06-JUN-1995
DEFINITION     yl75d11.r1 Homo sapiens cDNA clone 145077 5' similar to gb:V00518
               GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (HUMAN);.
ACCESSION      R77385
NID            g852017
KEYWORDS       EST.
SOURCE         human clone=145077 library=Soares placenta Nb2HP vector=pT7T3D
               (Pharmacia) with a modified polylinker host=DH10B (ampicillin

---

               resistant) primer=M13RP1 Rsite1-Not I Rsite2-Eco RI Female placenta
               obtained at birth (full term). 1st strand cDNA was primed with a
               Not I- oligo(dT) primer [5'
               AACTGGAAGAATTCGGCGGCGCGCGGGAATTTTTTTTTTTTTTTTT 3'], double-stranded
               cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
               I and cloned into the Not I and Eco RI sites of the modified pT7T3
               vector. Library went through one round of normalization. Library
               constructed by Bento Soares and M.Fatima Bonaldo.
ORGANISM       Homo sapiens
               Eukaryotae; Metazoa; Chordata; Eumetazoa; Bilateria; Coelomata;
               Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
               Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
               Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1  (bases 1 to 458)
AUTHORS        Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
               Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
               Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
               Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
               Wilson,R.
TITLE          The WashU-Merck EST Project
JOURNAL        Unpublished (1995)
COMMENT        Contact: Wilson RK
               WashU-Merck EST Project
               Washington University School of Medicine
               4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
               Tel: 314 286 1800
               Fax: 314 286 1810
               Email: est@watson.wustl.edu
               High quality sequence stops: 393
               Source: IMAGE Consortium, LLNL
               This clone is available royalty-free through LLNL; contact the
               IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES       Location/Qualifiers
   source      1..458
               /organism="Homo sapiens"
               /clone="145077"
BASE COUNT        119 a        109 c         97 g        133 t
ORIGIN

Query Match    22.1%;   Best Local Similarity 100.0%;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
Matches        254;     Score 254;   DB 11;   Length 458;

Db       16 AATGCACGCTACAGGAAAAACCCATTCTTCTCCCAGCCGGGGTGCCCCAATACTTCAGTGCA 75
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      882 AATGCACGCTACAGGAAAAACCCATTCTTCTCCCAGCCGGGGTGCCCCAATACTTCAGTGCA 941

Db       76 TGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGACGATGTTGG 135
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      942 TGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCACTAAGGTCCAAGAAGACGATGTTGG 1001

Db      136 TCCAAAAAGAACGTCACCTCAGAGTCCCACTTGCTGTGTAGCTAAATCATATAACAGGGTCA 195
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     1002 TCCAAAAAGAACGTCACCTCAGAGTCCCACTTGCTGTGTAGCTAAATCATATAACAGGGTCA 1061

Db      196 CAGTAATGGGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTACTTGTTATT 255
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     1062 CAGTAATGGGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTACTTGTTATT 1121

Db      256 ATCACAAAATCTTAA 269
            |||||||||||||||
Qy     1122 ATCACAAAATCTTAA 1135

RESULT 12

LOCUS          H03289          482 bp      mRNA      EST          20-JUN-1995
DEFINITION     yj44h10.r1 Homo sapiens cDNA clone 151651 5' similar to gb:V00518
               GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (HUMAN);.
ACCESSION      H03289
NID            g866222
KEYWORDS       EST.

SOURCE      human clone-151651 library-Soares placenta Nb2HP vector-pT7T3D
            (Pharmacia) with a modified polylinker host-DH10B (ampicillin
            resistant) primer-M13RP1 Rsitel-Not I Rsite2-Eco RI Female placenta
            obtained at birth (full term). 1st strand cDNA was primed with a
            Not I - oligo(dT) primer [5'
            AACTGGAAGAATTCGGCGCGCCGAGGAATTTTTTTTTTTTTTTTTTT 3'], double-stranded
            cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
            I and cloned into the Not I and Eco RI sites of the modified pT7T3
            vector. Library went through one round of normalization. Library
            constructed by Bento Soares and M.Fatima Bonaldo.
ORGANISM    Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 482)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohling,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High qality sequence stops: 301
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES    Location/Qualifiers
     source  1..482
             /organism="Homo sapiens"
             /clone="151651"
BASE COUNT    111 a    106 c    118 g    142 t    5 others
ORIGIN

Query Match             21.8%;  Score 250;  DB 12;  Length 482;
Best Local Similarity   99.2%;  Pred. No. 0.00e+00;
Matches  262;  Conservative   0;  Mismatches   0;  Indels   2;  Gaps   2;

Db         51 TTGCCCAGAATGCACGCTACAGGAAAAACCCATTCTTCTTCCCAGCCGCGGGTGCCCAATACT 110
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Qy        874 TTGCCCAGAATGCACGCTACAGGAAAAACCCATTCTTCTTCCCAGCCG-GGGTGCCCAATACT 933

Db        111 TCAGTGCATGGGCGTGCTGCTTCTCTAGAGCATATCCACTCAACTAAGGTCCAAGAAGAC 170
              |||||||||||||||||||||||||||||||||||||| |||||||||||||||| |||||
Qy        934 TCAGTGCATGGGCGTGCTGCTTCTCTAGAGCATATCCCACTCAACTAAGGTCCAAGAGAGAC 993

Db        171 GATGTTGGTCCAAAAGAAACGTCACCTCAGAGTCCACTTGCTGTGTGAGCTAAATCATATAA 230
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy        994 GATGTTGGTCCAAAAGAAACGTCACCTCAGAGTCCACTTGCTGTGTGAGCTAAATCATATAA 1053

Db        231 CAGGGTCACAGTAAATGGGGGGTTTCAAAAGTGGGAGAACCACACGGCGTGCCACTGCAGT 290
              |||||||||||||||||||||||||||||||||| |||||||||||| |||||||||||||
Qy       1054 CAGGGTCACAGTAAATGGGGGGTTTCAAAAGTGGG-AGAACCACACGG-CGTGCCACTGCAGT 1111

Db        291 ACTTGTTATTATCACAAATCTTAA 314
              ||||||||||||||||||||||||
Qy       1112 ACTTGTTATTATCACAAATCTTAA 1135

RESULT  13
LOCUS       HUM530G10B     336 bp    mRNA         EST       13-DEC-1995
DEFINITION  Human placenta cDNA 5'-end GEN-530G10.
ACCESSION   D79076
NID         g1180949

KEYWORDS    EST; EST(expressed sequence tag); Human placenta.
SOURCE      Homo sapiens placenta cDNA to mRNA, clone_lib:human placenta
            polyA+.
ORGANISM    Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
            Homo.
REFERENCE   1  (bases 1 to 336)
  AUTHORS   Fujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Nagata,M.,
            Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiya,H.,
            Takaichi,A., Takeda,S., Watanabe,T., Takahashi,E., Hirai,Y.,
            Maekawa,H., Shin,S. and Nakamura,Y.
  TITLE     Large-scale sequencing project at Otsuka GEN Research Institute
  JOURNAL   Unpublished (1995)
REFERENCE   2  (bases 1 to 336)
  AUTHORS   Fujiwara,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-NOV-1995) to the DDBJ/EMBL/GenBank databases. Tsutomu
            Fujiwara, Otsuka GEN Research Institute,Otsuka Pharmaceutical
            Co.,Ltd, 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01,
            Japan
COMMENT     Submitted (7-Nov-1995) to DDBJ by:
            Tsutomu Fujiwara
            Otsuka GEN Research Institute
            Otsuka Pharmaceutical CO.,Ltd
            463-10 Kagasuno Kawauchi-cho
            Tokushima, Tokushima
            771-01
            Japan
            Phone:0886-65-2888
            Fax  :0886-37-1035.
FEATURES    Location/Qualifiers
     source  1..336
             /organism="Homo sapiens"
             /db_xref="taxon:9606"
             /clone_lib="human placenta polyA+"
             /tissue_type="placenta"
BASE COUNT     76 a     89 c     78 g     93 t
ORIGIN

Query Match             21.7%;  Score 249;  DB 23;  Length 336;
Best Local Similarity   98.8%;  Pred. No. 0.00e+00;
Matches  252;  Conservative   0;  Mismatches   3;  Indels   0;  Gaps   0;

Db         47 TTGCCCAGAATGCACGCTACAGGAAAAACCCATTCTTCTTCCCAGCCGCGGGTGCCCAATACT 106
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy        874 TTGCCCAGAATGCACGCTACAGGAAAAACCCATTCTTCTTCCCAGCCGGGTGCCCAATACT 933

Db        107 TCAGTGCATGGGCGTGCTGCTTCTCTAGAGCATATCCACTCAACTAAGGTCCAAGAAGAC 166
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||| |||||
Qy        934 TCAGTGCATGGGCGTGCTGCTTCTCTAGAGCATATCCCACTCAACTAAGGTCCAAGAGAGAC 993

Db        167 GATGTTGGTCCAAAAGAAACGTCACCTCAGAGTCCACTTGCTGTGTGAGCTAAATCATATAA 226
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy        994 GATGTTGGTCCAAAAGAAACGTCACCTCAGAGTCCACTTGCTGTGTGAGCTAAATCATATAA 1053

Db        227 CAGGGTCACAGTAAATGGGGGGTTTCATAGTGGGAGGACCACCACACGGGCGTCCCACTGCAGT 286
              ||||||||||||||||||||||||||| |||||  |||  ||||||||||||| ||||||||
Qy       1054 CAGGGTCACAGTAAATGGGGGGTTTCAAAAGTGGGAGAACCACACGGGCGTGCCACTGCAGTAC 1113

Db        287 TTGTTATTATCACAA 301
              |||||||||||||||
Qy       1114 TTGTTATTATCACAA 1128

RESULT  14
LOCUS       AA779136      519 bp    mRNA         EST       05-FEB-1998
DEFINITION  zj46h11.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA
            clone 453381 3' similar to gb:V00518 GLYCOPROTEIN HORMONES ALPHA
            CHAIN PRECURSOR (HUMAN).
ACCESSION   AA779136
NID         g2838467

## Record 1

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KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 519)
AUTHORS     Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
            Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
            Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
TITLE       WashU-NCI human EST Project
JOURNAL     Unpublished (1997)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -40m13 fwd. EST from Amersham
            High quality sequence stop: 316.
FEATURES             Location/Qualifiers
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                     /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                     with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                     This is a modified version of the original Soares fetal
                     liver spleen INFLS library. 1st strand cDNA was primed
                     with a Pac I - oligo(dT) primer [5'
                     AACTGGAAGAATTAATTAAGAGATCTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia) digested with Pac I and cloned into the Pac I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M.Fatima Bonaldo."
                     /db_xref="GDB:1188737"
                     /clone_lib="Soares fetal liver spleen INFLS S1"
                     /clone="453381"
                     /dev_stage="20 week-post conception fetus"
                     /sex="male"
                     /lab_host="DH10B (ampicillin resistant)"
                     /db_xref="taxon:9606"
BASE COUNT   156 a   98 c   127 g   138 t
ORIGIN

Query Match            20.7%;  Score 238;  DB 31;  Length 519;
Best Local Similarity  96.6%;  Pred. No. 0.00e+00;
Matches  257;  Conservative   0;  Mismatches  7;  Indels  2;  Gaps  2;

Db  253 TTAAGATTTGTGATAATAACAAGTACTCCAGTGGCACCGTGTGGTTCTCCACTTTGAA 312
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Cp 1135 TTAAGATTTGTGATAATAACAAGTACTCCAGTGGCACCGTGTGGTTCTCCACTTTGAA 1076

Db  313 ACCCCCAATTACTGTGACCCGTGTTATATGATTTAGCTACACAGCAAGTGGACTCTGAGGT 372
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp 1075 ACCCCCAATTACTGTGACCCGTGTTATATGATTTAGCTACACAGCAAGTGGACTCTGAGGT 1016

Db  373 GACGTTCTTTTGGACCAACACATCGTCTTCTTGACCTTAGTGGATTAGCTCTAGA 432
        ||||||||||||||||||||||||||||| |||||||||||||||| ||||||||
Cp 1015 GACGTTCTTTTGGACCAACACATCGTCTTCTTGGACCTTAGTGGAGTGGGATATGCTCTAGA 956

Db  433 GAAGCAGCAGCCCATGCACTGAAGTAGTAGTGGGGGGGGGTTTC 492
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Cp  955 GAAGCAGCAGCCCATGCACTGAAGTAATGGGGGGGGGTTTC 896

Db  493 CTG-AGCGTG-ATTCTGGGGAATCTG 516
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Cp  895 CTGTAGCGTGTCAATCTGGGCAACCTG 870
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Record 2

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DEFINITION  Human placenta cDNA 5'-end GEN-555E01.
ACCESSION   C17966
NID         g1379568
KEYWORDS    EST; EST(expressed sequence tag); Human placenta.
SOURCE      Homo sapiens placenta cDNA to mRNA, clone:555E01.
ORGANISM    Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
            Homo.
REFERENCE   1  (sites)
AUTHORS     Fujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y.,
            Kyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y.,
            Shinomiya,H., Suzuki,M., Takaichi,A., Takeda,S., Watanabe,T.,
            Maekawa,H., Nakamura,Y. and Takahashi,E.
TITLE       Otsuka cDNA project
JOURNAL     Unpublished (1996)
REFERENCE   2  (bases 1 to 423)
AUTHORS     Fujiwara,T.
TITLE       Direct Submission
JOURNAL     Submitted (24-JUN-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu
            Fujiwara, Otsuka GEN Research Institute,Otsuka Pharmaceutical
            Co.,Ltd; 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01,
            Japan (Tel:+81-886-65-2888, Fax:+81-886-37-1035)
FEATURES             Location/Qualifiers
     source          1..423
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="555E01"
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BASE COUNT   113 a   117 c   90 g   103 t
ORIGIN

Query Match            20.6%;  Score 236;  DB 23;  Length 423;
Best Local Similarity  98.0%;  Pred. No. 0.00e+00;
Matches  251;  Conservative   0;  Mismatches  3;  Indels  2;  Gaps  2;

Qy  874 TTGCCCAGAATGCACGCTACAGGAAAAACCCATTCTTCTCCCAGCCCGGGGTGCCCAAATACT 933
        |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db  169 TTGCCCAGAATGCACGCTACAGGAAAAACCCATTCTTCTCCCAGCCCGGGGTGCCCAAATACT 228

Qy  934 TCAGTGCAIGGGCGCTGCTGCTTCTCTTAGAGCGCATATCCCACTCCACTAAGGTCCAAGAAGAC 993
        ||||||| ||||||| ||| |||||||||||||||||||||||||||||||||||||||||||||
Db  229 TCAGTGCATGGGCGTGCCTGCTTGTTCTCTTAGAGCGCATATCCCACTCCACTAAGGTCCAAGAAGAC 288

Qy  994 GATGTTGGTGTCCAAAAAGAACGTCACCTCAGAGTCCACTTCGCTGTGTGTAGCTAAAATCATATAA 1053
        ||||||||||||||||||||| |||||||||||||||||||||||||||||| ||||| ||||||||
Db  289 GATGTTGGTGTCCAAAAAGACCGTCACCTCACGAGTCCACTTCGCTGTGTGTGAGCTAAATACATATAA 348

Qy 1054 CAGGGTCACAGTAATGGGGGGGTTTCAAAAGTGGAGAACCACACGCGGCGTGCCACTGCAGTAC 1113
        ||||||||||||| |||||||||||||||| ||||||| |||||||||||||||||||||||||
Db  349 CAGGGTCACAGTAAATGGGGGGGGGTTTCAAAGTGGAGA-CCACACGCGGCGTGCCACTGCAGTAC 407

Qy 1114 TTGTTATT-ATCACAA 1128
        || ||| || |||||||
Db  408 TTTTTTTTTTATCACAA 423
```

```
**************************************************************************
*                                                                        *
*       |\/| |_ |_ |\ |_) |_ |_|                                         *
*       |  | |  |_ | \|   |  | | (TM)                                    *
*                                                                        *
**************************************************************************
```

MPsrch_pp   protein - protein database search, using Smith-Waterman algorithm

Release 3.0.5AA John F. Collins, Biocomputing Research Unit.
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Run on: Wed May 6 09:01:34 1998;   MasPar time 9.14 seconds
                                           466.133 Million cell updates/sec

Tabular output not generated.

Database: a-geneseq31
               1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
               8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
               14:part14 15:part15 16:part16 17:part17 18:part18
               19:part19 20:part20 21:part21 22:part22 23:part23
               24:part24 25:part25 26:part26

Title: >US-08-804-166-6
Description: (1-285) from US08804166.pep
Perfect Score: 2183
Sequence: 1 SRTSLLLAFGLLCLPWLQEG.........GFKVENHTACHCSTCYYHKS 285

Scoring table: PAM 150
               Gap 11

Searched: 120837 seqs, 14945562 residues

Post-processing: Minimum Match 0%
               Listing first 45 summaries

Statistics: Mean 31.870; Variance 121.907; scale 0.261

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES

Result   Query
NO.   Score Match Length DB ID   Description   Pred. No.
  1   2183   100.0   285   26   W33359 TBP(20-190)/hCG-alpha   2.81e-227
  2   1667   76.4   285   26   W33357 TBP(20-161)/hCG-alpha   1.50e-169
  3   1505   68.9   289   26   W33358 TBP(20-190)/hCG-beta   1.76e-151
  4   1306   59.8   336   26   W33360 TBP(20-190)/hCG-beta   2.45e-129
  5   1306   59.8   371   13   R07449 Tumour Necrosis Facto   2.45e-129
  6   1305   59.8   451   13   R70107 TNF-R-GBP 130 fusion   3.16e-129
  7   1306   59.8   455   4   R24000 TNF-alpha 55kD recept   2.45e-129
  8   1306   59.8   455   14   R25084 p55 TNF-R.   2.45e-129
  9   1306   59.8   455   8   R20787 TNF-R.   2.45e-129
 10   1306   59.8   455   4   R42059 Lambda derived TNF-R.   2.45e-129
 11   1306   59.8   455   2   R10986 30kD TNF inhibitor pr   2.45e-129
 12   1305   59.8   900   13   R11082 Human 55kD TNF-bindin   3.16e-129
 13   1303   59.7   309   13   R70103 TNF-R-GBP 130 fusion   3.16e-129
 14   1303   59.7   455   2   R70108 TNF-R-GBPH fusion pro   5.28e-129
 15   1303   59.7   547   13   R07451 Human Tumour Necrosis   5.28e-129
 16   1303   59.7 1604   13   R70104 TNF-R-GBPH fusion pro   5.28e-129
 17   1301   59.6 1245   13   R70105 TNF-R-EBA 175 fusion   5.28e-129
 18   1297   59.4   433   8   R51032 Mutant p55 tumour nec   2.45e-128
 19   1297   59.4   443   8   R51033 Mutant p55 tumour nec   2.45e-128
 20   1297   59.4   455   8   R42197 p55 Tumour necrosis f   2.45e-128
 21   1297   59.4   455   8   R51034 Mutant p55 tumour nec   2.45e-128
 22   1292   59.2   455   3   R12550 Type I TNF receptor.   8.80e-128
 23   1289   59.0   307   26   W33358 TBP(20-161)/hCG-beta   1.90e-127
 24   1247   57.1   161   5   R27496 Native 30 kD TNF inh1   8.73e-123
 25   1247   57.1   884   13   R70109 TNF-R-GBP 130 fusion   8.73e-123
 26   1236   56.6   199   4   R24080 Truncated TNF-alpha 5   1.45e-121
 27   994   45.5   168   4   R24084 Truncated TNF-alpha 5   9.63e-86
 28   994   45.5   168   4   R24081 Truncated TNF-alpha 5   9.63e-86
 29   907   41.5   461   2   R07450 Rat Tumour Necrosis F   3.42e-85
 30   715   32.8   234   15   R86254 Single chain gonadotr   4.68e-63
 31   705   32.3   234   15   R86276 Partially deglycosyla   4.68e-63
 32   705   32.3   234   15   R86266 Partially deglycosyla   4.68e-63
 33   705   32.3   234   15   R86270 Single chain gonadotr   4.68e-63
 34   697   31.9   234   15   R86248 Single chain gonadotr   1.1e-62
 35   696   31.9   234   15   R86249 Single chain gonadotr   4.0e-62
 36   694   31.8   226   15   R86235 Single chain gonadotr   7.40e-62
 37   693   31.7   222   15   R86256 Single chain gonadotr   9.51e-62
 38   693   31.7   222   15   R86268 Single chain gonadotr   9.51e-62
 39   689   31.6   234   15   R86270 Single chain gonadotr   2.60e-61
 40   689   31.6   237   15   R86252 Partially deglycosyla   2.60e-61
 41   689   31.6   234   15   R86253 Single chain gonadotr   2.60e-61
 42   687   31.5   229   15   R86250 Single chain gonadotr   4.29e-61
 43   687   31.5   234   15   R86271 Partially deglycosyla   4.29e-61
 44   687   31.5   234   15   R86261 Partially deglycosyla   4.29e-61
 45   686   31.4   234   15   R86275 Single chain gonadotr   5.51e-61
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                              ALIGNMENTS

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RESULT     1
ID    W33359; standard; Protein; 285 AA.
AC    W33359;
DT    19-MAR-1998  (first entry)
DE    TBP(20-190)/hCG-alpha fusion protein.
KW    Fusion protein; thrombopoietin; TPO; human chorionic gonadotrophin;
KW    alpha subunit; hCG-alpha.
OS    Homo sapiens.
PN    WO9730161-A1.
PD    21-AUG-1997.
PF    20-FEB-1997; U02315.
PR    20-FEB-1996; US-011936.
PA    (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
PI    Campbell RK, Chappel SC, Jameson BA;
DR    WPI; 97-425036/39.
DR    N-PSDB; T94021.
PT    Hybrid dimeric protein comprising two co-expressed units - each
PT    based on receptor or ligand and a subunit of a heterodimeric
PT    hormone, especially FSH, for inducing follicular maturation
PS    Example; Pages 37-38; 60pp; English.
PS    A novel fusion protein comprises 2 dimer forming co-expressed amino
CC    acid sequences, each consisting of a homodimeric or heterodimeric
CC    receptor chain or ligand, with ligand-receptor binding activity,
CC    bound directly or via a peptide linker to a subunit of a
CC    heterodimeric protein hormone capable of forming a heterodimer with
CC    the hormone's other subunits. The fusion protein, e.g. the
CC    thrombopoietin (TPO)/human chorionic gonadotrophin-alpha subunit
CC    (hCG-alpha) fusion protein denoted by the present sequence,
CC    significantly increases the biological activity of the hormone
CC    component, reducing the requirement for hormone itself and the
CC    number of injections needed.
SQ    Sequence  285 AA;

Query Match             100.0%;  Score 2183;  DB 26;  Length 285;
Best Local Similarity   100.0%;  Pred. No. 2.81e-227;
Matches  285;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

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Qy    61 tdcrecesgsftasenhlrhclscskckemqgveissctvdrdtvcgcrkngyrhvwse 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 tdcrecesgsftasenhlrhclscskckemqgveissctvdrdtvcgcrkngyrhvwse 120
```

```
Qy    61  TDCRECEGSGSFTASENHLRHCLSCSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHWSE 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  nlfgcfnctlclngtvhlscqekqntvctchagfflrenecvscsnckkslectklslpq 180
Qy   121  NLFQCFNCTLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQ 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  lenvkgtedsgttagaapgcpectlqenpffsqpgapllqcmgccfsrayptplrskktm 240
Qy   181  IENVKGTEDSGTTAGAAPGCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTM 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  lvqknvtsestccvaksynrvtvmggfkvenhtachcstcyyhks 285
Qy   241  LVQKNVTSESTCCVAKSYNRVTVMGGFKVENHTACHCSTCYYHKS 285
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RESULT  2
ID   W33357 standard; Protein; 256 AA.
AC   W33357;
DT   19-MAR-1998  (first entry)
DE   TBP(20-161)/hCG-alpha fusion protein.
KW   Fusion Protein; thrombopoietin; TPO; human chorionic gonadotrophin;
KW   alpha subunit; hCG-alpha.
OS   Homo sapiens.
PN   WO9730161-A1.
PD   21-AUG-1997.
PF   20-FEB-1997; US-011936.
PR   20-FEB-1996; US-011936.
PA   (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
PI   Campbell RK, Chappel SC, Jameson BA;
PR   WPI; 97-425036/39.
DR   N-PSDB; T94007.
PT   Hybrid dimeric protein comprising two co-expressed units - each
PT   based on receptor or ligand and a subunit of a heterodimeric
PT   hormone, especially FSH, for inducing follicular maturation
PS   Example; Pages 32-33; 60pp; English.
CC   A novel fusion protein comprises 2 dimer forming co-expressed amino
CC   acid sequences, each consisting of a homodimeric or heterodimeric
CC   receptor chain or ligand, with ligand-receptor binding activity,
CC   bound directly or via a peptide linker to a subunit of a
CC   heterodimeric protein hormone capable of forming a heterodimer with
CC   the hormone's other subunits. The fusion protein, e.g. the
CC   thrombopoietin (TPO)/human chorionic gonadotrophin-alpha subunit
CC   (hCG-alpha) fusion protein denoted by the present sequence,
CC   significantly increases the biological activity of the hormone
CC   component, reducing the requirement for hormone itself and the
CC   number of injections needed.
SQ   Sequence  256 AA;
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Query Match   76.4%;  Score 1667;  DB 26;  Length 256;
Best Local Similarity   89.1%;
Matches  254;  Conservative   2;  Pred. No. 1.50e-169;  Mismatches   0;  Indels  29;  Gaps   1;

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Qy     1  SRTSLLAFGLLCLPWLQEGSADSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQD 60
Db    61  tdcrecegsgsftasenhlrhclscscskcrkemgqveisscctvdrdtvcgcrknqyrhywse 120
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Qy   121  NLFQCFNCTLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSC 164
Db   165  ---------agaapgcpectlqenpffsqpgapllqcmgccfsrayptplrskktm 211
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Qy   165  IENVKGTEDSGTTAGAAPGCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTM 211
Db   212  lvqknvtsestccvaksynrvtvmggfkvenhtgchcstcyyhks 256
          |||||||||||||||||||||||||||||||||||||||||||||
Qy   212  LVQKNVTSESTCCVAKSYNRVTVMGGFKVENHTACHCSTCYYHKS 256
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```
RESULT  3
ID   W33360 standard; Protein; 336 AA.
AC   W33360;
DT   19-MAR-1998  (first entry)
DE   TBP(20-190)/hCG-beta fusion protein.
KW   Fusion protein; thrombopoietin; TPO; human chorionic gonadotrophin;
KW   beta subunit; hCG-beta.
OS   Homo sapiens.
PN   WO9730161-A1.
PD   21-AUG-1997.
PF   20-FEB-1997; US-011936.
PR   20-FEB-1996; US-011936.
PA   (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
PI   Campbell RK, Chappel SC, Jameson BA;
PR   WPI; 97-425036/39.
DR   N-PSDB; T94022.
PT   Hybrid dimeric protein comprising two co-expressed units - each
PT   based on receptor or ligand and a subunit of a heterodimeric
PT   hormone, especially FSH, for inducing follicular maturation
PS   Example; Pages 39-40; 60pp; English.
CC   A novel fusion protein comprises 2 dimer forming co-expressed amino
CC   acid sequences, each consisting of a homodimeric or heterodimeric
CC   receptor chain or ligand, with ligand-receptor binding activity,
CC   bound directly or via a peptide linker to a subunit of a
CC   heterodimeric protein hormone capable of forming a heterodimer with
CC   the hormone's other subunits. The fusion protein, e.g. the
CC   thrombopoietin (TPO)/human chorionic gonadotrophin-beta subunit
CC   (hCG-beta) fusion protein denoted by the present sequence,
CC   significantly increases the biological activity of the hormone
CC   component, reducing the requirement for hormone itself and the
CC   number of injections needed.
SQ   Sequence  336 AA;
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```
Query Match   68.9%;  Score 1505;  DB 26;  Length 336;
Best Local Similarity   98.0%;
Matches  196;  Conservative   2;  Pred. No. 1.76e-151;  Mismatches   2;  Indels   0;  Gaps   0;

Db     1  srtsllllafgllclplwlqegsadsvcpggkyihpqnnsicctkchkgtylyndcpgpgqd 60
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Qy     1  SRTSLLAFGLLCLPWLQEGSADSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQD 60
Db    61  tdcrecegsgsftasenhlrhclscscskcrkemgqveisscctvdrdtvcgcrknqyrhywse 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    61  TDCRECESGSSFTASENHLRHCLSCSCSKCRKEMGQVEISSCCTVDRDTVCGCRKNQYRHWSE 120
Db   121  nlfgcfnctlclngtvhlscqekqntvctchagfflrenecvscsnckkslectklclpq 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   121  NLFQCFNCTLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQ 180
Db   181  ienvkgtedsgttagapgc 200
          ||||||||||||||||| ||
Qy   181  IENVKGTEDSGTTAGAAPGC 200
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```
RESULT  4
ID   R07449 standard; protein; 371 AA.
AC   R07449;
DT   29-JAN-1991  (first entry)
DE   Tumour Necrosis Factor-binding protein from pTNF-BP15 cDNA.
KW   Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
KW   pTNF-BP15; infectious disease; parasitic disease; cachexia;
OS   Homo sapiens.
KW   autoimmune disease; shock.
PN   EP-393438-A.
PD   24-OCT-1990.
PF   06-APR-1990; 106624.
PR   29-APR-1989; DE-913101.
PR   21-APR-1989; DE-913101.
PR   21-JUN-1989; DE-920282.
PA   (BOEH ) BOEHRINGER INGELHEIMINT.
PI   Hauptmann R, Himmler A, Maurer-Fogy I, Stratowa C;
PR   WPI; 90-321987/43.
DR   N-PSDB; Q06282.
PT   DNA encoding TNF binding protein and TNF- receptor - used in
```

Left column:

```
PT  tumour treatment and to understand mechanismsm to TNF action
PS  Disclosure; Fig 1(1-3); 51pp; German.
CC  Clone pTNF-BP15 was used to contruct pADTNF-BP, for transfection of
CC  e.g. COS7 cells. The expressed proteins are useful
CC  prophylactically and therapeutically to control disorders which
CC  involve the damaging effects of TNF-alpha or -beta (e.g. infectious or
CC  parasitic diseases, shock, cachexia, autoimmune diseases, adult
CC  respiratory distress syndrome etc., or side effects of treatment with
CC  TNG-alpha). They can also be used as diagnostic reagents for
CC  assaying TNF and in study of TNF-receptor interactions.
CC  See also Q06282-Q06285.
SQ  Sequence 371 AA;
```

```
Query Match     59.8%;  Score 1306;  DB 2;  Length 371;
Best Local Similarity  98.8%;  Pred. No. 2.45e-129;
Matches 169;  Conservative  1;  Mismatches  1;  Indels  0;  Gaps  0;

Db   41  dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
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Db  101  scskcrkemgqveisscctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
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Qy   83  SCSKCRKEMGQVEISSCCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db  161  kqntvcctchagfflrenecvscsnckkslecctklclpqienvkgtedsgtt 211
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Qy  143  KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQIENVKGTEDSGTT 193
```

```
RESULT  5
ID   R70107  standard; Protein; 451 AA.
AC   R70107;
DT   10-NOV-1995  (first entry)
DE   TNF-R-GBP 130 fusion protein.
KW   Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;
KW   red blood cell; cytokine receptor; glycophorin binding peptide 130;
KW   GBP 130; GBPH; glycophorin binding protein A.
OS   Chimeric Homo sapiens.
OS   Chimeric Plasmodium falciparum.
PN   WO9506737-A.
PD   09-MAR-1995.
PF   09-SEP-1994; G01900.
PR   03-SEP-1993; GB-018350.
PR   23-AUG-1994; GB-017021.
PA   (PREN/) PRENDERGAST K F.
PI   Prendergast KF;
PT   WPI; 95-115452/15.
DR   
PT   New hybrid peptide(s) for binding cytokine(s) - comprising a
PT   malaria parasite peptide capable of binding a red blood cell and
PT   a receptor peptide.
PS   Example A: Page 53-54; 93pp; English.
CC   Hybrid peptides for binding cytokines, comprising a malaria parasite
CC   (Plasmodium falciparum) peptide (capable of binding to a red blood
CC   cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples
CC   of these hybrid peptides. R70107 is a fusion of tumour necrosis factor
CC   receptor (in accordance with H Loetscher et al Cell, Vol. 61, 351-359)
CC   and glycophorin binding protein (GBP) 130. The use of cytokine
CC   receptors not normally found on RBCs means that the cytokine can bind
CC   harmlessly to the RBC without deleterious effect. The RBC protects the
CC   hybrid peptides from excretion from the kidney, and due to steric
CC   hindrance prevents the cytokines binding to a receptor in another cell.
CC   GBP 130 or GBPH (GBP homologue) are the prefd. malaria parasite peptides
CC   used, others include EBA 175 (175 kDa erythrocyte binding antigen),
CC   PMMSA (pre major merozoite surface antigen) and the Duffy binding
CC   receptor molecule (eg. exhibited by Plasmodium vivax). These peptides
CC   bind to pref. glycophorin A, B and C, sialo glycoproteins, found on
CC   the surface of RBCs. The hybrid peptides are thus used to lower
CC   the levels of free cytokines in the circulation to reduce pathological
CC   damage.
SQ   Sequence  451 AA;
```

```
Query Match     59.8%;  Score 1305;  DB 13;  Length 451;
Best Local Similarity  98.8%;  Pred. No. 2.45e-129;
Matches 169;  Conservative  1;  Mismatches  1;  Indels  0;  Gaps  0;
```

Right column:

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Best Local Similarity  98.3%;  Pred. No. 3.16e-129;
Matches 169;  Conservative  1;  Mismatches  2;  Indels  0;  Gaps  0;

Db   20  dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 79
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   23  DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db   80  scskcrkemgqveisscctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 139
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   83  SCSKCRKEMGQVEISSCCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db  140  kqntvcctchagfflrenecvscsnckkslectklclpqienvkgtedsgtna 191
         ||||||| |||||||||||||||||||||||||||||||| |||||||||||||
Qy  143  KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQIENVKGTEDSGTTA 194
```

```
RESULT  6
ID   R24000  standard; Protein; 455 AA.
AC   R24000;
DT   05-NOV-1992  (first entry)
DE   TNF-alpha 55kD receptor.
KW   tumour necrosis factor alpha; extracellular binding domain;
KW   treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
KW   malaria; viral meningitis; graft versus host disease;
KW   autoimmune disease; rheumatoid arthritis.
OS   Homo sapiens.
FH   Key          Location/Qualifiers
FT   peptide      1..40
FT                /label= signal peptide
FT   modified_site 54..56
FT                /label= "N linked glycosylation site
FT                /note= "potential"
FT   modified_site 145..147
FT                /label= "N linked glycosylation site
FT                /note= "potential"
FT   modified_site 151..153
FT                /label= "N linked glycosylation site
FT                /note= "potential"
FT   domain       212..234
FT                /label= transmembrane domain
PN   WO9207076-A.
PD   30-APR-1992.
PF   18-OCT-1991; G01826.
PR   18-OCT-1990; GB-022648.
PA   (CHAR-) CHARING CROSS SUNLEY RES CENT.
PI   Brennan FM, Feldmann M, Gray PW, Turner MJC;
DR   WPI; 92-167156/20.
N-PSDB; Q24440.
PT   New polypeptide capable of binding human TNF alpha - comprises
PT   first three cysteine-rich subdomains of TNF alpha receptor for
PT   treating autoimmune disease, septic shock, HIV etc.
PS   Example: Fig 1; 43pp; English.
CC   This sequence was deduced from human TNF-alpha cDNA isolated as in
CC   Q24440. The first 35 amino acids are generally quite hydrophobic
CC   and probably represent a signal sequence. Residues 35-40 are highly
CC   charged (DREKR) and this is not normally found in secretory
CC   signal sequences. It is possible the receptor is processed by
CC   proteolysis after residue 40 which contains a dibasic cleavage site
CC   (KR). Hydropathy analysis of this sequence predicts a single
CC   transmembrane domain of 23 amino acids, dividing the sequence into
CC   an extracellular domain of 171 residues and a cytoplasmic domain of
CC   221 residues. The sequence contains a large number of cysteine
CC   residues, the arrangement of which is similar to that of other cell
CC   surface proteins, suggesting the TNF-alpha receptor is structurally
CC   related to a family of receptors.
CC   NOTE:- Residues 371,2 given in the sequence as T, L, are encoded by
CC   TGG  (W) and AAG (K).
CC   See also Q24440-51, R24000, R24080-84, R27585, Q29236-8
SQ   Sequence  455 AA;
```

```
Query Match     59.8%;  Score 1306;  DB 4;  Length 455;
Best Local Similarity  98.8%;  Pred. No. 2.45e-129;
Matches 169;  Conservative  1;  Mismatches  1;  Indels  0;  Gaps  0;
```

RESULT 7

```
ID   R75084 standard; Protein; 455 AA.
AC   R75084;
DT   19-JAN-1996 (first entry)
DE   p55 TNF-R.
KW   p55; tumour necrosis factor receptor; TNF-R; human; murine; chimera;
KW   epidermal growth factor receptor; EGF-R; protease; inhibitor;
KW   phorbol myristate acetate; PMA.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   peptide         41..53
FT                   /note= "N terminus of soluble p55 TNF-R"
FT   modified_site   54..56
FT                   /note= "glycosylation site"
FT   modified_site   145..147
FT                   /note= "glycosylation site"
FT   modified_site   161..163
FT                   /note= "glycosylation site"
FT   peptide         193..210
FT                   /note= "peptide used in creation of chimeras"
FT   region          198..210
FT                   /note= "spacer region"
FT   misc_difference 201
FT                   /note= "major C terminus for soluble p55 TNF-R"
FT   misc_difference 202
FT                   /note= "essential for shedding reaction"
FT   misc_difference 203
FT                   /note= "minor C terminus for soluble p55 TNF-R"
FT   region          212..234
FT                   /note= "transmembrane region"
PN   AU9475742-A.
PD   04-MAY-1995.
PF   11-OCT-1994; 075742.
PR   12-OCT-1993; IL-107268.
PA   (YEDA ) YEDA RES & DEV CO LTD.
PI   Batkin M, Brakebusch C, Varfolomeev E, Wallach D;
DR   WPI; 95-194342/26.
DR   N-PSDB; Q90513.
PT   New protease capable of cleaving soluble tumour necrosis factor
PT   (TNF) receptor - from cell-bound TNF- receptor, useful for
PT   antagonising deleterious effects of TNF.
PS   Disclosure; Fig 1; 40pp; English.
CC   This sequence represents human p55 tumour necrosis factor (TNF-R).
CC   Expression of this receptor is regulated by shedding of the extracellular
CC   receptor fragment. The p55 TNF-R can be shed in response to different
CC   inducing agents, e.g. phorbol myristate acetate (PMA), depending on cell
CC   type. The only region of the receptor whose structure affects the
CC   shedding response is the spacer region (see R75012) in the extracellular
CC   domain. This region is located close to a site of cleavage of the
CC   molecule, and links the Cys rich module to the transmembrane domain. The
CC   spacer region of the encoded protein was used to create the chimeras
CC   between human p55 TNF-R and murine epidermal growth factor receptor
CC   (EGF-R) that are represented by R75007-11. This spacer region was
CC   subjected to deletion mutations (R75013-25) and substitutions
CC   (R75026-47). Of the spacer region, the most important residues are
CC   Asn 172, Val 173, Lys 174 and Gly 175, with Val 173 being the most
CC   important of these. The shedding of the receptor is independent of the
CC   side chain identity of these residues, with the exception of a limited
CC   dependence on the identity of Val 173. Mutations which alter the
CC   conformation of the protein adversely effect the shedding process.
CC   The mutations shown in R75013-47 were introduced in order to create an
CC   inhibitor of a protease that is capable of cleaving the soluble TNF-R
CC   from the cell bound TNF-R. Fragments of these inhibitors can be seen in
CC   R75017-9, R75025, R75033-5 and R75042-3. These protease inhibitors can
CC   be used for enhancing TNF function.
SQ   Sequence 455 AA;

Query Match             59.8%;  Score 1306; DB 14; Length 455;
Best Local Similarity   98.8%;  Pred. No. 2.45e-129;
Matches   169;  Conservative   1;  Mismatches   1;  Indels   0;  Gaps   0;

Qy    41 dsvcpggkylhpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    41 dsvcpggkylhpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100

Qy    23 DSVCPGGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82
Db   101 scskcrkemgqveisscvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160

Qy    83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQE 142
Db   161 kqntvctchagfflrenecvscsnckksleetklclpqienvkgtedsgtt 211

Qy   143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQIENVKGTEDSGTT 193
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RESULT 8

```
ID   R20787 standard; Protein; 455 AA.
AC   R20787;
DT   11-MAY-1992 (first entry)
DE   TNF-alpha binding protein.
KW   Tumour necrosis factor alpha; autoimmune diseases; cachectin;
KW   extracellular domain.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   peptide         1..40
FT                   /note= "signal peptide"
FT   peptide         41..455
FT                   /note= "mature peptide"
FT   domain          30..199
FT                   /note= "extracellular domain"
FT   domain          212..234
FT                   /note= "transmembrane domain"
FT   modified_site   145..147
FT                   /note= "potential N-glycosylation site"
FT   modified_site   151..153
FT                   /note= "potential N-glycosylation site"
PN   GB2246569-A.
PD   05-FEB-1992.
PF   15-JUN-1990; 013410.
PR   15-JUN-1990; GB-013410.
PA   (CHAR-) CHARING CROSS SUNLE.
PI   Feldman M, Gray P, Turner M, Brennan F;
WPI; 92-043613/06.
DR   N-PSDB; Q20973.
PT   New tumour necrosis factor alpha binding protein and polypeptide
PT   - useful in treating cachexia, sepsis and auto immune diseases
PT   e.g. rheumatoid arthritis
PS   Disclosure; Fig 1; 25pp; English.
CC   The amino acid sequence is that of tumour necrosis factor alpha
CC   binding protein which contains the extracellular domain of human TNF
CC   alpha receptor. It is soluble and can be used in the regulation of
CC   TNF-mediated responses by binding and sequestering the cytokine. It
CC   can therefore be used therapeutically to treat disorders such as
CC   cachexia, sepsis and autoimmune diseases, specifically rheumatoid
CC   arthritis.
SQ   Sequence 455 AA;

Query Match             59.8%;  Score 1306; DB 4; Length 455;
Best Local Similarity   98.8%;  Pred. No. 2.45e-129;
Matches   169;  Conservative   1;  Mismatches   1;  Indels   0;  Gaps   0;

Qy    41 dsvcpggkylhpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
          |||||||||||||
Db    41 dsvcpggkylhpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
```

```
Qy   23  DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPQQDTDCRECESGSFFASENHLRHCL 82

Db  101  scskcrkemgqveisssctvdrdtvcgrknqyrhywsenlfqcfncslclngtvhlscqe 160
         ||||||||||||||||||||||:|||||||||||||||||||||||||||||||||
Qy   83  SCSKCRKEMGQVEISSSCTVDRDTVCGRKNQYRHWSENLFQCFNCTLCLNGTVHLSCQE 142

Db  161  kqntvctchagfflrenecvscsnckkslectklclpqienvkgtedsgtt 211
         ||||||||||||||||||||||||||||||||:|||||||||||||||||
Qy  143  KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQIENVKGTEDSGTT 193
```

RESULT 9

```
ID  R42059 standard; Protein; 455 AA.
AC  R42059;
DT  29-APR-1994 (first entry)
DE  Lambda derived TNF-R.
KW  Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;
KW  IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;
KW  rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;
KW  pulmonary fibrosis; silicosis; allograft; xenograft; rejection;
KW  graft verses host disease; sepsis; inflammation; allergy;
KW  autoimmune dysfunction.
OS  Homo sapiens.
FH  Lambda-gt10-7ctnfbp.
FT  Key           Location/Qualifiers
FT  peptide       1..40
FT                /note="Signal peptide"
FT  protein       41..455
FT                /note="Mature hTNF-R"
PN  WO9319777-A.
PD  14-OCT-1993;
PR  26-MAR-1993; U02938.
PR  30-MAR-1992; US-860710.
PA  (IMMV ) IMMUNEX CORP.
PI  Smith CA;
DR  WPI; 93-336592/42.
DR  N-PSDB; Q49932.
CC  New fusion protein tumour necrosis factor and human interleukin-1
CC  receptor - useful in therapy, diagnosis and assays of e.g.
CC  rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.
PS  Disclosure; Page 57-59; 85pp; English.
CC  The sequences given in R42058-59 represent human tumour necrosis
CC  factor receptor (TNF-R) and the sequences in R42060-61 represent
CC  human interleukin-1 receptor (IL-1R). These sequences were used in
CC  the production of a fusion protein which conformed to one of the
CC  formulae:
CC  TNF-R-linker-TNF-R-linker-IL-1R
CC  IL-1R-linker-TNF-R-linker-TNF-R
CC  TNF-R-linker-TNF-R
CC  The linker may comprise 5-100 amino acids selected from Gly, Asp,
CC  Ser, Thr and Ala. These linkers separate the individual moieties
CC  by such a distance that each component of the fusion protein is
CC  capable of folding into the secondary or tertiary structure required
CC  for its biological activity. These fusion proteins may be used in
CC  therapy, diagnosis and assays for conditions mediated by TNF or IL-1,
CC  particularly in conditions in which both TNF and IL-1 play a causitive
CC  role. They may be used to treat cachexia, rheumatoid arthritis,
CC  diabetes, multiple sclerosis, pulmonary fibrosis and silicosis,
CC  cerebral malaria, allograft and xenograft rejection in graft verses
CC  host disease, sepsis, septic shock, inflammation, allergies and
CC  autoimmune dysfunctions.
SQ  Sequence  455 AA;
```

Query Match   59.8%;   Score 1306;   DB 8;   Length 455;
Best Local Similarity 98.8%;   Pred. No. 2.45e-129;
Matches 169; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy   41  dsvcpqgkylhpqnnslcctkchkgtylyndcpgpqqdtdcrecesgsftasenhlrhcl 100
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   23  DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPQQDTDCRECESGSFTASENHLRHCL 82

Qy  101  scskcrkemgqveisssctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   83  SCSKCRKEMGQVEISSSCTVDRDTVCGCRKNQYRHWSENLFQCFNCTLCLNGTVHLSCQE 142

Qy  161  kqntvctchagfflrenecvscsnckkslectklclpqienvkgtedsgtt 211
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  143  KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQIENVKGTEDSGTT 193
```

```
Qy   83  SCSKCRKEMGQVEISSSCTVDRDTVCGRKNQYRHWSENLFQCFNCTLCLNGTVHLSCQE 142
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  161  kqntvctchagfflrenecvscsnckkslectklclpqienvkgtedsgtt 211

Qy  143  KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQIENVKGTEDSGTT 193
```

RESULT 10

```
ID  R10986 standard; Protein; 455 AA.
AC  R10986;
DT  13-MAY-1991 (first entry)
DE  30kD TNF inhibitor precursor.
KW  Tumour necrosis factor inhibitor.
OS  Homo sapiens.
FH  Key           Location/Qualifiers
FT  cleavage_site 40..41
FT                /note="cleavage gives active protein "
PN  AU9058976-A.
PD  24-JAN-1991.
PR  16-JUL-1990; 058976.
PR  18-JUL-1989; US-381080.
PR  11-DEC-1989; US-450329.
PR  07-FEB-1990; US-479661.
PA  (SYNE-) SYNERGEN INC.
DR  WPI; 91-073847/11.
DR  N-PSDB; Q10883.
CC  Tumour necrosis factor inhibitor - for suppression of TNF-alpha
CC  and -beta, useful as therapeutic agent.
PS  Disclosure; Fig 21; 142pp; English.
CC  The sequence comprises the entire 30 kD TNF inhibitor. The clone
CC  from which the sequence was deduced was isolated from a cDNA
CC  library prepd. from RNA form U937 cells treated with PMA/PHA.
CC  The whole gene can be inserted into expression vectors for prepn.
CC  of TNF inhibitor for use in the treatment of inflammatory and
CC  degenerative diseases. The active protein is claimed (Claim 8).
CC  See also R10984 and R11001.
SQ  Sequence  455 AA;
```

Query Match   59.8%;   Score 1306;   DB 2;   Length 455;
Best Local Similarity 98.8%;   Pred. No. 2.45e-129;
Matches 169; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Db   41  dsvcpqgkylhpqnnslcctkchkgtylyndcpgpqqdtdcrecesgsftasenhlrhcl 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   23  DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPQQDTDCRECESGSFTASENHLRHCL 82

Db  101  scskcrkemgqveisssctvdrdtvcgrknqyrhywsenlfqcfncslclngtvhlscqe 160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   83  SCSKCRKEMGQVEISSSCTVDRDTVCGRKNQYRHWSENLFQCFNCTLCLNGTVHLSCQE 142

Db  161  kqntvctchagfflrenecvscsnckkslectklclpqienvkgtedsgtt 211
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  143  KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQIENVKGTEDSGTT 193
```

RESULT 11

```
ID  R11082 standard; Protein; 455 AA.
AC  R11082;
DT  24-MAY-1991 (first entry)
DE  Human 55kD TNF-binding protein.
KW  Tumour Necrosis Factor; binding proteins; septic shock;
KW  autoimmune glomerulonephritis; lymphokine; cytokine.
FH  Key           Location/Qualifiers
FT  modified_site 54
FT                /label= putative N-glycosylation site
FT  modified_site 145
FT                /label= putative N-glycosylation site
FT  modified_site 151
FT                /label= putative N-glycosylation site
FT  modified_site 270
FT                /label= putative N-glycosylation site
FT  region        212..230
FT                /label= transmembrane region
```

FT   peptide
FT   1..28
FT   /label- signal peptide
PN   EP-417563-A.
PD   20-MAR-1991.
PN   31-AUG-1990; 116707.
PF   12-SEP-1989; CH-003319.
PR   08-MAR-1990; CH-000746.
PR   20-APR-1990; CH-001347.
PA   (HOFF) HOFFMANN-LA ROCHE AG.
PI   Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;
PI   Schlaeger EJ;
DR   WPI; 91-081851/12.
DR   N-PSDB; Q10955.
PT   Insoluble tumour necrosis factor binding proteins - and DNA
PT   encoding them, useful in pharmaceutical prods. and for antibody
PT   prodn.
PS   Claim 1; Fig 1; 26pp; German.
PT   Partial amino acid sequences were determined for the 55 and 75kD
CC   TNF-BPs (see R11072-R11081) and oligonucleotide primers were
CC   synthesised based on these partial sequences. The primers were used
CC   to produce a cDNA fragment for use as a probe to screen a human
CC   placental cDNA bank constructed in lambda gt11. Positive clones were
CC   identified and sequenced. DNA constructs comprising the TNF-BP coding
CC   sequence may also contain a fragment encoding a human Ig domain.
CC   Recombinant constructs are used to transform cells to confer
CC   improved TNF-binding properties.
CC   See also Q10956.
SQ   Sequence 455 AA;

Query Match   59.8%; Score 1306; DB 2; Length 455;
Best Local Similarity 98.8%; Pred. No. 2.45e-129;
Matches 169; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy   41 dsvcpggkylhpqnnsicctkchgkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
            ||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||
Db   23 DSVCPQGRYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Qy 101 scskcrkemgqvelssctvdrdtvcgcrknqyrhywsenlfqcfncsiclngtvhlscqe 160
            |||||||||||||||||||||:||||:||||||||||||||| ||||:|||||||||||
Db   83 SCSKCRKEMGQVELSSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQE 142

Qy 161 kqntvctchagfflrenecvscsnckkslectklclpqienvkgtedsgtt 211
            |||||||||||||||||||||||||||||| ||||:|||||||||||
Db 143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQIENVRGTEDSGTT 193

RESULT 12
ID   R70103 standard; Protein; 900 AA.
AC   R70103;
DT   02-NOV-1995 (first entry)
DE   TNF-R-GBP 130 fusion protein.
KW   Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;
KW   red blood cell; cytokine receptor; glycophorin receptor; glycophorin binding peptide 130;
KW   GBP 130; GBPH; glycophorin binding peptide homologue; glycophorin A.
OS   Chimeric Homo sapiens.
OS   Chimeric Plasmodium falciparum.
PN   WO9506737-A.
PN   09-MAR-1995.
PR   01-SEP-1994; G01900.
PR   03-SEP-1993; GB-018350.
PR   23-AUG-1994; GB-017021.
PA   (PREN/) PRENDERGAST K F.
PI   Prendergast KF;
DR   WPI; 95-115452/15.
PT   New hybrid peptide(s) for binding cytokine(s) - comprising a
PT   malaria parasite peptide capable of binding a red blood cell and
PT   a receptor peptide.
PS   Example A; Page 46-47; 93pp; English.
PT   Hybrid peptides for binding cytokines, comprising a malaria parasite
CC   (Plasmodium falciparum) peptide (capable of binding to a red blood
CC   cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples
CC   of these hybrid peptides. R70103 is a fusion of tumour necrosis factor
CC   receptor (in accordance with H Loetscher et al Cell, Vol. 61, 351-359)
CC   and glycophorin binding protein (GBP) 130. The use of cytokine
CC   receptors not normally found on RBCs means that the cytokine can bind
CC   harmlessly to the RBC without deleterious effect. The use of cytokine
CC   hybrid peptides from excretion from the kidney, and due to steric
CC   hindrance prevents the cytokines binding to a receptor in another cell.
CC   GBP 130 or GBPH (GBP homologue) are the prefd. malaria parasite peptides
CC   used, others include EBA 175 (175 kDa erythrocyte binding antigen),
CC   PMSA (pre major merozoite surface antigen) and the Duffy binding
CC   receptor molecule (eg. exhibited by Plasmodium vivax). These peptides
CC   bind to pref. glycophorin A, B and C, sialo glycoproteins, found on
CC   the surface of RBCs. The hybrid peptides are thus used to lower
CC   the levels of free cytokines in the circulation to reduce pathological
CC   damage.
SQ   Sequence 900 AA;

RESULT 13
ID   R70108 standard; Protein; 309 AA.
AC   R70108;
DT   10-NOV-1995 (first entry)
DE   TNF-R-GBPH fusion protein.
KW   Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;
KW   red blood cell; cytokine receptor; glycophorin receptor; glycophorin binding peptide 130;
KW   GBP 130; GBPH; glycophorin binding peptide homologue; glycophorin A;
KW   tumour necrosis factor receptor; TNF-R.
OS   Chimeric Homo sapiens.
OS   Chimeric Plasmodium falciparum.
FH   Key   Location/Qualifiers
FT   misc_difference 230..269
FT   /label= repeat_region
FT   /note= "can be repeated n times, where n is a real
FT   number"
PN   WO9506737-A.
PN   09-MAR-1995.
PR   01-SEP-1994; G01900.
PR   03-SEP-1993; GB-018350.
PR   23-AUG-1994; GB-017021.
PA   (PREN/) PRENDERGAST K F.
PI   Prendergast KF;
DR   WPI; 95-115452/15.
PT   New hybrid peptide(s) for binding cytokine(s) - comprising a
PT   malaria parasite peptide capable of binding a red blood cell and
PT   a receptor peptide.
PS   Example A; Page 54-55; 93pp; English.
PT   Hybrid peptides for binding cytokines, comprising a malaria parasite
CC   (Plasmodium falciparum) peptide (capable of binding to a red blood
CC   cell (RBC)) and a receptor peptide are claimed. R70108 is a fusion
CC   of these hybrid peptides. R70108 is a fusion of tumour necrosis factor
CC   receptor (in accordance with H Loetscher et al Cell, Vol. 61, 351-359)
CC   and glycophorin binding protein (GBP) homologue (GBPH). The
CC   use of cytokine receptors not normally found on RBCs means that the
CC   cytokine can bind harmlessly to the RBC without deleterious effect.
CC   The RBC protects the hybrid peptides from excretion from the kidney, and
CC   due to steric hindrance prevents the cytokines binding to a receptor in
CC   another cell. GBP 130 or GBPH are the prefd. malaria parasite peptides
CC   used, others include EBA 175 (175 kDa erythrocyte binding antigen), PMSA
CC   (pre major merozoite surface antigen) and the Duffy binding receptor

Query Match   59.8%; Score 1305; DB 13; Length 900;
Best Local Similarity 98.3%; Pred. No. 3.16e-129;
Matches 169; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy   20 dsvcpggkylhpqnnsicctkchgkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 79
            ||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||
Db   23 DSVCPQGRYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Qy   80 scskcrkemgqvelssctvdrdtvcgcrknqyrhywsenlfqcfncsiclngtvhlscqe 139
            |||||||||||||||||||||:||||:||||||||||||||| ||||:|||||||||||
Db   83 SCSKCRKEMGQVELSSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQE 142

Qy 140 kqntvctchagfflrenecvscsnckkslectklclpqienvkgtedsgtna 191
            ||||||||||||||||||||||||||||||||||:|||||||||||||
Db 143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQIENVRGTEDSGTTA 194

CC molecule (eg. exhibited by plasmodium vivax). These peptides bind to
CC pref. glycophorin A, B and C, sialo glycoproteins, found on the surface
CC of RBCs. The hybrid peptides are thus used to lower the levels of free
CC cytokines in the circulation to reduce pathological damage.
SQ Sequence 309 AA;

Query Match Best Local Similarity 59.7%; Score 1303; DB 13; Length 309;
Matches 168; Conservative 2; Pred. No. 5.28e-129; Mismatches 1; Indels 0; Gaps 0;

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Qy   20 dsvcpqggkylhpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl  79
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   20 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL   79

Qy   80 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfgcfncslclngtvhlscge  139
         |||||||||||||||||||||||||||||||||||||||||| ||| |||||||||| |
Db   83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQE  142

Qy  140 kqntvctchagfflrenecvscsnckkslectklclpqienvkgtedsgts  190
         ||||||||||||||||||||||||||||||||||||| |||||||||||||:
Db  143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQIENVKGTEDSGTT   193
```

RESULT 14
ID R07451 standard; protein; 455 AA.
AC R07451;
DT 29-JAN-1991 (first entry)
DE Human Tumour Necrosis Factor-Receptor from lambdaTNF-R2 cDNA insert.
KW Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
KW Infectious disease; parasitic disease; cachexia;
KW autoimmune disease; shock; lambdaTNF-R2; ratTNF-R8.
OS Homo sapiens.
PN EP-393438-A.
PD 24-OCT-1990.
PF 06-APR-1990; 106624.
PR 21-APR-1989; DE-913101.
PR 21-JUN-1989; DE-920282.
PA (BOEH) BOEHRINGER INGELHEIM INT.
PI Hauptmann R, Himmler A, Mauer-Fogy I, Stratowa C;
DR WPI; 90-321987/43.
DR N-PSDB; Q06285.
PT DNA encoding TNF binding protein and TNF- receptor - used in
PT tumour treatment and to understand mechanismsm to TNF action
PS Disclosure; Fig 9(1-2); 51pp; German;
CC ratTNF-R8 (Q06284) was used to screen the HS913T cDNA library.
CC LambdaTNF-R2 encodes the complete human TNF-R2 and was used to
CC construct a plasmid (pADTNF-R) expressing the product the same way
CC as pADTNF-BP (see Q06282). The expressed proteins are useful
CC prophylactically and therapeutically to control disorders which
CC involve the damaging effects of TNF-alpha or -beta (e.g. Infectious or
CC parasitic diseases, shock, cachexia, autoimmune diseases, adult
CC respiratory distress syndrome etc., or side effects of treatment with
CC TNG-alpha). They can also be used as diagnostic reagents for
CC assaying TNF and in study of TNF-receptor interactions.
CC See also Q06282-Q06285.
SQ Sequence 455 AA;

Query Match Best Local Similarity 59.7%; Score 1303; DB 2; Length 455;
Matches 168; Conservative 2; Pred. No. 5.28e-129; Mismatches 1; Indels 0; Gaps 0;

```
Qy   20 dsvcpqggkylhpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl  79
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   41 dsvcpqggkylhpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl  100

Qy   80 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfgcfncslclngtvhlscge  139
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  101 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfgcfncslclngtvhlscge  160

Qy  140 kqntvctchagfflrenecvscsnckkslectklclpqienvkgtedsgts  190
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  161 kqntvctchagfflrenecvscsnckkslectklclpqienvkgtedsgtt  211
```

RESULT 15
ID R70104 standard; protein; 547 AA.
AC R70104;
DT 02-NOV-1995 (first entry)
DE TNF-R-GBPH fusion protein.
KW Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;
KW red blood cell; cytokine receptor; glycophorin binding peptide 130;
KW GBP 130; GBPH; glycophorin binding peptide homologue; TNF-R.
KW tumour necrosis factor receptor; TNF-R.
OS Chimeric Homo sapiens.
OS Chimeric Plasmodium falciparum.
PN WO9506737-A.
PD 09-MAR-1995.
PF 01-SEP-1994; G01900.
PR 03-SEP-1993; GB-018350.
PR 23-AUG-1994; GB-0170021.
PA (PREN/) PRENDERGAST K F.
PI Prendergast KF;
DR WPI; 95-115452/15.
PT New hybrid peptide(s) for binding cytokine(s) - comprising a
PT malaria parasite peptide capable of binding a red blood cell and
PT a receptor peptide.
PS Example A; Page 47-48; 93pp; English.
CC Hybrid peptides for binding cytokines, comprising a malaria parasite
CC (Plasmodium falciparum) peptide (capable of binding to a red blood
CC cell (RBC)) and a receptor peptide are claimed. R70104-25 are examples
CC of these hybrid peptides. R70104 is a fusion of tumour necrosis factor
CC receptor (in accordance with H Loetscher et al Cell, Vol. 61, 351-359)
CC and glycophorin binding protein (GBP) homologue (GBPH). The use of
CC cytokine receptors not normally found on RBCs means that the
CC cytokine can bind harmlessly to the RBC without deleterious effect.
CC The RBC protects the hybrid peptides from excretion from the kidney, and
CC due to steric hindrance prevents the cytokines binding to a receptor in
CC another cell. GBP 130 or GBPH are the pref. malaria parasite peptides
CC used, others include EBA 175 (175 kDa erythrocyte binding antigen), PMMSA
CC (pre major merozoite surface antigen) and the Duffy binding receptor
CC molecule (eg. exhibited by Plasmodium vivax). These peptides bind to
CC pref. glycophorin A, B and C, sialo glycoproteins, found on the surface
CC of RBCs. The hybrid peptides are thus used to lower the levels of free
CC cytokines in the circulation to reduce pathological damage.
SQ Sequence 547 AA;

Query Match Best Local Similarity 59.7%; Score 1303; DB 13; Length 547;
Matches 168; Conservative 2; Pred. No. 5.28e-129; Mismatches 1; Indels 0; Gaps 0;

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Qy   20 dsvcpqggkylhpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl  79
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   41 dsvcpqggkylhpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl  100

Qy   80 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfgcfncslclngtvhlscge  139
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  101 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfgcfncslclngtvhlscge  160

Qy  140 kqntvctchagfflrenecvscsnckkslectklclpqienvkgtedsgts  190
         |||||||||||||||||||||||||||||||||||||||||||||||||||:
Db  143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQIENVKGTEDSGTT   193
```

```
***************************************************************
   M P S R C H                                          (TM)
***************************************************************
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   Copyright (c) 1993-1997 University of Edinburgh, U.K.
   Distribution rights by Oxford Molecular Ltd
***************************************************************
```

MPsrch_pp   protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 6 09:00:43 1998;   MasPar time 12.89 Seconds
                                              807.727 Million cell updates/sec

Tabular output not generated.

```
Title:
Description:     >US-08-804-166-6
                 (1-285) from US08804166.pep
Perfect Score:   2183
Sequence:        1 SRTSLLAFGLLCLPWLQEG..........GFKVENHTACHCSTCYYHKS 285
```

Scoring table: PAM 150
                 Gap 11

Searched: 120446 seqs, 36531193 residues

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database: pir56
                 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 40.957; Variance 71.278; scale 0.575

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match Length	DB	ID	Description	Pred. No.
1	1306	59.8	455	1	GQHUT1	tumor necrosis factor	1.60e-278
2	1241	56.8	160	5	IEXTA	tumor necrosis factor	8.41e-263
3	1222	56.0	158	5	IEXTB	tumor necrosis factor	3.27e-258
4	1119	51.3	142	5	INCFB	tumor necrosis factor	2.28e-233
5	1103	50.5	139	5	ITNRR	tumor necrosis factor	1.62e-229
6	1096	50.2	140	5	INCFA	tumor necrosis factor	7.85e-228
7	1012	46.4	461	2	JC4302	tumor necrosis factor	1.20e-207
8	944	43.2	454	1	I57826	tumor necrosis factor	2.33e-191
9	944	43.2	454	1	GQMST1	tumor necrosis factor	2.33e-191
10	928	42.5	461	1	GQRTT1	tumor necrosis factor	1.56e-187
11	672	30.8	116	5	TTHUAP	glycoprotein hormones	8.42e-127
12	650	29.8	86	5	1HRPA	glycoprotein hormones	1.23e-121
13	648	29.7	85	5	1XULA	chorionic gonadotropi	1.63e-121
14	648	29.7	85	5	1HCNA	chorionic gonadotropi	1.63e-121
15	552	25.3	120	2	A39555	Human chorionic gonad	3.63e-121
16	547	25.1	96	5	A05096	glycoprotein hormones	1.29e-97
17	549	25.1	120	1	TTBOA	glycoprotein hormones	4.44e-98
18	549	25.1	120	1	UTSHA	glycoprotein hormones	4.44e-98
19	544	24.9	120	1	TTRTA	glycoprotein hormones	6.39e-97
20	542	24.8	120	1	PN0138	glycoprotein hormones	1.86e-96
21	542	24.8	120	1	UTPGA	glycoprotein hormones	1.86e-96
22	542	24.8	120	1	TTMSA	glycoprotein hormones	1.86e-96
23	540	24.7	120	2	G00021	chorionic gonadotropi	5.39e-96
24	537	24.6	120	2	A45585	glycoprotein hormones	2.67e-95
25	537	24.6	120	2	I51241	pituitary glycoprotei	2.67e-95
26	507	23.2	120	2	A40554	glycoprotein hormones	2.25e-88
27	505	23.1	120	2	S53062	glycoprotein hormones	5.50e-88
28	503	23.0	96	1	TTHOA	gonadotropin alpha ch	1.88e-87
29	500	22.9	118	2	S16762	gonadotropin alpha ch	9.19e-87
30	500	22.9	118	2	UTCAA	gonadotropin alpha-su	9.19e-87
31	500	22.9	118	2	A60626	gonadotropin hormones	9.19e-87
32	478	21.9	93	2	S07091	glycoprotein hormones	1.03e-81
33	479	21.9	97	2	S20287	lutropin alpha chain	6.10e-82
34	474	21.7	117	2	A37198	glycoprotein hormones	1.02e-81
35	452	20.7	119	2	I51229	gonadotropin alpha 1	9.07e-76
36	450	20.6	114	2	B60627	glycoprotein hormones	2.59e-75
37	448	20.5	108	2	I51230	glycoprotein hormones	7.40e-75
38	448	20.5	114	2	I51230	gonadotropin alpha 2	7.40e-75
39	434	19.9	117	2	I50992	gonadotropin alpha-su	1.13e-71
40	435	19.9	117	2	I54182	tumor necrosis factor	1.53e-70
41	228	10.4	38	2	A60583	tumor necrosis factor	1.59e-26
42	228	10.3	325	2	B43692	T2 protein - rabbit f	6.39e-27
43	225	10.1	325	1	GQVZML	T2 protein - myxoma v	4.62e-26
44	221	10.1	349	2	D36858	gene G4R protein - va	1.20e-23
45	212	9.7	427	1	GQHUN	nerve growth factor r	3.08e-23

RESULT ENTRY   1

ALIGNMENTS

1   GQHUT1   #type complete

tumor necrosis factor receptor type 1 precursor - human ALTERNATE_NAM

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TITLE                tumor necrosis factor alpha inhibitor; tumor necrosis factor
CONTAINS             binding protein 1 (TNF blocking factor)
ORGANISM             #formal_name Homo sapiens #common_name man
DATE                 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
                     24-Oct-1997
ACCESSIONS           A38208; A34899; A34900; A36555; C36555; A38281; S12057;
                     JT0758; A60231; A38258; A60594; A35010; JC2404
REFERENCE            A38208
  #authors           Fuchs, P.; Strehl, S.; Dworzak, M.; Himmler, A.; Ambros, P.F.
  #journal           Genomics (1992) 13:219-224
  #title             Structure of the human TNF receptor 1 (p60) gene (TNFR1) and
                     localization to chromosome 12p13.
  ##accession        A38208
  ##molecule_type DNA
  ##residues         1-455 ##label FUC
  ##cross-references GB:M75864; GB:M75865; GB:M75866; NID:g339748;
                     PID:g339750
REFERENCE            A34899
  #authors           Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus,
                     M.; Tabuchi, H.; Lesslauer, W.
  #journal           Cell (1990) 61:351-359
  #title             Molecular cloning and expression of the human 55 kd tumor
                     necrosis factor receptor.
  #accession         A34899
  ##molecule_type mRNA
  ##residues         1-455 ##label LOE
  ##cross-references GB:M58286; GB:M33480; NID:g339753; PID:g339754
  ##experimental_source placenta
  ##note             part of this sequence, including the amino end of the
                     mature protein, confirmed by protein sequencing
REFERENCE            A34900
  #authors           Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.;
                     Wong, G.H.W.; Gatanaga, T.; Granger, G.A.; Lentz, R.; Raab,
                     H.; Kohr, W.J.; Goeddel, D.V.
  #journal           Cell (1990) 61:361-370
  #title             Molecular cloning and expression of a receptor for human
                     tumor necrosis factor.
  #accession         A34900
  ##molecule_type mRNA
  ##residues         1-455 ##label SCH
  ##cross-references GB:M33294; NID:g339744; PID:g339745
```

REFERENCE A36555
#authors Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.;
Pfizenmaier, K.; Lantz, M.; Olsson, I.; Hauptmann, R.;
Stratowa, C.; Adolf, G.
#journal DNA Cell Biol. (1990) 9:705-715
#title Molecular cloning and expression of human and rat tumor
necrosis factor receptor chain (p60) and its soluble
derivative, tumor necrosis factor-binding protein.
#cross-references MUID:91090841
#molecule_type mRNA
#accession A36555
##molecule_type mRNA
##residues 1-455 ##label HIM
##cross-references GB:M63121; NID:g339755; PID:g339756
##residues 30-38;41-53,'X',55-79,'NK';'XX','82-94,'NK';'XX','100-104;
107-128;162-167,'X',169-201 ##label HI2
#note the purified protein, called tumor necrosis factor
binding protein, is a soluble derivative of the
receptor

REFERENCE A38281
#authors Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann,
M.
#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:7380-7384
#title Cloning of human tumor necrosis factor (TNF) receptor cDNA
and expression of recombinant soluble TNF-binding protein.
#cross-references MUID:91017509
#molecule_type mRNA
#accession A38281
##molecule_type mRNA
##residues 1-455 ##label GRA
##cross-references GB:M37764
#note the authors translated the codon TGG for residue 371 as
Thr, AAG for residue 372 as Leu, and GAC for residue
427 as Asn

REFERENCE S12057
#authors Nophar, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang,
R.; Aderka, D.; Holtmann, H.; Wallach, D.
#journal EMBO J. (1990) 9:3269-3278
#title Soluble forms of tumor necrosis factor receptors (TNF-Rs).
The cDNA for the type I TNF-R, cloned using amino acid
sequence data of its soluble form, encodes both the cell
surface and a soluble form of the receptor.
#cross-references MUID:91006021
#molecule_type mRNA
#accession S12057
##molecule_type mRNA
##residues 1-455 ##label NOP
##cross-references EMBL:X55313; NID:g37223; PID:g37224
#note parts of soluble TNF binding protein 1, including its
amino and carboxyl ends, were confirmed by protein
sequencing

REFERENCE JT0758
#authors Kemper, O.; Wallach, D.
#journal Gene (1993) 134:209-216
#title Cloning and partial characterization of the promoter for the
human p55 tumor necrosis factor (TNF) receptor.
#accession JT0758
##molecule_type DNA
##residues 1-13 ##label KEM

REFERENCE A60231
#authors Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer,
J.M.
#journal Eur. J. Immunol. (1990) 20:1167-1174
#title Tumor necrosis factor inhibitor: purification, NH-2-terminal
amino acid sequence and evidence for anti-inflammatory and
immunomodulatory activities.
#accession A60231
##molecule_type protein
##residues 41-43,'X',45-53,'X',55-57 ##label SEC

REFERENCE A38258
#authors Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci III,
J.A.; Jeffes, E.W.B.; Lentz, R.; Tomich, J.; Yamamoto,
R.S.; Granger, G.A.

REFERENCE A35555
#authors Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thysell, H.;
Grubb, A.; Adolf, G.
#journal Eur. J. Haematol. (1989) 42:270-275
#title Isolation and characterization of a tumor necrosis factor
binding protein from urine.
#accession A60594
##molecule_type protein
##residues 41-60 ##label GAT
##experimental_source renal failure patient urine

REFERENCE A35010
#authors Engelmann, H.; Novick, D.; Wallach, D.
#journal J. Biol. Chem. (1990) 265:1531-1536
#title Two tumor necrosis factor-binding proteins purified from
human urine. Evidence for immunological cross-reactivity
with cell surface tumor necrosis factor receptors.
#cross-references MUID:90110215
#accession A35010
##molecule_type protein
##residues 41-45 ##label ENG

REFERENCE JC2404
#authors Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.
#journal Biosci. Biotechnol. Biochem. (1994) 58:2266-2268
#title Amino acid sequence of natural tumor necrosis factor alpha
inhibitor purified from human urine.
#accession JC2404
##molecule_type protein
##residues 41-53,'X',55-144,'X',146-150,'X',152-186,'X',188-201

COMMENT This protein is one of two known receptors for both TNF-alpha
(cachectin) and TNF-beta (lymphotoxin).

GENETICS
#gene GDB:TNFR1
##cross-references GDB:125913; OMIM:191190
#map_position 12p13.2-12p13.2
#introns 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 255/3; 353/1
CLASSIFICATION #superfamily tumor necrosis factor receptor type 1; NGF
receptor repeat homology

KEYWORDS duplication; glycoprotein; receptor; transmembrane protein

FEATURE
1-21 #domain signal sequence #status predicted #label SIG\
22-455 #product tumor necrosis factor receptor type 1 #status
predicted #label MAT\
30-211 #product TNF binding protein 1 (tumor necrosis factor
alpha inhibitor) #status experimental #label TBP1\
41-201 #domain extracellular #status predicted #label EXT\
44-82 #domain NGF receptor repeat homology #label NG1\
84-126 #domain NGF receptor repeat homology #label NG2\
127-167 #domain NGF receptor repeat homology #label NG3\
168-196 #domain NGF receptor repeat homology #label NG4\
212-234 #domain transmembrane #status predicted #label MEM\
235-455 #domain intracellular #status predicted #label INT\
54,145,151 #binding_site carbohydrate (Asn) (covalent) #status
predicted

SUMMARY
#length 455 #molecular-weight 50494 #checksum 153

Db
41 DSVCPQGKYIHPQNSICCTKCHKGTYLYNDCPGPGQDTCRECESGSFTASENHLRHCL 100

Query Match 59.8%; Score 1306; DB 1; Length 455;
Best Local Similarity 98.8%; Pred. No. 1.60e-278;
Matches 169; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy    23  DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL
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Qy   101  SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE  82
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    83  SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE  160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   161  KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT  211
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    83  SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE  142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   143  KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQIENVKGTEDSGTT  193
```

RESULT 2

ENTRY	1EXTA	#type complete

TITLE   tumor necrosis factor receptor extracellular domain, chain A
PDB_TITLE   extracellular domain of the 55kda tumor necrosis factor
             receptor. crystallized at ph3.7 in p 21 21 21.
ORGANISM   Homo sapiens man
#note   #formal_name Homo sapiens #common_name man
             expressed in Escherichia coli, the construct contains
             residues 12 to 172 of the mature sequence of the entire
             receptor. residue 11 is mutated to met as a result of the
             expression system
REFERENCE   A65560
#authors   Naismith, J.H.; Sprang, S.R.
#submission submitted to the Brookhaven Protein Data Bank, July 1996
#cross-references PDB:1EXT
REFERENCE   TN026248
#authors   Naismith, J.H.; Devine, T.Q.; Brandhuber, B.J.; Sprang, S.R.
#journal   J. Biol. Chem. (1995) 270:13303
#title   Crystallographic evidence for dimerization of unliganded
             tumor necrosis factor receptor.
REFERENCE   TN026249
#authors   Rodseth, L.E.; Brandhuber, B.; Devine, T.Q.; Eck, M.J.; Hale,
             K.; Naismith, J.H.; Sprang, S.R.
#journal   J. Mol. Biol. (1994) 239:332
#title   Two crystal forms of the extracellular domain of type 1 tumor
             necrosis factor receptor.
REFERENCE   A40737
#authors   Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
             H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
#journal   Cell (1993) 73:431-445
#title   Crystal structure of the soluble human 55 kd TNF
             receptor-human TNFbeta complex: implications for TNF
             receptor activation.
COMMENT   Resolution: 1.85 angstroms
COMMENT   Determination: X-ray diffraction
COMMENT   R-value: no refinement
KEYWORDS   binding protein; cytokine; signalling protein
FEATURE
       66-68   #region helix (right hand 3-10)\
      141-143   #region helix (right hand 3-10)\
      151-154   #region helix (right hand alpha)\
       7-9,17-19   #region beta sheet\
     131-134,137-140 #region beta sheet\
      25-29,39-42   #region beta sheet\
      71-74,83-85   #region beta sheet\
      90-96,99-104   #region beta sheet\
      61-76   #region beta sheet\
       3-17   #region beta sheet\
      18-31   #region beta sheet\
      21-40   #region beta sheet\
      43-58   #region beta sheet\
     111-115,124-127 #region beta sheet\
      86-102   #disulfide_bonds\
      64-84   #disulfide_bonds\
     105-117   #disulfide_bonds\
     108-125   #disulfide_bonds\
     127-138   #disulfide_bonds\
     141-154   #disulfide_bonds\
     144-150   #disulfide_bonds\
SUMMARY   #length 160   #molecular-weight 18065   #checksum 2297
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Query Match   56.8%;   Score 1241;  DB 5;  Length 160;
Best Local Similarity 98.8%;   Pred. No. 8.4le-263;
Matches  158;  Conservative  1;  Mismatches  1;  Indels  0;  Gaps  0;

Qy     1  SVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLS  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  SVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLS  60
Qy    24  SVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLS  83
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  CSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEK  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    61  CSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEK  120
          ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Qy    84  CSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQEK  143
          ||||||||||||||||||||||||||||||||||||||||||||::|||||||||||||||
Db   121  QNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIEN  160
          |||||||||||||||||||||||||||||||||||||||||
Db    84  CSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQEK  143
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   144  QNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQIEN  183
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RESULT 3

ENTRY	1EXTB	#type complete

TITLE   tumor necrosis factor receptor extracellular domain, chain B
PDB_TITLE   extracellular domain of the 55kda tumor necrosis factor
             receptor. crystallized at ph3.7 in p 21 21 21.
ORGANISM   Homo sapiens man
#note   #formal_name Homo sapiens #common_name man
             expressed in Escherichia coli, the construct contains
             residues 12 to 172 of the mature sequence of the entire
             receptor. residue 11 is mutated to met as a result of the
             expression system
REFERENCE   A65560
#authors   Naismith, J.H.; Sprang, S.R.
#submission submitted to the Brookhaven Protein Data Bank, July 1996
#cross-references PDB:1EXT
REFERENCE   TN026251
#authors   Naismith, J.H.; Devine, T.Q.; Brandhuber, B.J.; Sprang, S.R.
#journal   J. Biol. Chem. (1995) 270:13303
#title   Crystallographic evidence for dimerization of unliganded
             tumor necrosis factor receptor.
REFERENCE   TN026252
#authors   Rodseth, L.E.; Brandhuber, B.; Devine, T.Q.; Eck, M.J.; Hale,
             K.; Naismith, J.H.; Sprang, S.R.
#journal   J. Mol. Biol. (1994) 239:332
#title   Two crystal forms of the extracellular domain of type 1 tumor
             necrosis factor receptor.
REFERENCE   A40737
#authors   Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
             H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
#journal   Cell (1993) 73:431-445
#title   Crystal structure of the soluble human 55 kd TNF
             receptor-human TNFbeta complex: implications for TNF
             receptor activation.
COMMENT   Resolution: 1.85 angstroms
COMMENT   Determination: X-ray diffraction
COMMENT   R-value: no refinement
KEYWORDS   binding protein; cytokine; signalling protein
FEATURE
       68-70   #region helix (right hand 3-10)\
      143-145   #region helix (right hand 3-10)\
       9-11,19-21   #region beta sheet\
     133-136,139-142 #region beta sheet\
      27-31,41-44   #region beta sheet\
      73-76,85-87   #region beta sheet\
      92-98,101-106 #region beta sheet\
     113-117,126-129 #region beta sheet\
       5-19   #region beta sheet\
      20-33   #region beta sheet\
      23-42   #region beta sheet\
      45-60   #region beta sheet\
      63-78   #region beta sheet\
      66-86   #disulfide_bonds\
      88-104   #disulfide_bonds\
     107-119   #disulfide_bonds\
     110-127   #disulfide_bonds\
     129-140   #disulfide_bonds\
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        143-156          #disulfide_bonds\
        146-152          #disulfide_bonds
SUMMARY          #length 158    #molecular-weight 17827    #checksum 5022
        Query Match         56.0%;    Score 1222;  DB 5;   Length 158;
        Best Local Similarity  98.7%;   Pred. No. 3.27e-258;
        Matches   155;  Conservative    1;  Mismatches   1;  Indels   0;  Gaps   0;

Db    2   DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL  61
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   23   DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL  82

Db   62   SCSKCRKEMGQVEISSCTVRDRTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE  121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   83   SCSKCRKEMGQVEISSCTVRDRTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE  142

Db  122   KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLP  158
          |||||||||||||||||||||||||||||||:|| ||
Qy  143   KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLP  179

RESULT          4

ENTRY          1NCFB          #type complete
TITLE          tumor necrosis factor receptor 55 extracellular domain
                 contains residues 12 172 of the mature receptor sequence,
                 chain B - hu
ALTERNATE_NAMES  stnfri; type 1 receptor
ORGANISM         #formal_name Homo sapiens #common_name man
#note          expressed in Escherichia coli, residue 11 is mutated to met
                 as a result of the expression system
REFERENCE        A66195
#authors         Naismith, J.H.; Sprang, S.R.
#submission      submitted to the Brookhaven Protein Data Bank, October 1994
#cross-references PDB:1NCF
REFERENCE        TN029041
#authors         Rodseth, L.E.; Brandhuber, B.; Devine, T.Q.; Eck, M.J.; Hale,
                 K.; Naismith, J.H.; Sprang, S.R.
#journal         J. Mol. Biol. (1994) 239:332
#title           Two crystal forms of the extracellular domain of type 1 tumor
                 necrosis factor receptor.
REFERENCE        A40737
#authors         Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
                 H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
#journal         Cell (1993) 73:431-445
#title           Crystal structure of the soluble human 55 kd TNF
                 receptor-human TNFbeta complex: Implications for TNF
                 receptor activation.
COMMENT          Resolution: 2.25 angstroms
COMMENT          Determination: X-ray diffraction
COMMENT          R-value: no refinement
KEYWORDS         binding protein; cytokine; signalling protein
FEATURE
        2-16           #disulfide_bonds\
        17-30          #disulfide_bonds/
        20-39          #disulfide_bonds\
        42-57          #disulfide_bonds/
        60-75          #disulfide_bonds\
        63-83          #disulfide_bonds/
        85-101         #disulfide_bonds\
        104-116        #disulfide_bonds/
        107-124        #disulfide_bonds\
        126-137        #disulfide_bonds/
SUMMARY          #length 142    #molecular-weight 16046    #checksum 1225
        Query Match         51.3%;    Score 1119;  DB 5;   Length 142;
        Best Local Similarity  99.3%;   Pred. No. 2.28e-233;
        Matches   141;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db    1   VCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   25   VCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC  84
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Db   61   SKCRKEMGQVEISSCTVRDRTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQERQ  120
          ||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Qy   85   SKCRKEMGQVEISSCTVRDRTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQERQ  144

Db  121   NTVCTCHAGFFLRENECVSCSN  142
          ||||||||||||||||||||||
Qy  145   NTVCTCHAGFFLRENECVSCSN  166

RESULT          5

ENTRY          1TNRR          #type complete
TITLE          tumor necrosis factor receptor type 1 (P55 extracellular
                 receptor-human TNFbeta complex: Implications for TNF
                 receptor activation.
ORGANISM         #formal_name Homo sapiens #common_name man
#note          recombinant form expressed in Baculovirus SF9
REFERENCE        A52442
#authors         Banner, D.W.
#submission      submitted to the Brookhaven Protein Data Bank, May 1994
#cross-references PDB:1TNR
REFERENCE        A40737
#authors         Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
                 H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
#journal         Cell (1993) 73:431-445
#title           Crystal structure of the soluble human 55 kd TNF
                 receptor-human TNFbeta complex: Implications for TNF
                 receptor activation.
REFERENCE        TN034093
#authors         D'Arcy, A.; Banner, D.W.; Janes, W.; Winkler, F.K.;
                 Loetscher, H.; Schoenfeld, H.J.; Zulauf, M.; Gentz, R.;
                 Lesslauer, W.
#journal         J. Mol. Biol. (1993) 229:555
#title           Crystallization and preliminary analysis of tnf-beta and a
                 tnf-beta-55 kd tnf receptor complex.
COMMENT          Resolution: 2.85 angstroms
COMMENT          Determination: X-ray diffraction
KEYWORDS         Complex(lymphokineRECEPTOR)
FEATURE
        1-15           #disulfide_bonds\
        16-29          #disulfide_bonds/
        19-38          #disulfide_bonds\
        41-56          #disulfide_bonds/
        59-74          #disulfide_bonds\
        62-82          #disulfide_bonds/
        84-100         #disulfide_bonds\
        103-115        #disulfide_bonds/
        106-123        #disulfide_bonds\
        125-136        #disulfide_bonds/
SUMMARY          #length 139    #molecular-weight 15746    #checksum 5235
        Query Match         50.5%;    Score 1103;  DB 5;   Length 139;
        Best Local Similarity  99.3%;   Pred. No. 1.62e-229;
        Matches   138;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db    1   CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCS  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   26   CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCS  85

Db   61   KCRKEMGQVEISSCTVRDRTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQN  120
          |||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||
Qy   86   KCRKEMGQVEISSCTVRDRTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQEKQN  145

Db  121   TVCTCHAGFFLRENECVSC  139
          |||||||||||||||||||
Qy  146   TVCTCHAGFFLRENECVSC  164

RESULT          6

ENTRY          1NCFA          #type complete
TITLE          tumor necrosis factor receptor 55 kd extracellular domain
                 contains residues 12 172 of the mature receptor sequence,
                 chain A - hu
ALTERNATE_NAMES  stnfri; type 1 receptor
```

ORGANISM #formal_name Homo sapiens #common_name man
  #note expressed in Escherichia coli, residue 11 is mutated to met
    as a result of the expression system
REFERENCE
  #authors Naismith, J.H.; Sprang, S.R.
  #submission submitted to the Brookhaven Protein Data Bank, October 1994
  #cross-references PDB:1NCF
REFERENCE
  #authors Rodseth, L.E.; Brandhuber, B.; Devine, T.O.; Eck, M.J.; Hale,
    K.; Naismith, J.H.; Sprang, S.R.
  #cross-references TN029039
  #journal J. Mol. Biol. (1994) 239:332
  #title Two crystal forms of the extracellular domain of type 1 tumor
    necrosis factor receptor.
REFERENCE
  #authors Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
    H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
  #cross-references A40737
  #journal Cell (1993) 73:431-445
  #title Crystal structure of the soluble human 55 kd TNF
    receptor-human TNFbeta complex: implications for TNF
    receptor activation.
COMMENT Resolution: 2.25 angstroms
COMMENT Determination: X-ray diffraction
COMMENT R-value: no refinement
KEYWORDS binding protein; cytokine; signalling protein
FEATURE
  5-19   #disulfide_bonds\
  20-33   #disulfide_bonds\
  23-42   #disulfide_bonds\
  45-60   #disulfide_bonds\
  63-78   #disulfide_bonds\
  66-86   #disulfide_bonds\
  88-104 #disulfide_bonds\
  107-119 #disulfide_bonds\
  110-127 #disulfide_bonds\
  129-140 #disulfide_bonds
SUMMARY #length 140 #molecular-weight 15889 #checksum 6622

Query Match   Best Local Similarity 50.2%;
  Matches 138; Conservative 99.3%; Score 1096; DB 5; Length 140;
  Pred. No. 7.85e-228; Mismatches 0; Indels 0; Gaps 0;

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Db   2 DSVCPQGKYIHPQNNSICCTKCHKGTYLYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL  61
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL  82

Db  62 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 121
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQE 142

Db 122 KQNTVCTCHAGFFLRENEC 140
        |||||||||||||||||||
Qy 143 KQNTVCTCHAGFFLRENEC 161
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RESULT 7

ENTRY   JC4302   #type complete
TITLE tumor necrosis factor receptor p55 - pig
DATE 12-Dec-1997 #sequence_revision 08-Feb-1996 #text_change
    29-Nov-1995 #label SUT
ACCESSIONS JC4302; PC4093
REFERENCE
  #authors Suter, B.; Pauli, U.
  #journal Gene (1995) 163:263-266
  #title Cloning of the cDNA encoding the porcine p55 tumor necrosis
    factor receptor.
  #accession JC4302
    #molecule_type mRNA
    #residues 1-461 ##label SUT
    #cross-references GB:U19994; NID:g1141752; PID:g1141753
  #accession PC4093
    #molecule_type protein
    #residues 1-7 ##label SU2

GENETICS #experimental_source kidney cell line 15
  #gene tnfr
CLASSIFICATION #superfamily tumor necrosis factor receptor type 1; NGF
    receptor repeat homology
KEYWORDS glycoprotein; kidney; receptor; transmembrane protein; tumor
    necrosis factor receptor.
FEATURE
  1-29   #domain signal sequence #status predicted #label SIG\
  30-461 #product tumor necrosis factor receptor p55 #status
    predicted #label MAT\
  44-194 #domain extracellular cysteine rich #status predicted
    #label EXT\
  44-82   #domain NGF receptor repeat homology #label NG1\
  211-231 #domain transmembrane #status predicted #label TM\
  361-447 #domain signal transduction #status predicted #label
    SIT\
  54,145,151 #binding_site carbohydrate (Asn) (covalent) #status
    predicted
SUMMARY #length 461 #molecular-weight 50696 #checksum 8079

Query Match   Best Local Similarity 46.4%;
  Matches 123; Conservative 71.9%; Score 1012; DB 2; Length 461;
  Pred. No. 1.20e-207; Mismatches 25; Indels 22; Gaps 1;

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Db  41 ESLCPQGKYSHPQNRSICCTKCHKGTYLHNDCLGPGLDTDCRECDNGIFTASENHLTQCL 100
        : :|||||| |||| || ||||||||||||||| :||| :|||:|| ::|||||||| ||
Qy  23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL  82

Db 101 SCSKCRSEMSQVEISPCTVDRDTVCGCRKNQYRKYWSETLFQCLNCSLCPNGTVQLPCLE 160
        ||||||:||.|||| |||||||||||||||||:||||:||||:|| :|| |||| : | :
Qy  83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQE 142

Db 161 KQDTICNCHSGFFLRDKECVSCVNCKNA-DCKNLCPATSETRNDFQDIGTT 210
        |||:|| |||:|||:|:|||||:|:||.: ||| :| :|| : ::|:|||
Qy 143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQIENVKGTEDSGTT 193
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RESULT 8

ENTRY   I57826   #type complete
TITLE tumor necrosis factor receptor - mouse
DATE 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
    23-May-1997
ACCESSIONS I57826
REFERENCE
  #authors Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.;
    Steinmetz, M.
  #journal Mol. Immunol. (1993) 30:165-176
  #title Genomic organization and promoter function of the murine
    tumor necrosis factor receptor beta gene.
  #cross-references MUID:93156721
  #accession I57826
    #status preliminary; translated from GB/EMBL/DDBJ
    #molecule_type DNA
    #residues 1-454 ##label RES
    #cross-references GB:M76656; NID:g202100; PID:g202102
GENETICS
  #gene TNFR-2
  #introns 13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; 353/1
CLASSIFICATION #superfamily tumor necrosis factor receptor type 1; NGF
    receptor repeat homology
KEYWORDS cytokine receptor
SUMMARY #length 454 #molecular-weight 50030 #checksum 4267

Query Match   Best Local Similarity 43.2%;
  Matches 116; Conservative 67.4%; Score 944; DB 2; Length 454;
  Pred. No. 2.33e-191; Mismatches 27; Indels 28; Gaps 1;

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Db  41 DSLCPQGKYVHSKNNSICCTKCHGTYLVSDCPSPGRDTVCRECEKGTFTASQNYLRQCL 100
        ||:||||||:|.:|||||||||| |||| ||| |||:|||:| :|:|||:::||:|||
Qy  23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL  82

Db 101 SCKRCKEMSQVEISPCQADKDIVCGCKENQFQRYLSETHFQCVDCSPCFNGTVTIPCKE 160
Qy  83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQE 142
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Qy   83 SCSKCRKEMGQVEISSCTVDRDTVCGGCRKNQYRHVWSENLFQCFNCTLCLNGTVHLSCQE 142
         || ||||||| |||||| :| ||||| ||| | ||| ::|| ||| | | ||| :|| |
Db 161 ...   212
Qy 143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQ-IENVKGTEDSGTT 193

RESULT   9

ENTRY   GQMST1   #type complete
TITLE   tumor necrosis factor receptor type 1 precursor - mouseALTERNATE_NAMES
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE   30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
            05-Sep-1997
ACCESSIONS A38634; B40254; S16677; S19021; I54532
REFERENCE
   #authors Lewis, M.; Tartaglia, L. A.; Lee, A.; Bennett, G. L.; Rice,
            G. C.; Wong, G.H.W.; Chen, E.Y.; Goeddel, D.V.
  *journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:2830-2834
  *title   Cloning and expression of cDNAs for two distinct murine tumor
            necrosis factor receptors demonstrate one receptor is
            species specific.
   #cross-references MUID:91187885
   *accession A38634
   ##molecule_type mRNA
   *residues 1-454 #label G02
REFERENCE
   *accession A40254
   ##cross-references GB:M60468; NID:g199825; PID:g199826
   #authors Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan,
            C.I.; Copeland, N.G.; Jenkins, N.A.; Smith, C.A.
  *journal Mol. Cell. Biol. (1991) 11:3020-3026
  *title   Molecular cloning and expression of the type 1 and type 2
            murine receptors for tumor necrosis factor.
   #cross-references MUID:91246168
   *accession B40254
   ##molecule_type mRNA
   *residues 1-454 #label LEW
REFERENCE
   *accession S16677
   ##cross-references EMBL:X59238; NID:g53578; PID:g53579
   #authors A.M.; Gray, P.W.; Feldmann, M.; Foxwell, B.M.J.
  *journal Eur. J. Immunol. (1991) 21:1649-1656
  *title   Cloning, expression and cross-linking analysis of the murine
            p55 tumor necrosis factor receptor.
   #cross-references MUID:91285014
   *accession S16677
   ##molecule_type mRNA
   *residues 1-454 #label BAR
REFERENCE
   *accession S19021
   ##cross-references EMBL:X57796; NID:g54848; PID:g54849
   #authors Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.
  *journal Immunogenetics (1991) 34:338-340
  *title   Molecular cloning and expression of the mouse Tnf receptor
            type b.
   #cross-references MUID:92039815
   *accession S19021
   ##molecule_type mRNA
   *residues 1-454 #label ROT
REFERENCE
   *accession I54532
   #authors Bebo, B.F.
  *journal Immunogenetics (1994) 39:450-451
  *title   Nucleotide sequence of the TNF type I receptor from a mouse
            endothelioma cell line.
   #cross-references MUID:94245292
   *accession I54532
   ##status translated from GB/EMBL/DDBJ
   ##molecule_type mRNA
   *residues 1-454 #label RES
   ##cross-references GB:L26349; NID:g430732; PID:g430733
COMMENT   This protein is one of two distantly related receptors for both
            TNF-alpha (cachectin) and TNF-beta (lymphotoxin).

CLASSIFICATION *superfamily tumor necrosis factor receptor receptor type 1; NGF
                receptor repeat homology
                duplication: glycoprotein; receptor; transmembrane protein
KEYWORDS
FEATURE
   1-29   #domain signal sequence #status predicted #label SIG\
   30-454   #product tumor necrosis factor receptor type 1 #status
            #predicted #label MAT\
   30-212   #domain extracellular #status predicted #label EXT\
   44-82   #domain NGF receptor repeat homology #label NG1\
   84-126   #domain NGF receptor repeat homology #label NG2\
   127-167 #domain NGF receptor repeat homology #label NG3\
   168-204 #domain NGF receptor repeat homology #label NG4\
   213-235 #domain transmembrane #status predicted #label MEM\
   236-454 #domain intracellular #status predicted #label INT\
   54,151,202 #binding_site carbohydrate (Asn) (covalent) #status
            #predicted
SUMMARY   #length 454 #molecular-weight 50129 #checksum 4839

Query Match   43.2%; Score 944; DB 1; Length 454;
Best Local Similarity 67.4%; Pred. No. 2.33e-191;
Matches 116; Conservative 28; Mismatches 27; Indels 1; Gaps 1;

Db   41 DSLCPQGKYVHSKNNSICCTKCHKGTYLVSDCPSPGRDTVCRECEKGTFTASQNYLRQCL 100
         ||:||||||: ||||||:||||||||||| | ||:|| |:|||||:|| ||||:| ||:||
Qy   23 DSVCPQGKYIHPQNNSICCTKCHKGTIYLINDCPGPGQDTDCRECESGSFTASENLHRHCL 82

Db 101 SCKTCRKEMSQVEISPCQADKDTVCGCKENQFQRIISETHFQCVDCSPCENGTVTIPCKE 160
         |||:||||| |||||| | :||||| |:|||:: : ||| ||| ||: |||||| | | :
Qy   83 SCSKCRKEMGQVEISSCTVDRDTVCGGCRKNQYRHVWSENLFQCFNCTLCLNGTVHLSCQE 142

Db 161 ...   212
         |||||| ||||||||||||:||||:| |||| |||||||||||||:| ||
Qy 143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQ-IENVKGTEDSGTT 193

RESULT   10

ENTRY   GQRTT1   #type complete
TITLE   tumor necrosis factor receptor type 1 precursor - ratCONTAINS
ORGANISM   #formal_name Rattus norvegicus #common_name Norway rat
DATE   30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change
            05-Sep-1997
ACCESSIONS B36555
REFERENCE
   #authors Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.;
            Pfizenmaier, K.; Lantz, M.; Olsson, I.; Hauptmann, R.;
            Stratowa, C.; Adolf, G.R.
  *journal DNA Cell Biol. (1990) 9:705-715
  *title   Molecular cloning and expression of human and rat tumor
            necrosis factor receptor chain (p60) and its soluble
            derivative, tumor necrosis factor-binding protein.
   #cross-references MUID:91090841
   *accession B36555
   ##molecule_type mRNA
   *residues 1-461 #label HIM
   ##cross-references GB:M63122; NID:g207361; PID:g207362
COMMENT   This protein is one of two known receptors for both TNF-alpha
            (cachectin) and TNF-beta (lymphotoxin).
CLASSIFICATION *superfamily tumor necrosis factor receptor type 1; NGF
                receptor repeat homology
                duplication: glycoprotein; receptor; transmembrane protein
KEYWORDS
FEATURE
   1-29   #domain signal sequence #status predicted #label SIG\
   30-461   #product tumor necrosis factor receptor type 1 #status
            #predicted #label MAT\
   30-211   #domain extracellular #status predicted #label EXT\
   30-201   #product tumor necrosis factor binding protein #status
            #predicted #label TBP\
   44-82   #domain NGF receptor repeat homology #label NG1\
   84-126   #domain NGF receptor repeat homology #label NG2\
   127-167 #domain NGF receptor repeat homology #label NG3\
   168-204 #domain NGF receptor repeat homology #label NG4\
   212-234 #domain transmembrane #status predicted #label MEM\

```
                                    #domain intracellular #status predicted #label INT\
                                    #binding_site carbohydrate (Asn) (covalent) #status
                                    predicted
SUMMARY

         Query Match    42.5%;   Score 928;   DB 1;   Length 461;
         Best Local Similarity    66.1%;   Pred. No. 1.5e-187;
Matches 113;   Conservative 26;   Mismatches 32;   Indels 0;   Gaps 0;

                                    #length 461 #molecular-weight 50969 #checksum 1617

Qy   235-461
Db   54,151,201

Db    41  DNLCPQGKYAHPKNNSICCTKCHKGTYLVSDCPSPGQETVCEVCDKGTFTASQNHYRCL 100
          |:::|||||.:|||||||::.|||||||:|:||||| |:  ||  |::::|::|:::|:||:|
Qy    23  DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db   101  SCKTCREMFQVEISPCKADMDTVCGCKKNQFQRYLSETHFQCVDCSPCFNGTVTIPCKE 160
          |:|||||| :|||||||||:|||.|||||:| ||||:::|||:|||||:::::||:|.| |
Qy    83  SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCLCLNGTVHLSCQE 142

Db   161  KQNTVCNCHAGFFLSGNGECTPCSHCKKNQEMKLCLPPVANYTNPQDSGTA 211
          |||||| |||||:||||||:|:|.||  |||:| |||||||||:||||||||
Qy   143  KQNTVCTCHAGFFLRENECVSCSNCKSLECTKLSLPQIENVKGTEDSGTT 193
```

RESULT ENTRY 11

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ENTRY      TTHUAP    #type complete
TITLE      glycoprotein hormones alpha chain precursor - human ALTERNATE_NAMES cho
           alpha chain; follitropin alpha chain; interstitial
           cell-stimulating hormone alpha chain; luteinizing hormone
           alpha chain; lutropin alpha chain; thyroid-stimulating
           hormone alpha chain; thyrotropin alpha chain
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       13-Jul-1981 #sequence_revision 23-Oct-1981 #text_change
           05-Sep-1997
ACCESSIONS A93213; A92832; B92303; A90751; A90179; A91461; A92184;
           A94552; B92181; A92141; I58200; A01481
REFERENCE  A93213
  #authors Fiddes, J.C.; Goodman, H.M.
  #journal Nature (1979) 281:351-356
  #title   Isolation, cloning and sequence analysis of the cDNA for the
           alpha-subunit of human chorionic gonadotropin.
  #cross-references MUID:80011660
  #accession A93213
    #molecule_type mRNA
    #residues 1-116 ##label FID
REFERENCE  A92832
  #authors Fiddes, J.C.; Goodman, H.M.
  #journal J. Mol. Appl. Genet. (1981) 1:3-18
  #title   The gene encoding the common alpha subunit of the four human
           glycoprotein hormones.
  #cross-references MUID:82267643
  #accession A92832
    #molecule_type DNA
    #residues 1-98 ##label FI2
REFERENCE  A92303
  #authors Birken, S.; Fetherston, J.; Canfield, R.; Boime, I.
  #journal J. Biol. Chem. (1981) 256:1816-1823
  #title   The amino acid sequences of the prepeptides contained in the
           alpha and beta subunits of human choriogonadotropin.
  #cross-references MUID:81117268
  #accession B92303
    #molecule_type protein
    #residues 1-24 ##label BIR
  ##note restriction endonuclease evidence indicates that a
         single gene codes for the alpha chain common to the
         four dimeric hormones: thyrotropin, lutropin,
         follitropin, and choriogonadotropin
  ##note previously the mature alpha chain (residues 25-116) was
         isolated from each of the hormones and its sequence
         was determined, as documented below
REFERENCE
  #authors Sairam, M.R.; Li, C.H.
```

```
  #journal   Can. J. Biochem. (1977) 55:755-760
  #title     Human pituitary thyrotropin. The primary structure of the
             alpha and beta subunits.
    #cross-references MUID:77243687
    #accession A90751
      ##molecule_type protein
      ##residues 28-107,'/SC',110-116 ##label SAI
REFERENCE  A90179
  #authors Sairam, M.R.; Papkoff, H.; Li, C.H.
  #journal Biochem. Biophys. Res. Commun. (1972) 48:530-537
  #title   Human pituitary interstitial cell stimulating hormone:
           primary structure of the alpha subunit.
  #cross-references MUID:72242988
  #accession A90179
    ##molecule_type protein
    ##residues 28-107,'/SC',110-116 ##label SA2
REFERENCE  A91461
  #authors Keutmann, H.T.; Williams, R.M.; Bishop, W.H.; Ryan, R.J.
  #journal Fed. Proc. (1978) 37:1828
  #title   Structure of human luteinizing hormone.
  #accession A91461
    ##molecule_type protein
    ##residues 28-116 ##label KEU
REFERENCE  A92184
  #authors Rathnam, P.; Saxena, B.B.
  #journal J. Biol. Chem. (1975) 250:6735-6746
  #title   Primary amino acid sequence of follicle-stimulating hormone
           from human pituitary glands.
  #cross-references MUID:76005558
  #accession A92184
    ##molecule_type protein
    ##residues 25-28,'E',30-116 ##label RAT
REFERENCE  A94552
  #authors Shome, B.; Parlow, A.F.
  #submission submitted to the Atlas, April 1975
  #accession A94552
    ##molecule_type protein
    ##residues 28-116 ##label SHO
REFERENCE  A92181
  #authors Morgan, F.J.; Birken, S.; Canfield, R.E.
  #journal J. Biol. Chem. (1975) 250:5247-5258
  #title   The amino acid sequence of human chorionic gonadotropin. The
           alpha subunit and beta subunit.
  #cross-references MUID:75211304
  #accession B92181
    ##molecule_type protein
    ##residues 25-116 ##label MOR
  ##note heterogeneity is found at the amino end. Approximately
         10 and 30% of the chains lack residues 1-2 and 1-3,
         respectively
REFERENCE  A92141
  #authors Bellisario, R.; Carlsen, R.B.; Bahl, O.P.
  #journal J. Biol. Chem. (1973) 248:6796-6809
  #title   Human chorionic gonadotropin. Linear amino acid sequence of
           the alpha subunit.
  #cross-references MUID:74011266
  #accession A92141
    ##molecule_type protein
    ##residues 25-116 ##label BEL
REFERENCE  A92760
  #authors Shome, B.; Parlow, A.F.
  #journal J. Clin. Endocrinol. Metab. (1974) 39:199-202
  #title   Human follicle stimulating hormone (hFSH): first proposal for
           the amino acid sequence of the alpha-subunit (hFSHalpha)
           and first demonstration of its identity with the
           alpha-subunit of human luteinizing hormone (hLHalpha).
  #cross-references MUID:74262937
  #contents annotation
  #accession A90632
  #authors Fujiki, Y.; Rathnam, P.; Saxena, B.B.
  #journal Biochim. Biophys. Acta (1980) 624:428-435
  #title   Studies on the disulfide bonds in human pituitary
           follicle-stimulating hormone.
```

COMMENT
#cross-references MUID:81021713
#contents annotation: preliminary disulfide bonds
REFERENCE A44674
#authors Lapthorn, A.J.; Harris, D.C.; Littlejohn, A.; Lustbader, J.W.; Canfield, R.E.; Machin, K.J.; Morgan, F.J.; Isaacs, N.W.
#journal Nature (1994) 369:455-461
#title Crystal structure of human chorionic gonadotropin.
#contents annotation; X-ray crystallography; 3.0 angstroms; correction of disulfide bonds

REFERENCE I58200
#authors Miyoshi, I.; Kasai, N.; Hayashizaki, Y.
#journal Nippon Rinsho (1994) 52:940-947
#title [Structure and regulation of human thyroid-stimulating hormone (TSH) gene].
#status preliminary; translated from GB/EMBL/DDBJ
#molecule_type DNA
#residues 1-116 ##label RES
#cross-references GB:S70585; NID:g546844; PID:g546845
#accession I58200
#cross-references MUID:9425248

GENETICS
#gene GDB:CGA
#cross-references GDB:119774; OMIM:118850
#map_position 6q14-6q21
#introns 30/1; 91/3

CLASSIFICATION
#superfamily glycoprotein hormones alpha chain
KEYWORDS glycoprotein; heterodimer; hormone; pituitary
FEATURE
1-24 #domain signal sequence #status experimental #label SIG\
25-116 #product glycoprotein hormones alpha chain #status experimental #label MAT\
31-55,34-84,52-106, #disulfide_bonds #status experimental\
56-108,83-111
76,102 #binding_site carbohydrate (Asn) (covalent) #status experimental

SUMMARY #length 116 #molecular-weight 13075 #checksum 1664

RESULT 12
ENTRY 1HRPA #type complete
TITLE chorionic gonadotropin, chain A - humanORGANISM #formal_name Hc
#note placental origin, urinary extracted
REFERENCE A52806
#authors Lapthorn, A.J.; Harris, D.C.; Isaacs, N.W.
#submission submitted to the Brookhaven Protein Data Bank, August 1994
#cross-references PDB:1HRP
REFERENCE TN022062
#authors Lapthorn, A.J.; Harris, D.C.; Littlejohn, A.; Lustbader, J.W.; Canfield, R.E.; Machin, K.J.; Morgan, F.J.; Isaacs, N.W.
#journal Nature (1994) 369:455
#title Crystal structure of human chorionic gonadotropin.
REFERENCE TN022063
#authors Harris, D.C.; Machin, K.J.; Evin, G.M.; Morgan, F.J.; Isaacs, N.W.
#journal J. Biol. Chem. (1989) 264:6705
#title Preliminary x-ray diffraction analysis of human chorionic gonadotropin.
COMMENT Resolution: 3.0 angstroms

Query Match 30.8%; Score 672; DB 1; Length 116;
Best Local Similarity 93.5%; Pred. No. 8.42e-127;
Matches 87; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Db 24 SAPDVQDCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTC 83
       :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 193 TAGAAPCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTC 252

Db 84 CVAKSYNRVTVMGGFKVENHTACHCSTCYYHKS 116
       |||||||||||||||||||||||||||||||||
Qy 253 CVAKSYNRVTVMGGFKVENHTACHCSTCYYHKS 285

COMMENT
KEYWORDS Determination: X-ray diffraction
hormone
FEATURE
4-28 #disulfide_bonds\
7-57 #disulfide_bonds\
25-79 #disulfide_bonds\
29-81 #disulfide_bonds\
56-84 #disulfide_bonds\
SUMMARY #length 86 #molecular-weight 9572 #checksum 1371

Query Match 29.8%; Score 650; DB 5; Length 86;
Best Local Similarity 96.5%; Pred. No. 1.23e-121;
Matches 83; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TODCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAK 60
      :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 197 APGCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAK 256

Qy 61 SYNRVTVMGGFKVENHTACHCSTCYY 86
       ||||||||||||||||||||||||||
Db 257 SYNRVTVMGGFKVENHTACHCSTCYY 282

RESULT 13
ENTRY 1XULA #type complete
ORGANISM #formal_name Homo sapiens #common_name man
TITLE chorionic gonadotropin, chain A - humanPDB_TITLE theoretical
receptor complexed with human chorionic gonadotropin
REFERENCE A66957
#authors Jiang, X.; Dreano, M.; Buckler, D.R.; Cheng, S.; Ythier, A.;
TN032623
Wu, H.; Hendrickson, W.A.; El Tayar, N.
#journal Structure (London) (1996) 3:1341
#title Structural predictions for the ligand-binding region of glycoprotein hormone receptors and the nature of hormone-receptor interactions structure.
REFERENCE
#authors Wu, H.; Lustbader, J.W.; Liu, Y.; Canfield, R.E.;
TN032624
Hendrickson, W.A.
#journal Structure (London) (1994) 2:545
#title Structure of human chorionic gonadotropin at 2.6 a resolution from mad analysis of the selenomethionyl protein.
#submission submitted to the Brookhaven Protein Data Bank, December 1996
#cross-references PDB:1XUL

COMMENT Determination: theoretical model
COMMENT Resolution: not applicable
KEYWORDS complex; glycoprotein hormone receptor glycoprotein; hormone; phosphorylation; receptor
FEATURE
37-41 #region helix (right hand alpha)\
7-10,22-25 #region beta sheet\
49-53,26-34 #region beta sheet\
61-65,71-75 #region beta sheet\
55-60,77-81 #region beta sheet\
3-27 #disulfide_bonds\
6-56 #disulfide_bonds\
24-78 #disulfide_bonds\
28-80 #disulfide_bonds\
55-83 #disulfide_bonds\
SUMMARY #length 85 #molecular-weight 9471 #checksum 9656

Query Match 29.7%; Score 648; DB 5; Length 85;
Best Local Similarity 100.0%; Pred. No. 3.63e-121;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSYN 62
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 200 CPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSYN 259

Qy 63 RVTVMGGFKVENHTACHCSTCY 85
       ||||||||||||||||||||||
Db 63 RVTVMGGFKVENHTACHCSTCY 85

```
Qy    260  RVTVMGGFKVENHTACHCSTCYY 282
           |||||||||||||||||||||||
           |||||||||||||||||||||||

RESULT  14

ENTRY      1HCNA           #type complete

TITLE      Human chorionic gonadotropin, chain A - humanORGANISM
REFERENCE
#authors   A52587
           Wu, H.; Lustbader, J.W.; Liu, Y.; Canfield, R.E.;
           Hendrickson, W.A.
#submission    submitted to the Brookhaven Protein Data Bank, July 1994
#cross-references PDB:1HCN
REFERENCE  TN020262
#authors   Wu, H.; Lustbader, J.W.; Liu, Y.; Canfield, R.E.;
           Hendrickson, W.A.
#journal   Structure (1994) 2:545
#title     Structure of human chorionic gonadotropin at 2.6 angstroms
               resolution from mad analysis of the selenomethionyl
               protein.
COMMENT    Resolution: 2.6 angstroms                              #formal_n
COMMENT    Determination: X-ray diffraction
KEYWORDS   Hormone
FEATURE
   36-43       #region helix (right hand alpha)\
   4-11,21-28  #region beta sheet\
   29-35,48-54 #region beta sheet\
   3-27        #disulfide_bonds\
   6-56        #disulfide_bonds\
   24-78       #disulfide_bonds\
   28-80       #disulfide_bonds\
   55-83       #disulfide_bonds
SUMMARY    #length 85   #molecular-weight 9471   #checksum 9656

Query Match    29.7%;   Score 648;  DB 5;  Length 85;
Best Local Similarity 100.0%;  Pred. No. 3.63e-121;
   Matches 83; Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Db   3  CPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSYN 62
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  200  CPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSYN 259

Db   63  RVTVMGGFKVENHTACHCSTCYY 85
           |||||||||||||||||||||||
Qy  260  RVTVMGGFKVENHTACHCSTCYY 282


RESULT  15

ENTRY      A39555          #type complete

TITLE      glycoprotein hormones alpha chain precursor - rhesus macaqueORGANISM
DATE       08-Nov-1991  #sequence_revision 08-Nov-1991  #text_change
               13-Jan-1995
ACCESSIONS A39555
REFERENCE  A39555
#authors   Golos, T.G.; Durning, M.; Fisher, J.M.
#journal   DNA Cell Biol. (1991) 10:367-380
#title     Molecular cloning of the rhesus glycoprotein hormone
               alpha-subunit gene.
#cross-references MUID:9132174O
#accession A39555
##status       preliminary; not compared with conceptual translation
#molecule_type DNA
##residues 1-120  ##label GOL
CLASSIFICATION #superfamily glycoprotein hormones alpha chain
KEYWORDS   glycoprotein
SUMMARY    #length 120   #molecular-weight 13785   #checksum 5074

Query Match    25.3%;   Score 552;  DB 2;  Length 120;
Best Local Similarity 83.5%;  Pred. No. 8.95e-99;
   Matches 71; Conservative 4;  Mismatches 10;  Indels 0;  Gaps 0;

Db   35 CPECKPRENKFFSKPGAPIYQCMGCCFSRAYPTPVRSKKTMLVQKNVTSESTCCVAKSLT 94
```

```
Qy   200  CPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSYN 259
             |||  :||| |||   :||| ||||||||||||||||||||||||||||||||||||||
Db    95  RVMVMGSVRVENHTECHCSTCYYHK 119
             || ||| :||||| ||||||||||
Qy   260  RVTVMGGFKVENHTACHCSTCYYHK 284

Search completed: Wed May  6 09:01:17 1998
Job time : 34 secs.
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| |\  /| |‾‾| |‾‾| |‾‾| |‾‾|
| | \/ | |__| |__  |  | |    |__|
| |    | |    |    |  | |    | |
| |    | |    |__| |__| |__| | |    (TM)
**********************************************************************************
```

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****

MPsrch.pp   protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 6 08:58:14 1998;   MasPar time 8.40 seconds
                                             851.426 Million cell updates/sec

Tabular output not generated.

Title:
Description: >US-08-804-166-6
Perfect Score: (1-285) from US08804166.pep
Sequence: 2183
                     1 SRTSLLAFGLLCLPWLQEG..........GFKVENHTACHCSTCYYHKS 285

Scoring table: PAM 150
                     Gap 11

Searched: 69112 seqs, 25083644 residues

Post-processing: Minimum Match 0%
                     Listing first 45 summaries

Database: swiss-prot35
                     1:swiss1

Statistics: Mean 42.622; Variance 62.749; scale 0.679

                     Pred. No. is the number of results predicted by chance to have a
                     score greater than or equal to the score of the result being printed,
                     and is derived by analysis of the total score distribution.

                                               SUMMARIES

Result   %
No.   Score   Query   Length DB ID   Description   Pred. No.
----- -----   Match   --------
   1   1306   59.8   455   1   TNR1_HUMAN TUMOR NECROSIS FACTOR   0.00e+00
   2   1012   46.4   461   1   TNR1_PIG   TUMOR NECROSIS FACTOR   1.63e-244
   3   944   43.2   454   1   TNR1_MOUSE TUMOR NECROSIS FACTOR   2.69e-225
   4   928   42.5   461   1   TNR1_RAT   TUMOR NECROSIS FACTOR   8.75e-221
   5   672   30.8   116   1   GLHA_HUMAN GLYCOPROTEIN HORMONES   3.55e-149
   6   552   25.3   120   1   GLHA_MACMU GLYCOPROTEIN HORMONES   3.70e-116
   7   547   25.1   96   1   GLHA_RABIT GLYCOPROTEIN HORMONES   8.57e-115
   8   547   25.1   120   1   GLHA_BOVIN GLYCOPROTEIN HORMONES   8.57e-115
   9   549   25.1   120   1   GLHA_SHEEP GLYCOPROTEIN HORMONES   2.44e-115
  10   544   24.9   120   1   GLHA_RAT   GLYCOPROTEIN HORMONES   2.44e-115
  11   542   24.8   96   1   GLHA_BALAC GLYCOPROTEIN HORMONES   5.64e-114
  12   542   24.8   120   1   GLH2_RAT   GLYCOPROTEIN HORMONES   1.98e-113
  13   542   24.8   120   1   GLHA_MOUSE GLYCOPROTEIN HORMONES   1.98e-113
  14   542   24.8   120   1   GLHA_PIG   GLYCOPROTEIN HORMONES   1.98e-113
  15   539   24.7   96   1   GLHA_STRCA GLYCOPROTEIN HORMONES   1.30e-112
  16   540   24.7   120   1   GLHA_CALJA GLYCOPROTEIN HORMONES   6.95e-113
  17   536   24.6   96   1   GLHA_PHYCA GLYCOPROTEIN HORMONES   8.55e-112
  18   537   24.5   120   1   GLHA_MELGA GLYCOPROTEIN HORMONES   4.57e-112
  19   507   23.2   118   1   GLH2_CYPCA GLYCOPROTEIN HORMONES   6.51e-104
  20   505   23.1   120   1   GLHA_EQUAS GLYCOPROTEIN HORMONES   2.27e-103
  21   503   23.0   96   1   GLHA_HORSE GLYCOPROTEIN HORMONES   7.90e-103
  22   499   22.9   116   1   GLHA_CLAGA GLYCOPROTEIN HORMONES   9.58e-102
  23   500   22.9   118   1   GLHA_HYPMO GLYCOPROTEIN HORMONES   5.13e-102
  24   500   22.9   118   1   GLH1_CYPCA GLYCOPROTEIN HORMONES   5.13e-102
  25   500   22.9   118   1   GLHA_CTEID GLYCOPROTEIN HORMONES   5.13e-102
  26   478   21.9   93   1   GLHA_MURCI GLYCOPROTEIN HORMONES   4.53e-96
  27   479   21.9   97   1   GLHA_RANCA GLYCOPROTEIN HORMONES   2.43e-96
  28   474   21.7   117   1   GLHA_ANGAN GLYCOPROTEIN HORMONES   5.42e-95
  29   450   20.6   114   1   GLH2_ONCKE GLYCOPROTEIN HORMONES   1.53e-88
  30   448   20.5   108   1   GLH1_ONCKE GLYCOPROTEIN HORMONES   5.27e-88
  31   427   19.6   94   1   GLHA_THUOB GLYCOPROTEIN HORMONES   2.17e-82
  32   424   19.4   117   1   GLHA_ACALA GLYCOPROTEIN HORMONES   1.37e-81
  33   376   17.2   125   1   GLHA_FUNHE GLYCOPROTEIN HORMONES   6.97e-69
  34   247   11.3   417   1   WSL1_HUMAN WSL-1 PROTEIN PRECURSO   2.07e-35
  35   245   11.2   435   1   TNR_HUMAN   LYMPHOTOXIN-BETA RECEP   6.68e-36
  36   225   10.3   325   1   VT2_SFVKA   TUMOR NECROSIS FACTOR   1.55e-30
  37   225   10.1   326   1   VT2_MYXVL   TUMOR NECROSIS FACTOR   1.43e-29
  38   221   10.1   415   1   TNRC_MOUSE LYMPHOTOXIN-BETA RECEP   2.26e-28
  39   214   9.8   349   1   VC22_VARV   PROTEIN C22/B28 HOMOLO   3.53e-27
  40   211   9.7   425   1   NGFR_RAT   LOW-AFFINITY NERVE GRO   2.04e-27
  41   212   9.7   427   1   NGFR_HUMAN LOW-AFFINITY NERVE GRO   2.04e-27
  42   212   9.7   474   1   TNR2_MOUSE TUMOR NECROSIS FACTOR   2.04e-27
  43   204   9.3   260   1   CD27_HUMAN CD27L RECEPTOR PRECURS   1.61e-25
  44   191   8.7   323   1   FASA_BOVIN FASL RECEPTOR PRECURSO   1.77e-22
  45   183   8.4   595   1   CD30_HUMAN CD30L RECEPTOR PRECURS   1.24e-20
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                                              ALIGNMENTS

RESULT       1

ID   TNR1_HUMAN      STANDARD;       PRT;     455 AA.
AC   P19438;
DT   01-FEB-1991 (REL. 17, CREATED)
DT   01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (TUMOR NECROSIS FACTOR
DE   BINDING PROTEIN 1) (TBP1) (P60) (TNF-R1) (P55) (CD120A).
GN   TNFR1 OR TNFAR.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 90235284.
RA   LOETSCHER H., PAN Y.-C.E., LAHM H.-W., GENTZ R., BROCKHAUS M.,
RA   TABUCHI H., LESSLAUER W.;
RL   CELL 61:351-359(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PLACENTA;
RX   MEDLINE; 90235285.
RA   SCHALL T.J., LEWIS M., KOLLER K.J., LEE A., RICE G.C., WONG G.H.W.,
RA   GETRANAGA T., GRANGER G.A., LENTZ R., RAAB H., KOHR W.J., GOEDDEL D.V.;
RL   CELL 61:361-370(1990).
RN   [3]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 41-53; 110-124 AND 199-201.
RX   MEDLINE; 91006021.
RA   NOPHAR Y., KEMPER O., BRAKEBUSCH C., ENGELMANN H., ZWANG R.,
RA   ADERKA D., HOLTMANN H., WALLACH D.;
RL   EMBO J. 9:3269-3278(1990).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91090841.
RA   HIMMLER A., MAURER-FOGY I., KROENKE M., SCHEURICH P., PFIZENMAIER K.,
RA   LANTZ M., OLSSON I., HAUPTMANN R., STRATOWA C., ADOLF G.R.;
RL   DNA CELL BIOL. 9:705-715(1990).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PLACENTA;
RX   MEDLINE; 91017509.
RA   GRAY P.W., BARRETT K., CHANTRY D., TURNER M., FELDMAN M.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 87:7380-7384(1990).
RN   [6]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 92250049.
RA   FUCHS P., STREHL S., DWORZAK M., HIMMLER A., AMBROS P.F.;
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RL   GENOMICS 13:219-224(1992).
RN   [7]
RP   SEQUENCE OF 41-45.
RA   ENGELMANN H., NOVICK D., WALLACH D.;
RX   MEDLINE; 9010215.
RL   J. BIOL. CHEM. 265:1531-1536(1990).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211.
RA   BANNER D.W., D'ARCY A., JANES W., GENTZ R., SCHOENFELD H.-J.,
RA   BROGER C., LOETSCHER H., LESSLAUER W.;
RX   MEDLINE; 9325809.
RL   CELL 73:431-445(1993).
RN   [9]
RP   X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.
RA   NAISMITH J.H., DEVINE T.Q., KOHNO H., SPRANG S.R.;
RX   MEDLINE; 97094982.
RL   STRUCTURE 4:1251-1262(1996).
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC       RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC       AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC       PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC       SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC       PROTEASES) MEDIATING APOPTOSIS.
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC       HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC       PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC       WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC       PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC       TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC       ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR   EMBL; X55313; G37224; -.
DR   EMBL; M33294; G339745; -.
DR   EMBL; M58286; G339754; -.
DR   EMBL; M63121; G339756; -.
DR   EMBL; M75866; G339750; -.
DR   EMBL; M75864; G339750; JOINED.
DR   EMBL; M75865; G339750; JOINED.
DR   EMBL; M60275; G339760; -.
DR   EMBL; A21522; G579600; -.
DR   PIR; A34899; GQHUTI.
DR   PIR; A35010; A35010.
DR   PIR; S12057; S12057.
DR   PIR; A38208; A38208.
DR   PDB; 1TNR; 31-JUL-94.
DR   PDB; 1EXT; 11-JAN-97.
DR   PDB; 1NCF; 07-DEC-95.
DR   MIM; 191190; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS00050; TNFR_NGFR_2; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS;
KW   3D-STRUCTURE.
FT   SIGNAL         1     21
FT   CHAIN         22    455       TUMOR NECROSIS FACTOR RECEPTOR 1.
FT   CHAIN         41    291       TUMOR NECROSIS FACTOR BINDING PROTEIN 1.
FT   DOMAIN        22    211       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     212    234
FT   DOMAIN       235    455       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN        43    196       4 X TNFR-CYS.
FT   REPEAT        43     82       TNFR-CYS 1.
FT   REPEAT        83    125       TNFR-CYS 2.
FT   REPEAT       126    166       TNFR-CYS 3.
FT   REPEAT       167    196       TNFR-CYS 4.
FT   DOMAIN       356    441       DEATH DOMAIN.
FT   DISULFID      44     58
FT   DISULFID      59     72
FT   DISULFID      62     81
FT   DISULFID      84     99
FT   DISULFID     102    117
FT   DISULFID     105    125
FT   DISULFID     127    143
FT   DISULFID     146    158
FT   DISULFID     149    166
FT   DISULFID     168    179
FT   DISULFID     182    191
FT   DISULFID     185    195
FT   CARBOHYD      54     54       POTENTIAL.
FT   CARBOHYD     145    145       POTENTIAL.
FT   CARBOHYD     151    151       POTENTIAL.
FT   CONFLICT     412    412       MISSING (IN REF. 4).
FT   CONFLICT     443    446       GPAA -> APP (IN REF. 4).
SQ   SEQUENCE   455 AA;  50494 MW;  CE0EA06F CRC32;

Query Match             59.8%;  Score 1306;  DB 1;  Length 455;
Best Local Similarity   98.8%;  Pred. No. 0.0e+00;
Matches   169;  Conservative  1;  Mismatches  1;  Indels  0;  Gaps  0;

Db   41  DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSSFTASENHLRHCL  100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   23  DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSSFTASENHLRHCL   82

Db  101  SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHWSENLFQCFNCSLCLNGTVHLSCQE  160
             ||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Qy   83  SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHWSENLFQCFNCTLCLNGTVHLSCQE  142

Db  161  KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT  211
             |||||||||||||||||||||||||||||||||||:||||||||||||||
Qy  143  KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQIENVKGTEDSGTT  193
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RESULT 2

ID   TNR1_PIG       STANDARD;      PRT;    461 AA.
AC   P50555;
DT   01-OCT-1996 (REL. 34, CREATED)
DT   01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
GN   TNFR1.
OS   SUS SCROFA (PIG).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; ARTIODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=KIDNEY;
RX   MEDLINE; 96011645.
RA   SUTER B., PAULI U.H.;
RL   GENE 163:263-266(1995).
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC       RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC       AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC       PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC       SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC       PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC       HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC       PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC       WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC       PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC       TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC       ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR   EMBL; U19994; G1141753; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS00050; TNFR_NGFR_2; 2.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS.
FT   SIGNAL         1     21
FT   CHAIN         22    461       TUMOR NECROSIS FACTOR RECEPTOR 1.
FT   DOMAIN        22    210       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     211    233
FT   DOMAIN       234    461       CYTOPLASMIC (POTENTIAL).
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FT   DOMAIN      43    195    4 X TNFR-CYS.
FT   REPEAT      43     82    TNFR-CYS 1.
FT   REPEAT      83    125    TNFR-CYS 2.
FT   REPEAT     126    166    TNFR-CYS 3.
FT   REPEAT     167    195    TNFR-CYS 4.
FT   DOMAIN     362    447    DEATH DOMAIN.
FT   DISULFID    44     58    BY SIMILARITY.
FT   DISULFID    59     72    BY SIMILARITY.
FT   DISULFID    62     81    BY SIMILARITY.
FT   DISULFID   185    194    BY SIMILARITY.
FT   DISULFID   182    190    BY SIMILARITY.
FT   DISULFID   168    179    BY SIMILARITY.
FT   DISULFID   149    166    BY SIMILARITY.
FT   DISULFID   146    158    BY SIMILARITY.
FT   DISULFID   127    143    BY SIMILARITY.
FT   DISULFID   105    125    BY SIMILARITY.
FT   DISULFID   102    117    BY SIMILARITY.
FT   DISULFID    84     99    BY SIMILARITY.
FT   CARBOHYD    54     54    POTENTIAL.
FT   CARBOHYD    86     86    POTENTIAL.
FT   CARBOHYD   145    145    POTENTIAL.
FT   CARBOHYD   151    151    POTENTIAL.
FT   SEQUENCE   461 AA;  50696 MW;  8E2C350A CRC32;
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Query Match 46.4%; Score 1012; DB 1; Length 461;
Best Local Similarity 71.9%; Pred. No. 1.63e-244;
Matches 123; Conservative 25; Mismatches 22; Indels 1; Gaps 1;

SEQUENCE

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Db   41  ESLCPQGKYSHPQNRSICCTKCHKGTYLHNDCLGPGLDTDCRECDNGTFTASENHLTQCL 100
            :||||| ||||||.||||||||||||||||.|||.|||.|:||||| :||.||||||| ||
Qy   23  DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL  82

Db  101  SCSKCRSEMSQVEISPCTVDRDTVCGCRKNQYRKYWSETLFQCLNCSLCPNGTVQLPCLE 160
            |||||:|| ||||| ||||||||||||||||||.||||:||||:||:||:|||| | || 
Qy   83  SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHWSENLFQCFNCTLCLNGTVHLSCQE  142

Db  161  KQDTICNCHSGFFLRDKECVSCVNCKNA-DCKNLCPATSETRNDFQDTGTT          210
            ||:|:| ||:|||||.|||||||.||:    ::.|. |.::::| .::|||
Qy  143  KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQIENVKGTEDSGTT          193
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RESULT 3
ID   TNR1_MOUSE   STANDARD;   PRT;   454 AA.
AC   P25118;
DT   01-MAY-1992 (REL. 22, CREATED)
DT   01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
GN   TNFR1 OR TNFR-1.
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91187885.
RA   LEWIS M., TARTAGLIA L.A., LEE A., BENNETT G.L., RICE G.C.,
RA   WONG G.H., CHEN E.Y., GOEDDEL D.V.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 88:2830-2834(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91246168.
RA   GOODWIN R.G., ANDERSON D., JERZY R., DAVIS T., BRANNAN C.I.,
RA   COPELAND N.G., JENKINS N.A., SMITH C.A.;
RL   MOL. CELL. BIOL. 11:3020-3026(1991).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91285014.
RA   BARRETT K., TAYLOR-FISHWICK D.A., COPE A.P., KISSONERGHIS A.M.,
RA   GRAY P.W., FELDMANN M., FOXWELL B.M.J.;
RL   EUR. J. IMMUNOL. 21:1649-1656(1991).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=SPLEEN;

RX   MEDLINE; 92039815.
RA   ROTHE J.G., BROCKHAUS M., GENTZ R., LESSLAUER W.;
RL   IMMUNOGENETICS 34:338-340(1991).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 94245292.
RA   BEBO B.F., LINTHICUM D.S.;
RL   IMMUNOGENETICS 39:450-451(1994).
RN   [6]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 93156721.
RA   ROTHE J., BLUETHMANN H., GENTZ R., LESSLAUER W., STEINMETZ M.;
RL   IMMUNOL. 30:165-175(1993).
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC   RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC   AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC   PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC   SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC   PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC   HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC   PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC   WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC   PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC   TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC   ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC   NF-KAPPA B SIGNALING (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR   EMBL; M60468; G199826; -.
DR   EMBL; M59377; G202097; -.
DR   EMBL; X59238; G53579; -.
DR   EMBL; X57796; G54849; -.
DR   EMBL; L26349; G430733; -.
DR   EMBL; M76656; G202102; -.
DR   EMBL; M88067; G202102; JOINED.
DR   EMBL; M76655; G202102; JOINED.
DR   PIR; A38634; GOMSTI.
DR   PIR; S16677; S16677.
DR   PIR; S16677; JOINED.
DR   PIR; S19021; S19021.
DR   HSSP; P19438; 1TNR.
DR   MGD; MGI:98781; TNFR1.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS00050; TNFR_NGFR_2; 3.
DR   PROSITE; PS00017; DEATH_DOMAIN; 1.
KW   RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS.
FT   SIGNAL   1   21   POTENTIAL.
FT   CHAIN   22   454   TUMOR NECROSIS FACTOR RECEPTOR 1.
FT   DOMAIN   22   212   EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   213   235   POTENTIAL.
FT   DOMAIN   236   454   CYTOPLASMIC (POTENTIAL).
FT   DOMAIN   43   196   4 X TNFR-CYS.
FT   REPEAT   43   82   TNFR-CYS 1.
FT   REPEAT   83   125   TNFR-CYS 2.
FT   REPEAT   126   167   TNFR-CYS 3.
FT   REPEAT   167   196   TNFR-CYS 4.
FT   DOMAIN   356   441   DEATH DOMAIN.
FT   DISULFID   44   58   BY SIMILARITY.
FT   DISULFID   59   72   BY SIMILARITY.
FT   DISULFID   62   81   BY SIMILARITY.
FT   DISULFID   84   99   BY SIMILARITY.
FT   DISULFID   102   117   BY SIMILARITY.
FT   DISULFID   105   125   BY SIMILARITY.
FT   DISULFID   127   143   BY SIMILARITY.
FT   DISULFID   146   158   BY SIMILARITY.
FT   DISULFID   149   166   BY SIMILARITY.
FT   DISULFID   168   179   BY SIMILARITY.
FT   DISULFID   182   191   BY SIMILARITY.
FT   DISULFID   185   195   BY SIMILARITY.
FT   CARBOHYD   54   54   POTENTIAL.
FT   CARBOHYD   151   151   POTENTIAL.
FT   CARBOHYD   202   202   POTENTIAL.
FT   CONFLICT   394   394   R -> G (IN REF. 6).

RESULT 4

SQ SEQUENCE 454 AA; 50129 MW; 4B6EEC09 CRC32;

Query Match   43.2%; Score 944; DB 1; Length 454;
Best Local Similarity   67.4%; Pred. No. 2.69e-225;
Matches 116; Conservative 28; Mismatches 27; Indels 1; Gaps 1;

Qy   41 DSLCPQGKYVHSKNNSICCTKCHKGTYLLVSDCPSPGRDTVCREBCEKGTFTASQNYLRQCL 100
         |:|:||||:| |||||||||||||||:||| :| :| | |:||| ||||| | |:|||
Db   83 SCSKTCRKEMSQVEISPCCOADKDTVCGRCKENQFORYLSETHFQCCVDCSPCFNGTVTIPCKE 142

Qy   23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82
         |||||||:|| |||||||||:| |||:| || | |: |:|||:|||:|||:|
Db 101 SCKTCRKEMSQVEISPCCOADKDTVCGRCKENQFORYLSETHFQCCVDCSPCFNGTVTIPCKE 160

Qy 161 TONTVCNCHAGFFLRESECVPCSHCKKNEEOCMKLCLPPPLANVTNPQDSGTA 212
         ||:||| ||||||||| ||| |: ||| |::|||| || ||| |: |:|||:
Db 143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQ-IENVKGTEDSGTT 193

ID   TNR1_RAT   STANDARD;   PRT;   461 AA.
AC   P22934;
DT   01-AUG-1991 (REL. 19, CREATED)
DT   01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
GN   TNFR1 OR TNFR-1.
OS   RATTUS NORVEGICUS (RAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91090841.
RA   HIMMLER A., MAURER-FOGY I., KRONKE M., SCHEURICH P., PFIZENMAIER K.,
RA   LANTZ M., OLSSON I., HAUPTMANN R., STRATOWA C., ADOLF G.R.;
RL   DNA CELL BIOL. 9:705-715(1990).
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC   RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC   AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC   PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC   SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC   PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC   HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC   PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC   WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC   PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC   TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC   ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC   NF-KAPPA B SIGNALING (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR   EMBL; M63122; G207362; -.
DR   PIR; B36555; B36555.
DR   HSSP; P19438; 1TNR.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS00050; TNFR_NGFR_2; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS.
FT   SIGNAL   1   21   POTENTIAL.
FT   CHAIN   22   455   TUMOR NECROSIS FACTOR RECEPTOR 1.
FT   DOMAIN   22   211   EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   212   234   POTENTIAL.
FT   DOMAIN   235   461   CYTOPLASMIC (POTENTIAL).
FT   DOMAIN   43   196   4 X TNFR-CYS.
FT   REPEAT   43   82   TNFR-CYS 1.
FT   REPEAT   83   125   TNFR-CYS 2.
FT   REPEAT   126   166   TNFR-CYS 3.
FT   REPEAT   167   196   TNFR-CYS 4.
FT   DOMAIN   363   448   DEATH DOMAIN.
FT   DISULFID   44   58   BY SIMILARITY.
FT   DISULFID   59   72   BY SIMILARITY.
FT   DISULFID   62   81   BY SIMILARITY.
FT   DISULFID   84   99   BY SIMILARITY.
FT   DISULFID   102   117   BY SIMILARITY.
FT   DISULFID   105   125   BY SIMILARITY.
FT   DISULFID   127   143   BY SIMILARITY.
FT   DISULFID   146   158   BY SIMILARITY.
FT   DISULFID   149   166   BY SIMILARITY.
FT   DISULFID   168   179   BY SIMILARITY.
FT   DISULFID   182   191   BY SIMILARITY.
FT   DISULFID   185   195   BY SIMILARITY.
FT   CARBOHYD   54   54   POTENTIAL.
FT   CARBOHYD   151   151   POTENTIAL.
FT   CARBOHYD   201   201   POTENTIAL.
SQ   SEQUENCE 461 AA; 50969 MW; 82F68B08 CRC32;

RESULT 5

Query Match   42.5%; Score 928; DB 1; Length 461;
Best Local Similarity   66.1%; Pred. No. 8.75e-221;
Matches 113; Conservative 26; Mismatches 32; Indels 0; Gaps 0;

Qy   41 DNLCPQGKYAHPKNNSICCTKCHKGTYLVSDCSPGQETVCGDKGTFTASQNHVRQCL 100
         | ||||||| ||||||||||||||| |:||| | | |:|| |:|||||||:||||
Db   23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Qy 101 SCKTCRKEMQVEISPCKADMDTVCGCKKNQFQRYLSETHFQCVDCRECESGSFTASENHLRHCL 160
         ||| ||||| |||||| || |||| ||| | ||||||||| | |:|||:|||:||
Db   83 SCSKTCRKEMSQVEISPCCOADKDTVCGRCKENQFORYLSETHFQCCVDCSPCFNGTVTIPCKE 142

Qy 161 KQNTVCNCHAGFFLRGNECTPCSHCKKNQOECMKLCLPPVANVTNPQDSGTA 211
         ||||||||||||||| || | |: |||:| |||| || ||| ||||||||:
Db 143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLSLPQIENVKGTEDSGTT 193

ID   GLHA_HUMAN   STANDARD;   PRT;   116 AA.
AC   P01215;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR.
GN   CGA.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 80011660.
RA   FIDDES J.C., GOODMAN H.M.;
RL   NATURE 281:351-356(1979).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 94254248.
RA   MIYOSHI I., KASAI N., HAYASHIZAKI Y.;
RL   NIPPON RINSHO 52:940-947(1994).
RN   [3]
RP   SEQUENCE OF 1-98 FROM N.A.
RX   MEDLINE; 82267643.
RA   FIDDES J.C., GOODMAN H.M.;
RL   J. MOL. APPL. GENET. 1:3-18(1981).
RN   [4]
RP   SEQUENCE OF 1-24.
RX   MEDLINE; 81117268.
RA   BIRKEN S., FETHERSTON J., CANFIELD R.E., BOIME I.;
RL   J. BIOL. CHEM. 256:1816-1823(1981).
RN   [5]
RP   SEQUENCE OF 28-116.
RX   MEDLINE; 77243687.
RA   SAIRAM M.R., LI C.H.;
RL   CAN. J. BIOCHEM. 55:755-760(1977).
RN   [6]
RP   SEQUENCE OF 28-116.
RA   SAIRAM M.R., PAPKOFF H., LI C.H.;
RL   BIOCHEM. BIOPHYS. RES. COMMUN. 48:530-537(1972).
RN   [7]

RP   SEQUENCE, AND REVISIONS.
RA   KEUTMANN H.T., WILLIAMS R.M., BISHOP W.H., RYAN R.J.;
RL   FED. PROC. 37:1828-1828(1978).
RN   [8]
RP   SEQUENCE OF 25-116.
RX   MEDLINE; 76005558.
RA   RATHNAM P., SAXENA B.B.;
RL   J. BIOL. CHEM. 250:6735-6746(1975).
RN   [9]
RP   SEQUENCE OF 28-116.
RX   MEDLINE; 74262937.
RA   SHOME B., PARLOW A.F.;
RL   J. CLIN. ENDOCRINOL. METAB. 39:199-202(1974).
RN   [10]
RP   SEQUENCE OF 25-116.
RX   MEDLINE; 75211304.
RA   MORGAN F.J., BIRKEN S., CANFIELD R.E.;
RL   J. BIOL. CHEM. 250:5247-5258(1975).
RN   [11]
RP   SEQUENCE OF 25-116.
RX   MEDLINE; 74011266.
RA   BELLISARIO R., CARLSEN R.B., BAHL O.P.;
RL   J. BIOL. CHEM. 248:6796-6809(1973).
RN   [12]
RP   PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.
RX   MEDLINE; 81021713.
RA   FUJIKI Y., RATHNAM P., SAXENA B.B.;
RL   BIOCHIM. BIOPHYS. ACTA 624:428-435(1980).
RN   [13]
RP   PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.
RX   MEDLINE; 81066887.
RA   MISE T., BAHL O.P.;
RL   J. BIOL. CHEM. 255:8516-8522(1980).
RN   [14]
RP   STRUCTURE OF CARBOHYDRATES.
RX   MEDLINE; 91122088.
RA   WEISSHAAR G., HIYAMA J., RENWICK A.G.C., NIMTZ M.;
RL   EUR. J. BIOCHEM. 195:257-268(1991).
RN   [15]
RP   X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RX   MEDLINE; 94261179.
RA   LAPTHORN A.J., HARRIS D.C., LITTLEJOHN A., LUSTBADER J.W.,
RA   CANFIELD R.E., MACHIN K.J., MORGAN F.J., ISAACS N.W.;
RL   NATURE 369:455-461(1994).
RN   [16]
RP   STRUCTURE BY NMR.
RX   MEDLINE; 97054614.
RA   DE BEER T., VAN ZUYLEN C.W.E.M., LEEFLANG B.R., HARD K., BOELENS R.,
RA   KAPTEIN R., KAMERLING J.P., VLIEGENTHART J.F.G.;
RL   EUR. J. BIOCHEM. 241:229-242(1996).
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC   CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC   LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   EMBL; J00152; G183319; JOINED.
DR   EMBL; J00150; G183319; JOINED.
DR   EMBL; J00151; G183319; JOINED.
DR   EMBL; J00152; G183319; -.
DR   EMBL; S70585; G546845; -.
DR   EMBL; S70585; G546845; -.
DR   EMBL; S70583; G546845; JOINED.
DR   EMBL; S70584; G546845; JOINED.
DR   EMBL; S70584; G31869; JOINED.
DR   EMBL; V00518; G31869; -.
DR   EMBL; V00485; G669156; -.
DR   EMBL; V00486; G669156; JOINED.
DR   EMBL; V00487; G669156; JOINED.
DR   PIR; A01481; TTHUAP.
DR   PDB; 1HCN; 30-SEP-94.
DR   PDB; 1HRP; 01-NOV-94.
DR   MIM; 118850; -.
DR   MIM; 188530; -.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL; 3D-STRUCTURE.
FT   SIGNAL   1   24
FT   CHAIN   25   116   GLYCOPROTEIN HORMONES ALPHA CHAIN.

FT   DISULFID   31   55
FT   DISULFID   34   84
FT   DISULFID   52   106
FT   DISULFID   56   108
FT   DISULFID   56   111
FT   CARBOHYD   63   63
FT   CARBOHYD   76   76
FT   CARBOHYD   102   102
FT   CONFLICT   29   29   Q -> E (IN REF. 8).
FT   CONFLICT   108   109   CS -> SC (IN REF. 5 AND 6).
SQ   SEQUENCE   116 AA; 13075 MW; 3BA19E2F CRC32;

Query Match   30.8%; Score 672; DB 1; Length 116;
Best Local Similarity 93.5%; Pred. No. 3.55e-149;
Matches   87; Conservative   1; Mismatches   5; Indels   0; Gaps   0;

Db   24 SAPDVQDCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTC   83
          :| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   193 TAGAAPGCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTC 252

Db   84 CVAKSYNRVTVMGGFKVENNTACHCSTCYYHKS 116
          |||||||||||||||||||| |||||||||||||
Qy   253 CVAKSYNRVTVMGGFKVENHTACHCSTCYYHKS 285

RESULT 6
ID   GLHA_MACMU   STANDARD;   PRT;   120 AA.
AC   P22762;
DT   01-AUG-1991 (REL. 19, CREATED)
DT   01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR.
GN   CGA.
OS   MACACA MULATTA (RHESUS MACAQUE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91321740.
RA   GOLOS T.G., DURNING M., FISHER J.M.;
RL   DNA CELL BIOL. 10:367-380(1991).
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC   CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC   LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   PIR; A39555; A39555.
DR   HSSP; P01215; 1HCN.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL   1   24   BY SIMILARITY.
FT   CHAIN   25   120   GLYCOPROTEIN HORMONES ALPHA CHAIN.
FT   DISULFID   35   59   BY SIMILARITY.
FT   DISULFID   38   88   BY SIMILARITY.
FT   DISULFID   56   110   BY SIMILARITY.
FT   DISULFID   60   112   BY SIMILARITY.
FT   DISULFID   87   115   BY SIMILARITY.
FT   CARBOHYD   67   67   BY SIMILARITY.
FT   CARBOHYD   80   80   BY SIMILARITY.
FT   CARBOHYD   106   106   BY SIMILARITY.
SQ   SEQUENCE   120 AA; 13785 MW; 85E1F9F4 CRC32;

Query Match   25.3%; Score 552; DB 1; Length 120;
Best Local Similarity 83.5%; Pred. No. 3.70e-116;
Matches   71; Conservative   4; Mismatches   10; Indels   0; Gaps   0;

Db   35 CPECKPRENKFFSRPGAPIYQCMGCCFSRAYPTPVRSKKTMLVQKNVTSESTCCVAKSLT   94
          |||| ||||| || |||| ||||||||||||||| | |||||||||||||||||||| |
Qy   200 CPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSYN 259

Db   95 RVMMGSVRVENHTECHCSTCYYHK 119
          | | | | |||| ||||||||||
Qy   260 RVTVMGGFKVENHTACHCSTCYYHK 284

RESULT 7
ID   GLHA_RABIT   STANDARD;   PRT;   96 AA.
AC   P07474;
DT   01-APR-1988 (REL. 07, CREATED)
DT   01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   GLYCOPROTEIN HORMONES ALPHA CHAIN.
GN   CGA.
OS   ORYCTOLAGUS CUNICULUS (RABBIT)
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; LAGOMORPHA.
RN   [1]
RP   SEQUENCE.
RA   GLENN S.D., NAHM H.S., WARD D.N.;
RL   J. PROTEIN CHEM. 3:143-156(1984).
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC   CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC   LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   PIR; A05096; A05096.
DR   HSSP; P01233; 1HRP.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW   HORMONE; GLYCOPROTEIN.
FT   DISULFID   11   35   BY SIMILARITY.
FT   DISULFID   14   64   BY SIMILARITY.
FT   DISULFID   32   86   BY SIMILARITY.
FT   DISULFID   36   88   BY SIMILARITY.
FT   DISULFID   63   91   BY SIMILARITY.
FT   CARBOHYD   56   56   BY SIMILARITY.
FT   CARBOHYD   82   82   BY SIMILARITY.
SQ   SEQUENCE   96 AA; 10663 MW; CD56D255 CRC32;

Query Match   25.1%;
Best Local Similarity 76.7%;
Matches 69; Conservative   6; Mismatches 15; Indels   0; Gaps   0;
Score 547; DB 1; Length 96;
Pred. No. 8.57e-115;

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Db    7 AMGCGPECKLKENKYFSKLGAPIYQCMGCCFSRAYPTPARSKKTMLVPKNITSEATCCVA 66
          || |||| ||||     |  | ||||||||||||||||||| |||||||||  || | |||
Qy  196 AAPGCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKRNVTSESTCCVA 255

Db   67 KAFIKATVMGNAKVENHTECHCSTCYYHKS 96
          |:: |||| || ||||||| ||||||||||
Qy  256 KSYNRVTVMGGFKVENHTACHCSTCYYHKS 285
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RESULT 8
ID   GLHA_BOVIN   STANDARD;   PRT; 120 AA.
AC   P01217;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   23-OCT-1986 (REL. 02, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR.
GN   CGA.
OS   BOS TAURUS (BOVINE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; ARTIODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 84041490.
RA   GOODWIN R.G., MONCMAN C.L., ROTTMAN F.M., NILSON J.H.;
RL   NUCLEIC ACIDS RES. 11:6873-6882(1983).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 84024633.
RA   ERWIN C., CROYLE M.L., DONELSON J., MAURER R.;
RL   BIOCHEMISTRY 22:4856-4860(1983).
RN   [3]
RP   SEQUENCE OF 8-133 FROM N.A.
RX   MEDLINE; 83161058.
RA   NILSON J.H., THOMASON A.R., CSERBAK M.T., MONCMAN C.L., WOYCHIK R.P.;
RL   J. BIOL. CHEM. 258:4679-4682(1983).
RN   [4]
RP   SEQUENCE OF 25-120.
RX   MEDLINE; 71111428.
RA   LIAO T.-H., PIERCE J.G.;
RL   J. BIOL. CHEM. 246:850-865(1971).
RN   [5]
RP   PRELIMINARY PARTIAL SEQUENCE.
RX   MEDLINE; 71111429.
RA   PIERCE J.G., LIAO T.-H., CARLSEN R.B., REIMO T.;
RL   J. BIOL. CHEM. 246:866-872(1971).
RN   [6]
RP   SEQUENCE OF 80-91 AND 100-120.
RX   MEDLINE; 72012932.
RA   MAGHUIN-ROGISTER G., HENNEN G.P.;
RL   EUR. J. BIOCHEM. 21:489-497(1971).
RN   [7]
RP   PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.
RX   MEDLINE; 74307752.
RA   CORNELL J.S., PIERCE J.G.;
RL   J. BIOL. CHEM. 249:4166-4174(1974).
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC   CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC   LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   EMBL; X00003; E274391; -.
DR   EMBL; X00004; E274391; JOINED.
DR   EMBL; X00050; G607; -.
DR   PIR; A01483; TTBOA.
DR   PIR; A05132; A05132.
DR   HSSP; P01215; 1HCN.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL   1   24
FT   CHAIN   25   120   GLYCOPROTEIN HORMONES ALPHA CHAIN.
FT   DISULFID   35   59   BY SIMILARITY.
FT   DISULFID   38   88   BY SIMILARITY.
FT   DISULFID   56   110   BY SIMILARITY.
FT   DISULFID   60   112   BY SIMILARITY.
FT   DISULFID   87   115   BY SIMILARITY.
FT   CARBOHYD   80   80   BY SIMILARITY.
FT   CARBOHYD   106   106   BY SIMILARITY.
FT   CONFLICT   13   13   A -> T (IN REF. 2).
FT   CONFLICT   37   37   E -> Q (IN REF. 4).
FT   CONFLICT   52   52   P -> A (IN REF. 2).
FT   CONFLICT   84   87   EATC -> AZCT (IN REF. 6).
SQ   SEQUENCE 120 AA; 13616 MW; 99C153C5 CRC32;

Query Match   25.1%;
Best Local Similarity 77.0%;
Matches 67; Conservative   7; Mismatches 13; Indels   0; Gaps   0;
Score 549; DB 1; Length 120;
Pred. No. 2.44e-115;

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Db   34 GCPECKLKENKYFSKPDAPIYQCMGCCFSRAYPTPARSKKTMLVPKNITSEATCCVARAF 93
          |||| |||| |||| |  || ||||||||||||||||| |||||||||  || | ||||| |
Qy  199 GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKRNVTSESTCCVAKSY 258

Db   94 TKATVMGNVRVENHTECHCSTCYYHKS 120
          || ||||| ||||||| ||||||||||
Qy  259 NRVTVMGGFKVENHTACHCSTCYYHKS 285
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RESULT 9
ID   GLHA_SHEEP   STANDARD;   PRT; 120 AA.
AC   P01218;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR.
GN   CGA.
OS   OVIS ARIES (SHEEP).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; ARTIODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 90098887.

RA   BELLO P.A., MOUNTFORD P.S., BRANDON M.R., ADAMS T.E.;
RL   NUCLEIC ACIDS RES. 17:10494-10494(1989).
RN   [2]
RP   SEQUENCE OF 25-120.
RX   MEDLINE; 72211144.
RA   LIU W.-K., NAHM H.S., SWEENEY C.M., LAMKIN W.M., BAKER H.N.,
RA   WARD D.N.;
RL   J. BIOL. CHEM. 247:4351-4364(1972).
RN   [3]
RP   SEQUENCE OF 25-120.
RX   MEDLINE; 73190034.
RA   SAIRAM M.R., PAPKOFF H., LI C.H.;
RL   ARCH. BIOCHEM. BIOPHYS. 153:554-571(1972).
RN   [4]
RP   SEQUENCE OF 25-120.
RX   MEDLINE; 82213052.
RA   SAIRAM M.R.;
RL   BIOCHEM. J. 197:535-539(1981).
RN   [5]
RP   PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.
RA   CHUNG D., SAIRAM M.R., LI C.H.;
RL   ARCH. BIOCHEM. BIOPHYS. 159:678-682(1973).
RN   [6]
RP   STRUCTURE OF CARBOHYDRATES.
RX   MEDLINE; 91006170.
RA   WEISSHAAR G., HIYAMA J., RENNICK A.G.C.;
RL   EUR. J. BIOCHEM. 192:741-751(1990).
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC   CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC   LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   EMBL; X16977; G1366; -.
DR   PIR; A01483; TTBOA.
DR   PIR; A01484; UTSHA.
DR   PIR; S06935; S06935.
DR   PIR; S13200; S13200.
DR   HSSP; P01215; 1HCN.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL   1   24
FT   CHAIN   25   120   GLYCOPROTEIN HORMONES ALPHA CHAIN.
FT   DISULFID   35   59   BY SIMILARITY.
FT   DISULFID   38   88   BY SIMILARITY.
FT   DISULFID   56   110   BY SIMILARITY.
FT   DISULFID   60   112   BY SIMILARITY.
FT   DISULFID   87   115   BY SIMILARITY.
FT   CARBOHYD   106   106   BY SIMILARITY.
FT   CARBOHYD   27   27   BY SIMILARITY.
FT   CARBOHYD   29   29   BY SIMILARITY.
FT   CONFLICT   37   37   E -> Q (IN REF. 2).
FT   CONFLICT   112   113   CS -> SC (IN REF. 2 TO 4).
SQ   SEQUENCE   120 AA; 13588 MW; 13BA4DE1 CRC32;

Query Match   25.1%;
Best Local Similarity   77.0%;   Score 549; DB 1; Length 120;
Matches   67; Conservative   7; Mismatches 13; Indels   0; Gaps   0;

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Db        34  GCPECKLKENKYFSKPDAPIYQCMGCCFSRAYPTPARSKKTMLVPKNITSEATCCVAKAF  93
              |||| || :|| :|| |||||||||||||||| :|||||||||||||||||||||||||||::
Qy       199  GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVPKNITSEATCCVAKSY  258

Db        94  TKATVMGNVRVENHTECHCSTCYYHKS  120
              :|||  |||||||:|||||||||||||
Qy       259  NRVTVMGGFKVENHTACHCSTCYYHKS  285
```

RESULT 10
ID   GLH1_RAT   STANDARD;   PRT;   120 AA.
AC   P11962; P70516;
DT   01-OCT-1989 (REL. 12, CREATED)
DT   01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   GLYCOPROTEIN HORMONES ALPHA CHAIN 1 PRECURSOR.
OS   RATTUS NORVEGICUS (RAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=PITUITARY;
RX   MEDLINE; 82214055.
RA   GODINE J.E., CHIN W.W., HABENER J.F.;
RL   J. BIOL. CHEM. 257:8368-8371(1982).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 89169918.
RA   BURNSIDE J., BUCKLAND P.R., CHIN W.W.;
RL   GENE 70:67-74(1988).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=WISTAR-IMAMICHI; TISSUE=ANTERIOR PITUITARY;
RA   KATO Y., EZASHI T., HIRAI T., KATO T.;
RL   ZOOL. SCI. 7:877-885(1990).
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC   CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC   LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   EMBL; V01252; G56580; -.
DR   EMBL; J00757; G206111; -.
DR   EMBL; M22829; -; NOT_ANNOTATED_CDS.
DR   EMBL; M25543; G204470; -.
DR   EMBL; M25544; G204471; -.
DR   EMBL; D00575; G220842; -.
DR   PIR; JT0408; TTRTA.
DR   PIR; S27385; S27385.
DR   HSSP; P01233; 1HRP.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL   1   24
FT   CHAIN   25   120   GLYCOPROTEIN HORMONES ALPHA CHAIN 1.
FT   DISULFID   35   59   BY SIMILARITY.
FT   DISULFID   38   88   BY SIMILARITY.
FT   DISULFID   56   110   BY SIMILARITY.
FT   DISULFID   60   112   BY SIMILARITY.
FT   DISULFID   87   115   BY SIMILARITY.
FT   CARBOHYD   106   106   PROBABLE.
FT   CARBOHYD   80   80   PROBABLE.
FT   CONFLICT   84   84   E -> Q (IN G206111).
SQ   SEQUENCE   120 AA; 13453 MW; 5E507A0D CRC32;

Query Match   24.9%;
Best Local Similarity   78.2%;   Score 544; DB 1; Length 120;
Matches   68; Conservative   6; Mismatches 13; Indels   0; Gaps   0;

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Db        34  GCPECKLKENKYFSKLGAPIYQCMGCCFSRAYPTPARSKKTMLVPKNITSEATCCVAKSF  93
              |||| ||   || ||| |||||||||||||||| :|||||||||||||||||||||||||||
Qy       199  GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVPKNITSEATCCVAKSY  258

Db        94  TKATVMGNARVENHTDCHCSTCYYHKS  120
              :|||  || ||||||:||||||||||||
Qy       259  NRVTVMGGFKVENHTACHCSTCYYHKS  285
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RESULT 11
ID   GLHA_BALAC   STANDARD;   PRT;   96 AA.
AC   P37036;
DT   01-JUN-1994 (REL. 29, CREATED)
DT   01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   GLYCOPROTEIN HORMONES ALPHA CHAIN.
GN   CGA.
OS   BALAENOPTERA ACUTOROSTRATA (MINKE WHALE) (LESSER RORQUAL).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; CETACEA.
RN   [1]
RP   SEQUENCE.

RA KARASEV V. S., PANKOV Y. A.;
RL BIOKHIMIIA 50:1972-1986(1985).
CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC   CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC   LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR PIR; PN0138; PN0138.
HSSP; P01215; 1HCN.
DR PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW HORMONE; GLYCOPROTEIN.
FT DISULFID   11   35   BY SIMILARITY.
FT DISULFID   14   64   BY SIMILARITY.
FT DISULFID   32   86   BY SIMILARITY.
FT DISULFID   36   88   BY SIMILARITY.
FT DISULFID   63   91   BY SIMILARITY.
FT CARBOHYD   56   BY SIMILARITY.
FT CARBOHYD   82   BY SIMILARITY.
SQ SEQUENCE   96 AA; 10720 MW; E2CD30DF CRC32;

Qy 259 NRVTVMGGFKVENHTACHCSTCYYHKS 285

Db 70 TKATVMGBARYZNHTCHCSTCYYHKS 96
        |||| :|:|||| |||||||||||||
Qy 259 NRVTVMGGFKVENHTACHCSTCYYHKS 285

RESULT 12

ID GLH2_RAT   STANDARD;   PRT;   120 AA.
AC P11963;
DT 01-OCT-1989 (REL. 12, CREATED)
DT 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE GLYCOPROTEIN HORMONES ALPHA CHAIN 2 PRECURSOR.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 82214055.
RA GODINE J. E., CHIN W.W., HABENER J.F.;
RL J. BIOL. CHEM. 257:8368-8371(1982).
CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC   CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC   LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR EMBL; V01253; G56583; -.
DR PIR; S27386; S27386.
HSSP; P01215; 1HCN.
DR PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW HORMONE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL   1   24
FT CHAIN   25   120   GLYCOPROTEIN HORMONES ALPHA CHAIN 2.
FT DISULFID   35   59   BY SIMILARITY.
FT DISULFID   38   88   BY SIMILARITY.
FT DISULFID   56   110   BY SIMILARITY.
FT DISULFID   60   112   BY SIMILARITY.
FT DISULFID   87   115   BY SIMILARITY.
FT CARBOHYD   80   PROBABLE.
FT CARBOHYD   106   PROBABLE.
SQ SEQUENCE   120 AA; 13565 MW; 4E4FAB2E CRC32;

Query Match   24.8%; Score 542; DB 1; Length 120;
Best Local Similarity   70.1%; Pred. No. 1.98e-113;
Matches   61; Conservative   13; Mismatches 13; Indels   0; Gaps   0;

Qy 199 GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVPKNITSZATCCVAKAF 69
        |||:||| || ::| ||||||||||||||| |:||:|||||||| |:|||||||||:
Db 10 GCPZCKLKZBKYFSKLGAPIYZCMGCCFSRAYPTPARSKKTMLVPKNITSZATCCVAKAF 69

Db 70 TKATVMGBARYZNHTCHCSTCYYHKS 96
        |||| :|:|||| |||||||||||||
Qy 259 NRVTVMGGFKVENHTACHCSTCYYHKS 285

RESULT 13

ID GLHA_MOUSE   STANDARD;   PRT;   120 AA.
AC P01216;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR.
GN CGA.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 82060239.
RA CHIN W.W., KRONENBERG H.M., DEE P.C., MALOOF F., HABENER J.F.;
RL PROC. NATL. ACAD. SCI. U.S.A. 78:5329-5333(1981).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89170115.
RA GORDON D.F., WOOD W.M., RIDGWAY E.C.;
RL DNA 7:679-690(1988).
CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC   CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC   LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR EMBL; J00643; G202180; -.
DR EMBL; V00852; G547799; -.
DR EMBL; M22991; -; NOT_ANNOTATED_CDS.
DR EMBL; M22992; G575520; -.
DR PIR; A01482; TTMSA.
DR PIR; A31598; A31598.
HSSP; P01215; 1HCN.
MGD; MGI:88390; CGA.
DR PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW HORMONE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL   1   24
FT CHAIN   25   120   GLYCOPROTEIN HORMONES ALPHA CHAIN.
FT DISULFID   35   59   BY SIMILARITY.
FT DISULFID   38   88   BY SIMILARITY.
FT DISULFID   56   110   BY SIMILARITY.
FT DISULFID   60   112   BY SIMILARITY.
FT DISULFID   87   115   BY SIMILARITY.
FT CARBOHYD   80   PROBABLE.
FT CARBOHYD   106   PROBABLE.
SQ SEQUENCE   120 AA; 86F1F31A CRC32;

Query Match   24.8%; Score 542; DB 1; Length 120;
Best Local Similarity   77.0%; Pred. No. 1.98e-113;
Matches   67; Conservative   7; Mismatches 13; Indels   0; Gaps   0;

Qy 199 GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSY 258
        ||| ||| |||||||||||||||||||||||| |:||:|||||||||||||||||||||:
Db 34 GCPECKLKENKYFSKLGAPIYQCMGCCFSRAYPTPARSKKTMLVPKNITSEATCCVAKAF 93

Db 94 TKATVMGNARVENHTECHCSTCYYHKS 120
        : |||| ||||||||||||||||||||
Qy 259 NRVTVMGGFKVENHTACHCSTCYYHKS 285

RESULT 14

ID GLHA_PIG   STANDARD;   PRT;   120 AA.
AC P01219;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR.

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GN   CGA.
OS   SUS SCROFA (PIG).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; ARTIODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 89325834.
RA   HIRAI T., TAKIKAWA H., KATO Y.;
RL   MOL. CELL. ENDOCRINOL. 63:209-217(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   KATO Y., EZASHI T., HIRAI T., KATO T.;
RL   SUBMITTED (MAR-1992) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN   [3]
RP   SEQUENCE OF 31-120.
RA   MAGHUIN-ROGISTER G., COMBARNOUS Y., HENNEN G.;
RL   MEDLINE; 74075725.
RN   [4]
RA   MAGHUIN-ROGISTER G., COMBARNOUS Y., HENNEN G.;
RL   EUR. J. BIOCHEM. 39:255-263(1973).
RN   [5]
RP   PRELIMINARY SEQUENCE OF 25-120.
RA   CLOSSET J., MAGHUIN-ROGISTER G., HENNEN G.;
RL   ENDOCRINOL. EXP. 8:164(1974).
RP   PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.
RX   MEDLINE; 75093922.
RA   COMBARNOUS Y., HENNEN G.;
RL   BIOCHEM. SOC. TRANS. 2:915-917(1974).
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
EMBL; D00768; G217699; -.
EMBL; D00767; G217699; JOINED.
PIR; A01485; UTPGA.
PIR; A30339; A30339.
HSSP; P01215; 1HCN.
PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL        1     24
FT   CHAIN        25    120     GLYCOPROTEIN HORMONES ALPHA CHAIN.
FT   DISULFID     35     59     BY SIMILARITY.
FT   DISULFID     38     88     BY SIMILARITY.
FT   DISULFID     56    110     BY SIMILARITY.
FT   DISULFID     60    112     BY SIMILARITY.
FT   DISULFID     87    115     BY SIMILARITY.
FT   CARBOHYD     80     80     BY SIMILARITY.
FT   CARBOHYD    106    106     BY SIMILARITY.
SQ   SEQUENCE    120 AA;  13532 MW;  8749DBA5 CRC32;

Query Match     24.8%;  Score 542; DB 1; Length 120;
Best Local Similarity   77.0%;  Pred. No. 1.98e-113;
Matches    67;  Conservative    7;  Mismatches   13;  Indels    0;  Gaps    0;

Qy   199 GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSY 258
Db    34 GCPECKLKENKYFSKLGAPIYQCMGCCFSRAYPTPARSKKTMLVPKNITSEATCCVAKAF 93

Db    94 TKAIVMGNARVENHTECHCSTCYYHKS 120
Qy   259 NRVTVMGGFKVENHTACHCSTCYYHKS 285
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RESULT   15
ID   GLHA_STRCA     STANDARD;     PRT;    96 AA.
AC   P80065;
DT   01-OCT-1996 (REL. 34, CREATED)
DT   01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   GLYCOPROTEIN HORMONES ALPHA CHAIN.
OS   STRUTHIO CAMELUS (OSTRICH).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES;
OC   PALAEOGNATHAE; STRUTHIONIFORMES.
RN   [1]
RP   SEQUENCE.
RX   MEDLINE; 97025333.
RA   KOIDE Y., PAPKOFF H., KAWAUCHI H.;
RL   EUR. J. BIOCHEM. 240:262-267(1996).
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
HORMONE; GLYCOPROTEIN.
FT   DISULFID     11     35     BY SIMILARITY.
FT   DISULFID     14     64     BY SIMILARITY.
FT   DISULFID     32     86     BY SIMILARITY.
FT   DISULFID     36     88     BY SIMILARITY.
FT   DISULFID     63     91     BY SIMILARITY.
FT   CARBOHYD     56     56     POTENTIAL.
FT   CARBOHYD     82     82     POTENTIAL.
SQ   SEQUENCE     96 AA;  10781 MW;  DDF7B4BB CRC32;

Query Match     24.7%;  Score 539; DB 1; Length 96;
Best Local Similarity   74.7%;  Pred. No. 1.30e-112;
Matches    65;  Conservative    10;  Mismatches   12;  Indels    0;  Gaps    0;

Qy   199 GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSY 258
Db    10 GCPECKLGENRFFSKPGAPVYQCTGCCFSRAYPTPLRSKKTMLVPKNITSEATCCVAKAF 69

Db    70 TKITLKDNVKIENHTECHCSTCYYHKS 96
Qy   259 NRVTVMGGFKVENHTACHCSTCYYHKS 285

Search completed: Wed May  6 08:58:56 1998
Job time : 42 secs.
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MPsrch_pp   protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May   6 08:59:13 1998; MasPar time 14.96 Seconds
                                              802.180 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-6
Description: (1-285) from US0804166.pep
Perfect Score: 2183
Sequence: 1 SRTSLLLAFGLLCLPWLOEG.........GFKVENHTACHCSTCYHKS 285

Scoring table: PAM 150
                Gap 11

Searched: 140555 seqs, 42109429 residues

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database: sptrembl5
                1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
                5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
                9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
                13:sp_unclassified

Statistics: Mean 41.694; Variance 64.494; scale 0.646

                Pred. No. is the number of results predicted by chance to have a
                score greater than or equal to the score of the result being printed,
                and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description	Pred. No.
1	959	43.9	471	4	O19131	TUMOR NECROSIS FACTOR-	7.07e-219
2	943	43.2	180	4	Q95185	TUMOR NECROSIS FACTOR	1.42e-214
3	453	20.8	107	12	Q90286	GONADOTROPIN ALPHA SUB	3.04e-85
4	454	20.8	108	12	Q90287	GONADOTROPIN ALPHA SUB	1.68e-85
5	452	20.7	119	12	Q91370	GONADOTROPIN ALPHA SUB	5.48e-85
6	448	20.5	114	12	Q91371	GONADOTROPIN ALPHA 2	5.78e-84
7	433	19.8	117	12	Q91119	GONADOTROPIN ALPHA 1	3.90e-80
8	334	15.3	55	10	O62589	GLYCOPROTEIN HORMONES	2.97e-55
9	249	11.4	277	2	O14866	ALPHA SUBUNIT OF GLYCO	1.12e-34
10	249	11.4	426	2	O14865	SOLUBLE DEATH RECEPTOR	1.12e-34
11	247	11.3	253	2	O00276	DEATH RECEPTOR 3 BETA.	3.31e-34
12	247	11.3	380	2	O00280	LYMPHOCYTE ASSOCIATED	3.31e-34
13	247	11.3	418	2	O00275	LYMPHOCYTE ASSOCIATED	3.31e-34
14	214	9.8	348	11	O85407	HOMOLOG OF VACCINIA VI	1.52e-26
15	214	9.8	349	11	O85118	SOMALIA-1977 RIGHT	1.52e-26
16	214	9.8	349	11	O89098	GARCIA-1966 RIGHT NEA	1.52e-26
17	210	9.6	355	11	O85308	SECRETED RECEPTOR BIND	1.24e-25
18	206	9.4	459	10	O62327	TUMOR NECROSIS FACTOR	1.00e-24
19	204	9.3	401	10	O08727	OSTEOPROTEGERIN.	2.84e-24
20	194	8.9	401	2	O00300	OSTEOPROTEGERIN.	5.02e-22
21	191	8.7	401	10	O08712	OSTEOPROTEGERIN.	2.34e-21
22	187	8.6	267	4	O02764	OX40 PRECURSOR (FRAGME	1.80e-20
23	181	8.3	324	10	O63199	FAS ANTIGEN PRECURSOR.	3.77e-19
24	181	8.3	411	2	O15517	CYTOTOXIC TRAIL RECEPT	3.77e-19
25	181	8.3	411	2	O15508	CYTOTOXIC TRAIL RECEPT	3.77e-19
26	181	8.3	411	2	O14720	P53-REGULATED DNA DAMA	3.77e-19
27	181	8.3	440	2	O15531	DEATH RECEPTOR 5.	3.77e-19
28	181	8.3	440	2	O14763	APOPTOSIS INDUCING PRO	3.77e-19
29	180	8.2	259	2	O14755	APOPTOSIS INDUCING REC	3.90e-19
30	180	8.2	283	2	O92956	TRAIL RECEPTOR 3.	6.24e-19
31	178	8.2	299	2	O92956	HERPESVIRUS ENTRY MEDI	6.24e-19
32	179	8.2	425	2	O16042	CYTOTOXIC TRAIL RECEPT	4.19e-11
33	173	7.9	625	10	O35305	TUMOR NECROSIS FACTOR	1.71e-18
34	167	7.7	202	2	O14405	RANK.	2.08e-17
35	167	7.7	217	2	O16631	SOMATOTROPIN PRECURSOR	4.07e-16
36	160	7.3	202	2	O14643	SOMATOTROPIN PRECURSOR	4.07e-16
37	160	7.3	245	2	O14644	PLACENTAL GROWTH HORMO	1.25e-14
38	159	7.3	468	2	O00220	PLACENTAL GROWTH HORMO	1.25e-14
39	154	7.1	199	2	O14406	CYTOTOXIC LIGAND TRAIL	2.04e-14
40	150	7.1	217	2	O14407	CHORIONIC SOMATOMAMMOT	2.28e-13
41	150	6.9	274	2	O13663	CHORIONIC SOMATOMAMMOT	1.41e-13
42	147	6.7	217	4	O07367	CHORIONIC SOMATOMAMMOT	5.39e-12
43	146	6.7	217	4	O07369	SOMATOTROPIN 1 PRECURS	1.54e-12
44	143	6.6	212	4	O07368	SOMATOTROPIN 2 PRECURS	4.19e-11
45	142	6.5	314	2	O14293	FAS SOLUBLE PROTEIN.	6.68e-11
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ALIGNMENTS

RESULT 1
ID   O19131   PRELIMINARY;   PRT;   471 AA.
AC   O19131;
DT   01-JAN-1998 (TREMBLREL. 05, CREATED)
DT   01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   TUMOR NECROSIS FACTOR-RECEPTOR I.
GN   TNF-RI.
OS   BOS TAURUS (BOVINE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; ARTIODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=AORTA;
RA   LEE E.-K., TALYOR M.J., KEHRLI M.E.;
RL   SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U90937; G2290398; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
SQ   SEQUENCE   471 AA; 51368 MW; 1D60FF4A CRC32;

Query Match   43.9%; Score 959; DB 4; Length 471;
Best Local Similarity   66.7%; Pred. No. 7.07e-219;
Matches   114; Conservative 28; Mismatches 28; Indels 1; Gaps 1;

Qy   41 ESPCPQGKYIHPQNSTICCTKCHKGTYLYNDCGPGRDTDCRVCAPGTYTALENHLRRCL 100
          :|.||||||.:|||||||||:|:||||||||:|||.|||||||||:|:|||||||:|:||
Db   41 ESPCPQGKYIHPQNSTICCTKCHKGTYLYNDCGPGRDTDCRVCAPGTYTALENHLRRCL 100

Qy   23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82
          :|.||||||.:|||.:||||||||:||||||||:|:||||.||:|:|||:|:|||||||:||
Db   101 SCSRCRDEMFQVEISPCVVDRDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQE 160

Qy   83 SCSKCRKEMGQVEISSCCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNGTVHLSCQE 142
          |||:||.|||||||:||||||||||||||||||:::||.|:|||||||||::||||:|||
Db   161 RQDTICHCMGFFLKGAKCICISCHDCKNK-ECEKLCPTRPSTGKDSQDPGTT 210

Qy   143 KQNTVCTCHAGFFLRENECVSCSNCKRSLECTKLSLPOIENVKGTEDSGTT 193
          ::|:|:||||::|||:|:||||:||||||:||||:|||:|||||:|||||

RESULT 2
ID   Q95185   PRELIMINARY;   PRT;   180 AA.
AC   Q95185;
DT   01-FEB-1997 (TREMBLREL. 02, CREATED)
DT   01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)

DT   01-JAN-1998 (TREMBLREL, 05, LAST ANNOTATION UPDATE)
DE   TUMOUR NECROSIS FACTOR RECEPTOR P60 (FRAGMENT).
GN   TNFR-1.
OS   FELIS SILVESTRIS CATUS (CAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; CARNIVORA.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   DUTHIE S., NASIR L., ECKERSALL P.D.;
RL   SUBMITTED (OCT-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U72344; G1613880; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
FT   NON_TER   180   180
SQ   SEQUENCE   180 AA;   20399 MW;   2O399A6B2 CRC32;

Query Match   43.2%; Score 943; DB 4; Length 180;
Best Local Similarity   85.3%;   Pred. No. 1.42e-214;
Matches 116; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

Qy   45 CPQGKYIHPQDNSICCTKCHRGYTYLYNDCAGPGLDTDCRECENGTFTASENYLRQCLSCS 104
         |||||||||| ||||||||||| ||||||||| ||| |||||||||||||| |||| ||||
Db   26 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGGDTDCRECESGSFTASENHLRHCLSCS   85

Qy 105 KCRKEMYQVEISPCTVYRDTVCGGCRKNQYRYWSETHFQCLNCSLCLNGTVQISCKETQN 164
         ||||||||||| |||| ||||||||||||||| |||| || || |||||||| | | |
Db   86 KCRKEMYQVEISSCTVRDTVCGGCRKNQYRHVWSENLFQCFNCTLCLNGTVHLSCQEKQN 145

Qy 165 TVCTCHAGFFLRGNEC   180
         |||||||||||| ||
Db 146 TVCTCHAGFFLRENEC   161

RESULT 3
ID   Q90286   PRELIMINARY;   PRT;   107 AA.
AC   Q90286;
DT   01-NOV-1996 (TREMBLREL, 01, CREATED)
DT   01-NOV-1996 (TREMBLREL, 01, LAST SEQUENCE UPDATE)
DT   01-NOV-1996 (TREMBLREL, 01, LAST ANNOTATION UPDATE)
DE   GONADOTROPIN ALPHA SUBUNIT (FRAGMENT).
OS   CARASSIUS AURATUS (GOLDFISH).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OC   OSTEICHTHYES; ACTINOPTERYGII; CYPRINIFORMES.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   KOBAYASHI M., KATO Y., YOSHIURA Y., AIDA K.;
RL   SUBMITTED (AUG-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; D86551; G1469836; -.
FT   NON_TER   1   1
SQ   SEQUENCE   107 AA;   11959 MW;   880C6840 CRC32;

Query Match   20.8%; Score 453; DB 12; Length 107;
Best Local Similarity   72.0%;   Pred. No. 3.04e-85;
Matches 59; Conservative 7; Mismatches 15; Indels 1; Gaps 1;

Qy 199 GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVPKNITSEATCCVAKEV   258
         | ||| ||||| || ||| |||| |||||||||||||||||||||||| | ||||
Db   27 GCEECKLKENNIFSKPGAPVYQCMGCCFSRAYPTPLRSKKTMLVPKNITSEATCCVAKEV   86

Qy 259 NRVTVMGGFKVENHTACHCSTC   280
         ||||| ||| |||| ||||
Db   87 KRVLV-NDVRLVNHTDCHCSTC   107

DE   GONADOTROPIN ALPHA SUBUNIT (FRAGMENT).
OS   CARASSIUS AURATUS (GOLDFISH).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OC   OSTEICHTHYES; ACTINOPTERYGII; CYPRINIFORMES.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   KOBAYASHI M., KATO Y., YOSHIURA Y., AIDA K.;
RL   SUBMITTED (AUG-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
FT   EMBL; D86552; G1469838; -.
FT   NON_TER   1   1
SQ   SEQUENCE   108 AA;   12129 MW;   B2B1A212 CRC32;

RESULT 5
ID   Q91370   PRELIMINARY;   PRT;   119 AA.
AC   Q91370;
DT   01-NOV-1996 (TREMBLREL, 01, CREATED)
DT   01-NOV-1996 (TREMBLREL, 01, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL, 05, LAST ANNOTATION UPDATE)
DE   GONADOTROPHIN ALPHA 1 SUBUNIT.
OS   ONCORHYNCHUS MASOU (CHERRY SALMON) (MASU SALMON).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OC   OSTEICHTHYES; ACTINOPTERYGII; SALMONIFORMES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 94197892.
RA   GEN K., MARUYAMA O., KATO T., TOMIZAWA K., WAKABAYASHI K., KATO Y.;
RL   J. MOL. ENDOCRINOL. 11:265-273(1993).
DR   EMBL; S69273; G546258; -.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
SQ   SEQUENCE   119 AA;   13131 MW;   2EEF28F4 CRC32;

Query Match   20.8%; Score 454; DB 12; Length 108;
Best Local Similarity   72.0%;   Pred. No. 1.68e-85;
Matches 59; Conservative 7; Mismatches 15; Indels 1; Gaps 1;

Qy 199 GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVPKNITSEATCCVAKEV   258
         | ||| ||||| || ||| |||| |||||||||||||||||||||||| | ||||
Db   28 GCEECKLKENNIFSKPGAPVYQCMGCCFSRAYPTPLRSKKTMLVPKNITSEATCCVAKEV   87

Qy 259 NRVTVMGGFKVENHTACHCSTC   280
         ||||| ||| |||| ||||
Db   88 KRVLV-DDVKLVNHTDCHCSTC   108

Query Match   20.7%; Score 452; DB 12; Length 119;
Best Local Similarity   67.8%;   Pred. No. 5.48e-85;
Matches 59; Conservative 11; Mismatches 16; Indels 1; Gaps 1;

Qy 199 GCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLQSKRAMLVPKNITSEATCCVAKEG   258
         | || ||||| || ||| |||| ||||||||||| || ||||||||||||||||
Db   34 GCEECKLKENKLFSNPGAPVYQCTGCCFSRAYPTPLRSKKTMLVPKNITSEATCCVAKEG   93

Qy 259 NRVTVMGGFKVENHTACHCSTCYHKS   285
         ||||| ||| |||| ||||||||
Db   94 ERV-VVDNIKLTNHTECWCNTCYHHKS 119

RESULT 6
ID   Q91371   PRELIMINARY;   PRT;   114 AA.
AC   Q91371;
DT   01-NOV-1996 (TREMBLREL, 01, CREATED)
DT   01-NOV-1996 (TREMBLREL, 01, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL, 05, LAST ANNOTATION UPDATE)
DE   GONADOTROPHIN ALPHA 2 SUBUNIT.
OS   ONCORHYNCHUS MASOU (CHERRY SALMON) (MASU SALMON).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OC   OSTEICHTHYES; ACTINOPTERYGII; SALMONIFORMES.
RN   [1]
RP   SEQUENCE FROM N.A.

RESULT 4
ID   Q90287   PRELIMINARY;   PRT;   108 AA.
AC   Q90287;
DT   01-NOV-1996 (TREMBLREL, 01, CREATED)
DT   01-NOV-1996 (TREMBLREL, 01, LAST SEQUENCE UPDATE)
DT   01-NOV-1996 (TREMBLREL, 01, LAST ANNOTATION UPDATE)

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RX   MEDLINE; 94197892.
RA   GEN K., MARUYAMA O., KATO T., TOMIZAWA K., WAKABAYASHI K., KATO Y.;
RL   J. MOL. ENDOCRINOL. 11:265-273(1993).
DR   EMBL; S69274; G546260; -.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
SQ   SEQUENCE   114 AA;  12519 MW;  473D3C83 CRC32;

Query Match             58.3%;  Score  448;  DB 12;  Length 114;
Best Local Similarity   58.3%;  Pred. No. 5.78e-84;
  Matches   67;  Conservative  11;  Mismatches  33;  Indels   4;  Gaps   2;

Db      4 LKSTGSLILSALLVIADSYPNSDKINMGCEECTLKPNTIF--PN--IIQCTGCCFSRAY 59
            |  |||   :  ::          ||  |||||      |  :  |  | ||||||
Qy    171 LECTKLSLPQIENVKGTEDSGGTAGAAPGCPECTLQENPFFSQPGAPILQCMGCCFSRAY 230

Db     60 PTPLRSKQTMLVPKNITSEATCCVAKEGERVTTKDGFPVTNHTECHCSTCYYHKS 114
          ||||||:||| ||||||||||||||  ::||||||| ||  | |||||||||||||
Qy    231 PTPLRSKKTMLVQKNVTSESTCCVAKSYNRVTVMGGFKVENHTACHCSTCYYHKS 285
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RESULT 7
ID   Q91119   PRELIMINARY;   PRT;   117 AA.
AC   Q91119;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (GONADOTROPIN ALPHA
DE   CHAIN) (GTH-ALPHA).
OS   MORONE SAXATILIS (STRIPED BASS).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OC   OSTEICHTHYES; ACTINOPTERYGII; PERCIFORMES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PITUITARY GLAND;
RX   MEDLINE; 96020549.
RA   HASSIN S., ELIZUR A., ZOHAR Y.;
RL   J. MOL. ENDOCRINOL. 15:23-35(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PITUITARY GLAND;
RA   HASSIN S.;
RL   SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC   -!- FUNCTION: INVOLVED IN GAMETOGENESIS AND STEROIDOGENSIS (BY
CC       SIMILARITY).
CC   -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN (BY SIMILARITY).
DR   EMBL; L35071; G2322657; -.
DR   PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR   PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL        1     23       BY SIMILARITY.
FT   CHAIN        24    117       GLYCOPROTEIN HORMONES ALPHA CHAIN.
FT   DISULFID     34     57       BY SIMILARITY.
FT   DISULFID     37     86       BY SIMILARITY.
FT   DISULFID     54    107       BY SIMILARITY.
FT   DISULFID     58    109       BY SIMILARITY.
FT   DISULFID     85    112       BY SIMILARITY.
FT   CARBOHYD     78     78       POTENTIAL.
FT   CARBOHYD    103    103       POTENTIAL.
SQ   SEQUENCE   117 AA;  13066 MW;  CAFB9D0C CRC32;

Query Match             65.58%;  Score  433;  DB 12;  Length 117;
Best Local Similarity   65.58%;  Pred. No. 3.90e-80;
  Matches   57;  Conservative  14;  Mismatches  12;  Indels   4;  Gaps   4;

Db     33 GCEECTLRKNSVFSR-DRPVYQCMGCCFSRAYPTPLKAMKTMTIPKNITSEATCCVAKHS 91
          || :|||::| ::|    |:||||||||||||||| :: |:||:|:||:||:||||||:
Qy    199 GCPECTLQENPFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAK-S 257

Db     92 YE-TEV-AGIKVRNHTDCHCSTCYFHK 116
          |  |:|  ||:|.||| ||||||||:||
Qy    258 YNRVTVMGGFKVENHTACHCSTCYYHK 284
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RESULT 8
ID   Q62589   PRELIMINARY;   PRT;   55 AA.
AC   Q62589;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   ALPHA SUBUNIT OF GLYCOPROTEIN HORMONES (FRAGMENT).
OS   PHODOPUS SUNGORUS (STRIPED HAIRY-FOOTED HAMSTER) (DJUNGARIAN HAMSTER).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PITUITARY;
RX   MEDLINE; 96198779.
RA   BOCKMANN J., BOCKERS T.M., VENNEMANN B., NIKLOWITZ P., MÜLLER J.,
RA   WITTKOWSKI W., SABEL B., KREUTZ M.R.;
RL   ENDOCRINOLOGY 13?:1804-1813(1996).
DR   EMBL; X90776; E195654; -.
FT   NON_TER       1      1
SQ   SEQUENCE   55 AA;  6047 MW;  E5AAE0F8 CRC32;

Query Match             76.4%;  Score  334;  DB 10;  Length 55;
Best Local Similarity   76.4%;  Pred. No. 2.97e-55;
  Matches   42;  Conservative   6;  Mismatches   7;  Indels   0;  Gaps   0;

Db      1 PTPARSKKTMLVPKNITSEATCCVAKAFTKATVMGNARVENHTECHCSTCYYHKS 55
          ||| ||||||||:||:||:|||||||::   ||:||| .||||||:||||||||||
Qy    231 PTPLRSKKTMLVQKNVTSESTCCVAKSYNRVTVMGGFKVENHTACHCSTCYYHKS 285
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RESULT 9
ID   O14866   PRELIMINARY;   PRT;   277 AA.
AC   O14866;
DT   01-JAN-1998 (TREMBLREL. 05, CREATED)
DT   01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   SOLUBLE DEATH RECEPTOR 3 BETA.
GN   DR3.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   WARZOCHA K., RIBEIRO P., RENARD N., CHARLOT C., COIFFIER B.,
RA   SALLES G.;
RL   SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; AF026071; G2570833; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
SQ   SEQUENCE   277 AA;  29111 MW;  06E165C7 CRC32;

Query Match             31.8%;  Score  249;  DB 2;  Length 277;
Best Local Similarity   31.8%;  Pred. No. 1.12e-34;
  Matches   57;  Conservative  31;  Mismatches  76;  Indels  15;  Gaps  11;

Db      3 TSLLLAFGLLCLPWLQEGSADSVCP-QSKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDT 61
           : ||   .||.   :  |:|  | |  : :| ||:|.|| :| ::|.|| : |||| | |
Qy     13 AALLLIV--LLG-ARAQGGTRSPRCDCAGDF-HKKIGLFCCRCCPAGHYLKAPCTEPCGNS 68

Db     62 DCRECESGGSFTASENHLR-HCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYW-S 119
          .|  | .  :|  :|||:   ||.|| || :   |||::| || |.|||| |::|  | :
Qy     69 TCLVCPQDTFLAWENHHNSECARCQACDEQASGVALENCSAVADTRGCGCKPGNFVECQVS 128

Db    120 ENLFQC-FNCTLCLN-GTVH----LSCQEKONTVC-TCHAGFFLRENECVSCSNCKKSL 171
          : :: | |.|.||:   |.:    | | .    ||  || .|:  .. |||| |   .||
Qy    129 QCVSSSPFYCQPCLDCGALHRTHRLLC-SRRDTDCGTCLPGFYEHGDGCVSCPTPPSL 186
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RESULT 10
ID   O14865   PRELIMINARY;   PRT;   426 AA.
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AC   O14865;
DT   01-JAN-1998 (TREMBLREL. 05, CREATED)
DT   01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   DEATH RECEPTOR 3 BETA.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   WARZOCHA K., RIBEIRO P., RENARD N., CHARLOT C., COIFFIER B.,
RA   SALLES G.;
RL   SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; AF026070; G2570831; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
SQ   SEQUENCE   426 AA;  45950 MW;  87E00821 CRC32;

Query Match             11.4%;  Score 249;  DB 2;  Length 426;
Best Local Similarity   31.8%;  Pred. No. 1.1e-34;
  Matches   57;  Conservative   57;  Mismatches   76;  Indels  15;  Gaps  11;

Qy   13 AALLLV--LLG-ARAQGGTRSPRCDCAGDF-HKKIGLFCCRGCRGCPAGHYLKAPCTEPCGNS 68
          ::|||  ||| |||| :: ::|||:|||||  :|||||||:||||||||| :::|| ::
Db    3 TSLLLAFGLLCLPWLQEGSADSVCP-QGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDT 61

Qy   69 TCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVS 128
          ||| ||| :||| ||| :| ||| ::| || :|| :||:||||||||||||:|| |:|
Db   62 DCRECESGSFTASENHLR-HCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYW-S 119

Qy  120 ENLFQC-FNCTLCLN-GTVH-----LSCQEKQNTVC-TCHAGFFLRENECVSCSNCKKSL 171
         |||:| |: : ||| |:|:      | ||:|| |: ||||| ||| |||||
Db  129 QCVSSSPFYCQPCLDCGALHRHTRLLC-SRRDTDCGTCLPGFYEHGDGCVSCPTPPPSL 186
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RESULT 11
ID   O00276    PRELIMINARY;  PRT;   253 AA.

AC   O00276;
DT   01-JUL-1997 (TREMBLREL. 04, CREATED)
DT   01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 2.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   SCREATON G., XU X.N., OLSEN A., COWPER A., TAN R., MCMICHAEL A.,
RA   BELL J.;
RL   SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U94503; G2071953; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
SQ   SEQUENCE   253 AA;  26934 MW;  A21C863E CRC32;

Query Match             31.8%;  Score 247;  DB 2;  Length 253;
Best Local Similarity   31.8%;  Pred. No. 3.31e-34;
  Matches   55;  Conservative   31;  Mismatches   72;  Indels  15;  Gaps  11;

Qy   13 AALLLV--LLG-ARAQGGTRSPRCDCAGDF-HKKIGLFCCRGCRGCPAGHYLKAPCTEPCGNS 68
          ::|||  ||| |||| :: ::|||:|||||  :|||||||:||||||||| :::|| ::
Db    3 TSLLLAFGLLCLPWLQEGSADSVCP-QGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDT 61

Qy   69 TCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVS 128
          ||| ||| :||| ||| :| ||| ::| || :|| :||:||||||||||||:|| |:|
Db   62 DCRECESGSFTASENHLR-HCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYW-S 119

Qy  120 ENLFQC-FNCTLCLN-GTVH-----LSCQEKQNTVC-TCHAGFFLRENECVSCS 165
         |||:| |: : ||| |:|:      | ||:|| |: ||||| ||| |||||
Db  129 QCVSSSPFYCQPCLDCGALHRHTRLLC-SRRDTDCGTCLPGFYEHGDGCVSCP 180
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RESULT 12
ID   O00280    PRELIMINARY;  PRT;   380 AA.

AC   O00280;
DT   01-JUL-1997 (TREMBLREL. 04, CREATED)
DT   01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 9.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   SCREATON G., XU X.N., OLSEN A., COWPER A., TAN R., MCMICHAEL A.,
RA   BELL J.;
RL   SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U94510; G2071967; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
SQ   SEQUENCE   380 AA;  41192 MW;  17C92A14 CRC32;

Query Match             31.8%;  Score 247;  DB 2;  Length 380;
Best Local Similarity   31.8%;  Pred. No. 3.31e-34;
  Matches   55;  Conservative   31;  Mismatches   72;  Indels  15;  Gaps  11;

Qy   13 AALLLV--LLG-ARAQGGTRSPRCDCAGDF-HKKIGLFCCRGCRGCPAGHYLKAPCTEPCGNS 68
          ::|||  ||| |||| :: ::|||:|||||  :|||||||:||||||||| :::|| ::
Db    3 TSLLLAFGLLCLPWLQEGSADSVCP-QGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDT 61

Qy   69 TCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVS 128
          ||| ||| :||| ||| :| ||| ::| || :|| :||:||||||||||||:|| |:|
Db   62 DCRECESGSFTASENHLR-HCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYW-S 119

Qy  120 ENLFQC-FNCTLCLN-GTVH-----LSCQEKQNTVC-TCHAGFFLRENECVSCS 165
         |||:| |: : ||| |:|:      | ||:|| |: ||||| ||| |||||
Db  129 QCVSSSPFYCQPCLDCGALHRHTRLLC-SRRDTDCGTCLPGFYEHGDGCVSCP 180
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RESULT 13
ID   O00275    PRELIMINARY;  PRT;   418 AA.

AC   O00275;
DT   01-JUL-1997 (TREMBLREL. 04, CREATED)
DT   01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 1B.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   SCREATON G., XU X.N., OLSEN A., COWPER A., TAN R., MCMICHAEL A.,
RA   BELL J.;
RL   SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U94502; G2071951; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
SQ   SEQUENCE   418 AA;  45456 MW;  3D04954A CRC32;

Query Match             31.8%;  Score 247;  DB 2;  Length 418;
Best Local Similarity   31.8%;  Pred. No. 3.31e-34;
  Matches   55;  Conservative   31;  Mismatches   72;  Indels  15;  Gaps  11;

Qy   13 AALLLV--LLG-ARAQGGTRSPRCDCAGDF-HKKIGLFCCRGCRGCPAGHYLKAPCTEPCGNS 68
          ::|||  ||| |||| :: ::|||:|||||  :|||||||:||||||||| :::|| ::
Db    3 TSLLLAFGLLCLPWLQEGSADSVCP-QGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDT 61

Qy   69 TCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVS 128
          ||| ||| :||| ||| :| ||| ::| || :|| :||:||||||||||||:|| |:|
Db   62 DCRECESGSFTASENHLR-HCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYW-S 119

Qy  120 ENLFQC-FNCTLCLN-GTVH-----LSCQEKQNTVC-TCHAGFFLRENECVSCS 165
         |||:| |: : ||| |:|:      | ||:|| |: ||||| ||| |||||
Db  129 QCVSSSPFYCQPCLDCGALHRHTRLLC-SRRDTDCGTCLPGFYEHGDGCVSCP 180
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RESULT  14
ID      Q85407              PRELIMINARY;    PRT;    348 AA.
AC      Q85407;
DT      01-NOV-1996 (TREMBLREL. 01, CREATED)
DT      01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT      01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE      HOMOLOG OF VACCINIA VIRUS CDS B28R.
GN      G2R.
OS      VARIOLA VIRUS.
OC      VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPOXVIRINAE;
OC      ORTHOPOXVIRUSES.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=BANGLADESH-1975;
RX      MEDLINE; 94088747.
RA      MASSUNG R.F., ESPOSITO J.J., LIU L.I., QI J., UTTERBACK T.R.,
RA      KNIGHT J.C., AUBIN L., YURAN T.E., PARSONS J.M., LOPAREV V.N.;
RL      NATURE 366:748-751(1993).
DR      EMBL; L22579; G439102; -.
DR      PROSITE; PS00652; TNFR_NGFR_1; 2.
SQ      SEQUENCE   348 AA;  38075 MW;  2A91IAF6 CRC32;

Query Match           9.8%;    Score 214;   DB 11;   Length 348;
Best Local Similarity  38.5%;    Pred. No. 1.52e-26;
Matches   30;  Conservative  14;  Mismatches  32;  Indels  2;  Gaps  2;

Db     39 HNLCCLSCPPGTIYASRLCDSKI-NTQCTPCGSGTFTSRNNHLPACLSCNG-RCNSNQVET 96
           :::||:| ||   ||||   |||| | ||| ||:||:: :||| :||||  : |||  |||
Qy     37 NSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEI 96

Db     97 RSCNTTHNRICECSPGYY 114
          ||   :|| | |
Qy     97 SSCTVDRDTVCGCRKNQY 114


RESULT  15
ID      Q89118              PRELIMINARY;    PRT;    349 AA.
AC      Q89118;
DT      01-NOV-1996 (TREMBLREL. 01, CREATED)
DT      01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT      01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE      SOMALIA-1977 RIGHT NEAR-TERMINAL REGION.
OS      VARIOLA VIRUS.
OC      VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPOXVIRINAE;
OC      ORTHOPOXVIRUSES.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=SOMALIA-1977;
RA      MASSUNG R.F., LOPAREV V.N., KNIGHT J.C., CHIZHIKOV V.E., PARSONS J.M.,
RA      TOTMENIN A.V., SHCHELKUNOV S.N., ESPOSITO J.J.;
RL      SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR      EMBL; U18341; G885855; -.
DR      PROSITE; PS00652; TNFR_NGFR_1; 2.
SQ      SEQUENCE   349 AA;  38272 MW;  0FDCC784 CRC32;

Query Match           9.8%;    Score 214;   DB 11;   Length 349;
Best Local Similarity  38.5%;    Pred. No. 1.52e-26;
Matches   30;  Conservative  14;  Mismatches  32;  Indels  2;  Gaps  2;

Db     40 HNLCCLSCPPGTIYASRLCDSKT-NTQCTPCGSGTFTSRNNHLPACLSCNG-RCNSNQVET 97
           :::||:| ||   ||||   |||: | ||| ||:||:: :||| :||||  : |||  |||
Qy     37 NSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEI 96

Db     98 RSCNTTHNRICECSPGYY 115
          ||   :|| | |
Qy     97 SSCTVDRDTVCGCRKNQY 114
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Search completed: Wed May 6 09:00:25 1998
Job time : 72 secs.

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**         M P S R C H  (TM)             **
**                                       **
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MPsrch_nn   n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed May 6 14:22:01 1998;   MasPar time 1326.51 Seconds
                                              1499.916 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-7
Description: (1-1301) from US08804166.seq
Perfect Score: 1301
N.A. Sequence: 1   CTCGAGATGGCCTACAGGTAA.................CACAATAAGGATCCCTCGAG 1301
Comp: GAGCTCTACCGGATGTCCATT.................GTGTTATTCCTAGGAGAGCTC

Scoring table: TABLE default
                  Gap 6

Nmatch STD :   Dbase 0: Query 0

Searched: 436399 seqs, 764661465 bases x 2

Post-processing: Minimum Match 0&
                  Listing first 45 summaries

Database: embl53
                  1:em_in 2:em_om 3:em_ov 4:em_ov 5:em_p1 6:em_htg
                  7:em_hum1 8:em_hum2 9:em_ba 10:em_ro 11:em_un 12:em_vi
                  13:em_pat

Database: genbank105
                  14:gb_om 15:gb_ov 16:gb_ov 17:gb_in 18:gb_p1 19:gb_ba
                  20:gb_st 21:gb_v1 22:gb_ph 23:gb_sy 24:gb_un 25:gb_pat
                  26:gb_htg 27:gb_pr1 28:gb_pr2

Statistics: Mean 11.236; Variance 5.267; scale 2.134

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES

Result   %
No.   Score Query   Length DB ID   Description   Pred. No.
            Match   DB
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  1   514   39.5   1331   25 A29103   H.sapiens mRNA for TNF   0.00e+00
  2   514   39.5   1368   25 A29099   Synthetic DNA for TNF-   0.00e+00
  3   514   39.5   1350   27 A21525   Human tumor necrosis f   0.00e+00
  4   514   39.5   2050   27 HUMTNFRP Human tumor necrosis f   0.00e+00
  5   514   39.5   2062   25 A21522   TNF alpha gene.   0.00e+00
  6   514   39.5   2062   25 143805   Sequence 24 from paten   0.00e+00
  7   514   39.5   2087   27 HUMTNFR   Human tumor necrosis f   0.00e+00
  8   514   39.5   2111   27 A26412   cDNA for (55kD TNF-BP)   0.00e+00
  9   514   39.5   2112   27 HUMTNFRB Homo sapiens tumor nec   0.00e+00
 10   514   39.5   2111   27 HUMTNFRC Human tumor necrosis f   0.00e+00
 11   514   39.5   2161   27 HSTNFR1A H.sapiens TNF-R mRNA f   0.00e+00
 12   514   39.5   2175   25 A43873   Sequence 1 from patent   0.00e+00
 13   514   39.5   2176   25 164751   Sequence 1 from patent   0.00e+00
 14   514   39.5   6889   25 A19907   Synthetic nucleotide s   0.00e+00
 15   507   39.0   2061   25 A20255   Synthetic nucleotide s   0.00e+00
 16   483   37.1   483   25 A29099   55kD receptor gene for   0.00e+00
 17   483   37.1   510   25 A21525   Synthetic DNA for TNF-   0.00e+00
 18   478   36.7   600   25 A20257   oligonucleotide probe.   0.00e+00
 19   474   36.4   600   25 143808   Synthetic nucleotide s   0.00e+00
 20   420   32.3   539   27 HUMCGB   Synthetic nucleotide s   2.83e-242
 21   383   29.4   504   25 143813   Human chorionic gonado   2.71e-259
 22   383   29.4   504   25 A20713   Sequence 56 from paten   0.00e+00
 23   381   29.3   501   25 143786   Human chorionic gonado   0.00e+00
 24   374   28.7   500   25 A20254   Sequence 1 from patent   0.00e+00
 25   372   28.6   372   25 A20253   Synthetic nucleotide 5   5.19e-295
 26   372   28.6   372   25 143787   Sequence 3 from patent   3.19e-295
 27   354   27.2   474   25 A20259   Synthetic nucleotide s   4.88e-279
 28   354   27.2   474   25 143809   Sequence 49 from paten   4.88e-279
 29   336   25.8   642   27 BABBCGA   Baboon beta-chorionic   7.02e-263
 30   332   25.5   332   25 HUMGHCSA Human growth hormone (2.71e-259
 31   313   24.1   581   15 FCU72344 Felis catus tumour nec   2.83e-242
 32   314   24.1   1665   27 HSGG02   Human chorionic gonado   3.60e-243
 33   312   24.0   468   27 HUMCGBBA3 Human chorionic gonado   2.22e-241
 34   312   24.0   475   27 HUMCGBEL03 Human chorionic gonado 2.22e-241
 35   312   24.0   1665   27 HSCG01   Human chorionic gonado   2.22e-241
 36   307   23.6   2004   15 SSU19994 Sus scrofa p55 TNF rec   6.58e-237
 37   305   23.4   1826   25 I02855   Sequence 1 from patent   1.04e-235
 38   304   23.4   1964   27 HSGROW2   Human germ line gene f   4.16e-234
 39   304   23.4   1964   27 HDMGH   Human growth hormone (3.16e-234
 40   304   23.4   2771   25 I41411   Human growth hormone 9   3.16e-234
 41   303   23.3   2657   27 HUMGHN   Human growth hormone 9   2.48e-233
 42   303   23.3   4283   25 I63120   Sequence 3 from patent   2.48e-233
 43   285   21.9   426   25 I08477   Sequence 18 from patent 2.90e-217
 44   267   20.5   2130   14 RATTNFR   Rat tumor necrosis fac   3.10e-201
 45   257   19.8   477   25 A20263   Synthetic nucleotide s   2.38e-192
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                              ALIGNMENTS

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RESULT      1
LOCUS       A29103              1331 bp    DNA                PAT        03-JUL-1995
DEFINITION  H.sapiens mRNA for TNF-binding polypeptide from patent EP0393438.
ACCESSION   A29103
NID         g1247517
KEYWORDS    .
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1331)
AUTHORS     Hauptmann,R., Himmler,A., Maurer-Fogy,I. and Stratowa,C.
TITLE       TNF-receptor, TNF-binding protein and DNA coding therefor
JOURNAL     Patent: EP 0393438-A 53 24-OCT-1990;
            BOEHRINGER INGELHEIM INTERNATIONAL G.M.B.H
FEATURES             Location/Qualifiers
     source          1..1331
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      298 a    407 c    343 g    283 t
ORIGIN

Query Match            39.5%;  Score 514;  DB 25;  Length 1331;
Best Local Similarity 100.0%;
Matches   514;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy   345 GATAGTGTGTGTGTCCCCAAGGAGAAAAATATATCCACCCTCAAGAAAATAATTCGAATTGCGTACC 404
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Db   345 GATAGTGTGTGTGTCCCCAAGGAGAAAAATATATCCACCCTCAAGAAAATAATTCGAATTGCGTACC 404

Qy   393 AAGTGCCACAAAAGGAACCTACTTGTTACAATGACTGTCCAGCGCCGGGGCCAGGATACGGAC 452
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   393 AAGTGCCACAAAAGGAACCTACTTGTTACAATGACTGTCCAGCGCCGGGGCCAGGATACGGAC 452

Qy   405 AAGTGCCACAAAAGGAACCTACTTGTTACAATGACTGTCCAGCGCCGGGGCCAGGATACGGAC 464
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   453 AAGTGCCACAAAAGGAACCTACTTGTTACAATGACTGTCCAGCGCCGGGGCCAGGATACGGAC 512

Qy   465 TGCAGGGAGTGTGAGAGCGGCGTCTTCACCGCCTTCAGAAAAACCACCTCAGACACTCGGAC 524
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   453 TGCAGGGAGTGTGAGAGCGGCGTCTTCACCGCCTTCAGAAAAACCACCTCAGACACTCGGAC 512
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Db 513 AGCTGCTTCCAAATGCCGAAAGGAAAGGGTCAGGTGGAGATCTCTTCTTCTTGCACAGTGGGAC 572
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Qy 525 AGCTGCTTCCAAATGCCGAAAGGAAAGGGTCAGGTGGAGATCTCTTCTTCTTGCACAGTGGGAC 584

Db 573 CGGGACACCGTGTGTGGGCTGCGGAGGAAGAACCAGTACCGGGCCATTATTGGAGTGAAAACCTT 632
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 585 CGGGACACCGTGTGTGGGCTGCGGAGGAAGAACCAGTACCGGGCCATTATTGGAGTGAAAACCTT 644

Db 633 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCCTCCCAATGGGACCAGTACCGGGCACTGTCCAGGAG 692
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCCTCCCAATGGGACCAGTACCGGGCACTGTCCAGGAG 704

Db 693 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTTCTTAAGAGAAAACGAGTGTGTC 752
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Qy 705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTTCTTAAGAGAAAACGAGTGTGTC 764

Db 753 TCCTGTAGTAACTGTAAGAAAGCCTGGAGTGCACGAAGTGTTGCCTACCCCAGATTGAG 812
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Qy 765 TCCTGTAGTAACTGTAAGAAAGCCTGGAGTGCACGAAGTGTTGCCTACCCCAGATTGAG 824

Db 813 AATGTTAAGGGCCACTGAGGACTCAGGCACCACACAG 846
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Qy 825 AATGTTAAGGGCCACTGAGGACTCAGGCACCACACAG 858

RESULT 2

LOCUS   A29098   1368 bp   DNA   PAT   03-JUL-1995
DEFINITION Synthetic DNA for TNF-receptor from patent EP0393438.
ACCESSION   A29098
NID   g1248892
KEYWORDS   .
SOURCE   unidentified.
  ORGANISM unidentified
            unclassified.
REFERENCE   1 (bases 1 to 1368)
  AUTHORS   Hauptmann,R., Himmler,A., Maurer-Fogy,I. and Stratowa,C.
  TITLE   TNF-receptor, TNF-binding protein and DNA coding therefor
  JOURNAL   Patent: EP 0393438-A 48 24-OCT-1990;
            BOEHRINGER INGELHEIM INTERNATIONAL G.M.B.H
FEATURES   Location/Qualifiers
     source   1..1368
                     /organism="unidentified"
                     /db_xref="taxon:32644"
     source   1..1368
                     /organism="artificial sequence"
                     /db_xref="taxon:29278"
BASE COUNT   293 a   424 c   375 g   276 t
ORIGIN

Query Match   39.5%; Score 514; DB 25; Length 1368;
Best Local Similarity 100.0%;
Matches 514; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy 121 GATAGTGTGTGTCCCCAAGGAAAGAAAATATATCCACCCTCAAAATAATTGATTTGCTGTACC 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 345 GATAGTGTGTGTCCCCAAGGAAAAATATATCCACCCTCAAAAATAATTGATTTGCTGTACC 404

Qy 181 AAGTGCCACAAAAGGAACCTACTTGTTACAATGACTGTCCAGCGCCCGGGGCAGGATACGGAC 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 405 AAGTGCCACAAAAGGAACCTACTTGTTACAATGACTGTCCAGCGCCCGGGGCAGGATACGGAC 464

Qy 241 TGCAGGGAGTGTGAGGAGAGCGGCGGCCTCCTTCCTTCAGGAAAAACCACCTCAACACTGCCTC 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 465 TGCAGGGAGTGTGAGGAGAGCGGCGGCCTCCTTCCTTCAGGAAAAACCACCTCAACACTGCCTC 524

Qy 301 AGCTGCTGTCCAAATGCCGAAAATGGGGTCAGGTGGAGATCTCTTCTTCTTCACGGTGGGAC 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 525 AGCTGCTGTCCAAATGCCGAAAATGGGGTCAGGTGGAGATCTCTTCTTCTTCACGGTGGGAC 584

Db 361 CGGGACACCGTGTGTGGGCTGCGGAGGAAGAACCAGTACCGGGCCATTATTGGAGTGAAAACCTT 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 585 CGGGACACCGTGTGTGGGCTGCGGAGGAAGAACCAGTACCGGGCCATTATTGGAGTGAAAACCTT 644
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 421 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCCTCCCAATGGGAC 480

Qy 645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCCTCCCAATGGGAC 704
         |||||||||||||||||||||||||||||||||||||||||||
Db 481 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTTCTTAAGAGAAAACGAGTGTGTC 540

Qy 705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTTCTTAAGAGAAAACGAGTGTGTC 764
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 541 TCCTGTAGTAACTGTAAGAAAGCCTGGAGTGCACGAAGTGTTGCCTACCCCAGATTGAG 600

Qy 765 TCCTGTAGTAACTGTAAGAAAGCCTGGAGTGCACGAAGTGTTGCCTACCCCAGATTGAG 824
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 601 AATGTTAAGGGCCACTGAGGACTCAGGCACCACACAG 634

Qy 825 AATGTTAAGGGCCACTGAGGACTCAGGCACCACACAG 858
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RESULT 3

LOCUS   HUMTNFRP   2050 bp   mRNA   PRI   11-OCT-1991
DEFINITION Human tumor necrosis factor receptor (TNF) mRNA, complete cds.
ACCESSION   M60275 M37764
NID   g339759
KEYWORDS   TNF receptor; transmembrane receptor; tumor necrosis factor
            receptor.
SOURCE   Human placenta, cDNA to mRNA.
  ORGANISM Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 2050)
  AUTHORS   Gray,P.W., Barrett,R.J., Chantry,D., Turner,M. and Feldman,M.
  TITLE   Cloning of human tumor necrosis factor (TNF) receptor cDNA and
            expression of recombinant soluble TNF-binding protein
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384 (1990)
  MEDLINE   91017509
COMMENT   Draft entry and computer-readable sequence for [Proc. Natl. Acad.
            Sci. U.S.A. (1990) In press] kindly submitted
            by P.W.Gray, 13-AUG-1990.
FEATURES   Location/Qualifiers
     source   1..2050
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BASE COUNT   429 a   611 c   566 g   444 t
ORIGIN

Query Match   39.5%; Score 514; DB 27; Length 2050;
Best Local Similarity 100.0%;
Matches 514; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db 275 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 334
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RESULT 4

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LOCUS       A21522    2062 bp    RNA    PAT    26-JUL-1994
DEFINITION  TNF alpha gene.
ACCESSION   A21522
NID         g579599
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2062)
  AUTHORS   .
  JOURNAL   Patent: GB 2246569-A 1 05-FEB-1992;
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     source          1. .2062
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BASE COUNT     429 a    617 c    573 g    443 t
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Query Match     39.5%;  Score 514;  DB 25;  Length 2062;
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Qy    825 AATGTTAAGGGCACTGAGGACTCAGGCACCACACAG 858
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RESULT 5

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LOCUS       I43805    2062 bp    DNA    PAT    10-JUL-1997
DEFINITION  Sequence 24 from patent US 5633145.
ACCESSION   I43805
NID         g2468903
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2062)
  AUTHORS   Feldmann,M., Gray,P.W., Turner,M.J.C. and Brennan,F.M.
  TITLE     TNF.alpha. receptor-derived binding protein
  JOURNAL   Patent: US 5633145-A 24 27-MAY-1997;
FEATURES             Location/Qualifiers
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BASE COUNT     429 a    617 c    573 g    443 t
ORIGIN

Query Match     39.5%;  Score 514;  DB 25;  Length 2062;
Best Local Similarity 100.0%;
Matches  514;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    275 GATAGTGTGTGTCCCAAGGAAAATATACCCACCTTCAAAATAATTCGATTTGCTGTACC 334
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Qy    525 AGCTGCTCCAAAATGGGCCGAAAGGAAAATGGGTGGTGGGGAGATCTCTTCTTGCACAGTGGAC 584
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RESULT 6

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Qy    635  AAACAGAACACCGTGTGCACCTCTGCCATGCAGCCTCTGCCTCCCTCAATTGGGACCGGTGCACCTCTCTGCCCAGGAG  694
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Db    645  TTCCAGTGCTTCAAATTGCAGCCTCTGCCTCCCTCAATTGGGACCGGTGCACCTCTCTGCCCAGGAG  704

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Db    765  TCCCTGTAGTAACTGTAAGAAACCCTGGAGTGTGCCTACCCCAGATTGAG  824

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Qy    825  AATGTTAAGGGCCACTGAGGACTCAGGCACCACCACAG  858
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LOCUS       HUMTNFR      2087 bp    mRNA             PRI       10-NOV-1993
DEFINITION  Human tumor necrosis factor receptor mRNA, complete cds.
ACCESSION   M33294
NID         g339744
KEYWORDS    cell surface receptor; tumor necrosis factor receptor.
SOURCE      Human placenta, cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2087)
  AUTHORS   Schall,T.J., Lewis,M., Koller,K.J., Lee,A.L., Rice,G.C., Wong,G.H.,
            Gatanaga,T., Granger,G.A., Lentz,R., Raab,H., Kohr,W.J. and
            Goeddel,D.V.
  TITLE     Molecular cloning and expression of a receptor for human tumor
            necrosis factor
  JOURNAL   Cell 61, 361-370 (1990)
  MEDLINE   9035285
COMMENT     Draft entry and computer-readable sequence for [1] kindly submitted
            by T.Schall, 26-MAR-1990.
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     CDS             182..1549
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BASE COUNT    433 a    624 c    581 g    449 t
ORIGIN
Query Match     39.5%;  Score 514;  DB 27;  Length 2087;
Best Local Similarity 100.0%;
Matches  514;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;
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Qy    345  GATAGTGTGTGTCCCCAAGGAGAAAAATATATCCACCCTCAAAATAATAATTGGATTTGCTGTACC  404

Db    362  AAGTGCCACAAGGACTACTTGTACAATGACTGTCCAGGCCCGGGCCAGGACATACGGAC  421
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Qy    405  AAGTGCCACAAGGACTACTTGTACAATGACTGTCCAGGCCCGGGCCAGGACATACGGAC  464

Db    422  TGCAGGGAGTGTGAGAGCGGCGTCCTTCACCGCTTCAGAAAACCACTCAGACACTGCCTC  481
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Qy    465  TGCAGGGAGTGTGAGAGCGGCGTCCTTCACCGCTTCAGAAAACCACTCAGACACTGCCTC  524

Db    482  AGCTCGCTCCAAATGCCGAAAGGAGAGGGTCTTCCACGGCTTCAGAAAACCACCTCAGACAGTGGGAC  541
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Qy    525  AGCTCGCTCCAAATGCCGAAAGGAGAGGGTCTTCCACGGCTTCAGAAAACCACCTCAGACAGTGGGAC  584

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Qy    765  TCCCTGTAGTAACTGTAAGAAACCCTGGAGTGCACGAAGCGAAGTTGTGCCTACCCCAGATTGAG  824

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LOCUS       A26412       2111 bp    DNA              PAT       26-APR-1995
DEFINITION  cDNA for (55kD TNF-BP) tumor necrosis factor binding protein from
            patent EP0417563.
ACCESSION   A26412
NID         g904968
KEYWORDS    unidentified.
SOURCE      unidentified.
  ORGANISM  unclassified.
REFERENCE   1  (bases 1 to 2111)
  AUTHORS   Brockhaus,M., Dembic,Z., Gentz,R., Lesslauer,W., Loetscher,H. and
            Schlaeger,E.J.
  TITLE     TNF-binding proteins
  JOURNAL   Patent: EP 0417563-A 24 20-MAR-1991;
            F. HOFFMANN-LA ROCHE AG
FEATURES             Location/Qualifiers
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BASE COUNT    445 a    629 c    587 g    450 t
ORIGIN
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Query Match   39.5%;   Score 514;   DB 25;   Length 2111;
Best Local Similarity 100.0%;   Pred. No. 0.00e+00;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   307 GATAGTGTGTGTCCCCAAGGAAAAATAATATCCACCCTCAAAATAATTCGATTTGCTGTACC 366
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Db   367 AAGTGCCACAAAGGAAACCTACTTGTACAAATGACTGTGTCCAGGGCCCCGGGGATACGGAC 426
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Qy   405 AAGTGCCACAAAGGAAACCTACTTGTACAAATGACTGTGTCCAGGGCCCCGGGGATACGGAC 464

Db   427 TGCAGGGAGTGTGAGAGCGGGCTCCTTCACCGGCTTCAGAAAACCACCTCAGACACTGCCTC 486
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Qy   465 TGCAGGGAGTGTGAGAGCGGGCTCCTTCACCGGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db   487 AGCTGCTCCAAAATGCCGAAAGGAAAAATGGGTCAGGTGGGACGATCTCTTCTTCACAGTGGAC 546
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Qy   525 AGCTGCTCCAAAATGCCGAAAGGAAAAATGGGTCAGGTGGGAGATCTCTTCTTGCACAGTGGAC 584

Db   547 CGGGACACCGTGTGTGCCTGCACCTGCCACGTGACCAGTGACTACCGGCATGTGAAAAACCTT 606
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Db   727 TCCTGTAGTAACTGTAAGAAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGAGATTGAG 786
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Qy   765 TCCTGTAGTAACTGTAAGAAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGAGATTGAG 824

Db   787 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 820
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Qy   825 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 858

RESULT
LOCUS   8   HUMTNFRB   2111 bp   mRNA   PRI   14-NOV-1990
DEFINITION   Homo sapiens tumor necrosis factor receptor mRNA, complete cds.
ACCESSION   M58286 M33480
NID   g339753
KEYWORDS   tumor necrosis factor receptor.
SOURCE   Human cell line HL60, cDNA to mRNA.
ORGANISM   Homo sapiens
             Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
             Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 2111)
AUTHORS   Loetscher,H., Pan,Y.-C.E., Lahm,H.-W., Gentz,R., Brockhaus,M.,
             Tabuchi,H. and Lesslauer,W.
TITLE   Molecular cloning and expression of the human 55 kd tumor necrosis
             factor receptor
JOURNAL   Cell 61, 351-359 (1990)
MEDLINE   9035284
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BASE COUNT   445 a   629 c   587 g   450 t
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Query Match   39.5%;   Score 514;   DB 27;   Length 2111;
Best Local Similarity 100.0%;   Pred. No. 0.00e+00;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   307 GATAGTGTGTGTCCCCAAGGAAAAATAATATCCACCCTCAAAATAATTCGATTTGCTGTACC 366
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Db   367 AAGTGCCACAAAGGAAACCTACTTGTACAAATGACTGTGTCCAGGGCCCCGGGGATACGGAC 426
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Qy   405 AAGTGCCACAAAGGAAACCTACTTGTACAAATGACTGTGTCCAGGGCCCCGGGGATACGGAC 464

Db   427 TGCAGGGAGTGTGAGAGCGGGCTCCTTCACCGGCTTCAGAAAACCACCTCAGACACTGCCTC 486
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Qy   465 TGCAGGGAGTGTGAGAGCGGGCTCCTTCACCGGCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db   487 AGCTGCTCCAAAATGCCGAAAGGAAAAATGGGTCAGGTGGGAGATCTCTTCTTGCACAGTGGAC 546
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Qy   525 AGCTGCTCCAAAATGCCGAAAGGAAAAATGGGTCAGGTGGGAGATCTCTTCTTGCACAGTGGAC 584

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Db   607 TTCCAGTGCTTCAAATTGCACCGTCGACCTGCCACCTCGCCTCAAATGGGACCGTGCACCTCTCCTGCCAGGAG 666
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Qy   645 TTCCAGTGCTTCAAATTGCACCGTCGACCTGCCACCTCGCCTCAAATGGGACCGTGCACCTCTCCTGCCAGGAG 704

Db   667 AAACAGAACACCGTGTGCACCTGCCACGTGCAGCAGGTTTCTTTCTTCTTAAGAGAGAAAACGAGTGTGTC 726
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Qy   705 AAACAGAACACCGTGTGCACCTGCCACGTGCAGCAGGTTTCTTTCTTAAGAGAGAAAACGAGTGTGTC 764

Db   727 TCCTGTAGTAACTGTAAGAAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGAGATTGAG 786
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Qy   765 TCCTGTAGTAACTGTAAGAAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGAGATTGAG 824

Db   787 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 820
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Qy   825 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 858

RESULT
LOCUS   9   HUMTNFRC   2112 bp   mRNA   PRI   30-SEP-1991
DEFINITION   Human tumor necrosis factor receptor (TNF receptor) mRNA, complete
             cds.
ACCESSION   M63121 M75861
NID   g339755
KEYWORDS   tumor necrosis factor receptor.
SOURCE   Human cDNA to mRNA.
ORGANISM   Homo sapiens
             Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
             Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 2112)
AUTHORS   Himmler,A., Maurer-Fogy,I., Kronke,M., Scheurich,P.,

Left column

TITLE   Pfizenmaier,K., Lantz,M., Olsson,I., Hauptmann,R., Stratowa,C., and
          Adolf,G.R.
          Molecular cloning and expression of human and rat tumor necrosis
          factor receptor chain (p60) and its soluble derivative, tumor
          necrosis factor-binding protein
JOURNAL   DNA Cell Biol. 9, 705-715 (1990)
MEDLINE   91090841
FEATURES   Location/Qualifiers
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ORIGIN

Query Match   39.5%; Score 514; DB 27; Length 2112;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db   327 GATAGTGTGTGTCCCCAAGGAGAAAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 386
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Qy   345 GATAGTGTGTGTCCCCAAGGAAAAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404

Db   387 AAGTGCCACAAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCCGGGGGCCAGGATACGGAC 446
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Qy   405 AAGTGCCACAAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCCGGGGGCCAGGATACGGAC 464

Db   447 TGCAGGGAGTGTGAAGCGCGCTCCTTCCACCGGCTTCAGAGAAAACCACCTCAGACACTGCCTC 506
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Qy   465 TGCAGGGAGTGTGAGAGCGGCGGTCCTTCACCGGCTTCAGAAAAACCACCTCAGACACTGCCTC 524

Db   507 AGCTGCTCCAAATGCCGAAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTTGCACAGTGGAC 566
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Qy   525 AGCTGCTCCAAATGCCGAAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTTGCACAGTGGAC 584

Db   567 CGGGACCACCGTGTGTGGGCTGCGAGGAAGAACCAGTACCGGCACATTATTGGAGTGAAAACCTT 626
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Qy   585 CGGGACACCCGTGTGTGGGCTGCGAGGAAGAACCAGTACCGGCACATTATTGGAGTGAAAACCTT 644

Db   627 TTCCAGTGCTTCAAATTGCACGCCTCGCCTCAACTTGCACCTCTCCTCGCCAGGAG 686
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Qy   645 TTCCAGTGCTTCAAATTGCACGCCTCTCGCCTCAACTTGGACACCTCTCCTCGCCAGGAG 704

Db   687 AAACAGAACACCGTGTGCACCTGCCATGCAGCTCAGCAGTTTCTTCTCTAAGAGAAAACGAGTGTGTC 746
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Qy   705 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTCTTCTTAAGAGAAAACGAGTGTGTC 764

Db   747 TCCTGTAGTAACTGTAAGAAAAAGCCTGGAGTGCCAGAGTTGTGCCTACCCCAGATTGAG 806
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Qy   765 TCCTGTAGTAACTGTAAGAAAAAGCCTGGAGTGCCAGAAGTTGTGCCTACCCCAGATTGAG 824

Db   807 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 840
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Qy   825 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 858

RESULT 10

LOCUS   HSTNFR1A   2161 bp   RNA   PRI   18-JAN-1993
DEFINITION H.sapiens TNF-R mRNA for tumor necrosis factor receptor 1.
ACCESSION   X55313
NID   g37223
KEYWORDS   TNF-R gene; tumor necrosis factor receptor 1.
SOURCE   human.
  ORGANISM Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 2161)
  AUTHORS   Nophar,Y., Kemper,O., Brakebusch,C., Englemann,H., Zwang,R.,
            Aderka,D., Holtmann,H. and Wallach,D.
  TITLE   Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA
            for the type I TNF-R, cloned using amino acid sequence data of its
            soluble form, encodes both the cell surface and a soluble form of
            the receptor
  JOURNAL   EMBO J. 9 (10), 3269-3278 (1990)
  MEDLINE   91006021
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BASE COUNT   459 a   642 c   604 g   456 t
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Query Match   39.5%; Score 514; DB 27; Length 2161;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   345 GATAGTGTGTGTCCCCAAGGAAAAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 404
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Qy   405 AAGTGCCACAAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCCGGGGGCCAGGATACGGAC 464
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Qy   ... AAGTGCCACAAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCCGGGGGCCAGGATACGGAC 464
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Qy   465  TGCAGGGAGTGTGTGAGGACGCGGCTCCTTCACCGGCTTCAGAAAACCACCTCAGACACTGCCTC  524
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Qy   525  AGCTGCTCCAAATGCCGAAAAGAAAGAAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC  584
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Qy   585  CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCCATTATTGGAGTGAAAACCTT      644
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Qy   616  CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCCATTATTGGAGTGAAAACCTT      675
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Qy   556  AGCTGCTCCAAATGCCGAAAAGAAAGAAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC  615
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Qy   676  TTCCAGTGCTTCAATTGCAGCCCTCTGCCCTCAAATGGGACCGTGCCACCTCGTCTCCTGCCAGGAG  735
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Qy   645  TTCCAGTGCTTCAATTGCAGCCCTCTGCCCTCAAATGGGACCGTGCCACCTCGTCTCCTGCCAGGAG  704
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Qy   736  AAACAGAACACCGTGTGCACCTGCCACTCGGTGTTTCTTCTTAAGAGAAAACAGAGTGTGTC  795
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Qy   705  AAACAGAACACCGTGTGCACCTGCCACTCGGTGTTTCTTCTTAAGAGAAAACAGAGTGTGTC  764
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Qy   796  TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG  855
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Qy   765  TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG  824
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Qy   856  AATGTTAAGGGCACTGAGGACTCAGGCACCACAG  889
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Qy   825  AATGTTAAGGGCACTGAGGACTCAGGCACCACAG  858
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RESULT  11

LOCUS        A43873      2175 bp      DNA        PAT        06-MAR-1997
DEFINITION   Sequence 1 from Patent EP0657536.
ACCESSION    A43873
NID          g2299022
KEYWORDS     .
SOURCE       unidentified.
  ORGANISM   unidentified
             unclassified.
REFERENCE    1  (bases 1 to 2175)
  AUTHORS    Wallach,D., Brakebusch,C., Varfolomeev,E. and Batkin,M.
  TITLE      Proteases capable of shedding the soluble TNF-receptor and TNF-R
             derived peptides and antibodies against the proteases inhibiting
             the shedding
  JOURNAL    Patent: EP 0657536-A 1 14-JUN-1995;
             YEDA RES & DEV (IL);
COMMENT      Other publication ZA 9407962 951121
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             Other publication AU 7574294 950504
             Other publication CA 2133872 950413.
FEATURES             Location/Qualifiers
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BASE COUNT      474 a      641 c      604 g      456 t
ORIGIN

Query Match     39.5%;  Score 514;  DB 25;  Length 2175;
Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
Matches  514;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;
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Db   585  CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCCATTATTGGAGTGAAAACCTT      644
Db   616  CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCCATTATTGGAGTGAAAACCTT      675
Db   556  AGCTGCTCCAAATGCCGAAAAGAAAGAAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC  615
Db   676  TTCCAGTGCTTCAATTGCAGCCCTCTGCCCTCAAATGGGACCGTGCCACCTCGTCTCCTGCCAGGAG  735
Db   705  AAACAGAACACCGTGTGCACCTGCCACTCGGTGTTTCTTCTTAAGAGAAAACAGAGTGTGTC  764
Db   736  AAACAGAACACCGTGTGCACCTGCCACTCGGTGTTTCTTCTTAAGAGAAAACAGAGTGTGTC  795
Db   796  TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG  855
Db   765  TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG  824
Db   856  AATGTTAAGGGCACTGAGGACTCAGGCACCACAG  889
Db   825  AATGTTAAGGGCACTGAGGACTCAGGCACCACAG  858
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Right column

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Db   376  GATAGTGTGTGTCCCCAAGGAGAAATATATCCACCCTCAAAATAATTCGATTGCTGTACC  435
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Qy   465  TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTAGCGAGAACCACCTCAGACACTGCCTC  524
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Qy   525  AGCTGCTCCAAATGCCGAAAAGAAAGAAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC  584
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Db   616  CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCCATTATTGGAGTGAAAACCTT  675
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Db   676  TTCCAGTGCTTCAATTGCAGCCCTCTGCCCTCAAATGGGACCGTGCCACCTCGTCTCCTGCCAGGAG  735
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Qy   645  TTCCAGTGCTTCAATTGCAGCCCTCTGCCCTCAAATGGGACCGTGCCACCTCGTCTCCTGCCAGGAG  704
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Qy   705  AAACAGAACACCGTGTGCACCTGCCACTCGGTGTTTCTTCTTAAGAGAAAACAGAGTGTGTC  764
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Db   796  TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG  855
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Qy   765  TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG  824
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Qy   825  AATGTTAAGGGCACTGAGGACTCAGGCACCACAG  858
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RESULT  12

LOCUS        I64751      2175 bp      DNA        PAT        26-SEP-1997
DEFINITION   Sequence 1 from patent US 5665859.
ACCESSION    I64751
NID          g2481645
KEYWORDS     .
SOURCE       Unknown.
  ORGANISM   Unknown
             Unclassified.
REFERENCE    1  (bases 1 to 2175)
  AUTHORS    Wallach,D., Brakebusch,C., Varfolomeev,E. and Batkin,M.
  TITLE      Molecules influencing the shedding of the TNF receptor, their
             preparation and their use
  JOURNAL    Patent: US 5665859-A 1 09-SEP-1997;
FEATURES             Location/Qualifiers
     source          1..2175
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BASE COUNT      474 a      641 c      604 g      456 t
ORIGIN

Query Match     39.5%;  Score 514;  DB 25;  Length 2175;
Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
Matches  514;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;
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Db   376  GATAGTGTGTGTCCCCAAGGAGAAATATATCCACCCTCAAAATAATTCGATTGCTGTACC  435
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Qy   345  GATAGTGTGTGTCCCCAAGGAGAAATATATCCACCCTCAAAATAATTCGATTGCTGTACC  404
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Qy   405  AAGTGCCACAAAAGGAAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCCAGGATACGGAC  464
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Db   496  TGCAGGGAGTGTGAGAGCGGCCTCCTTCACGGCTTCAGAAAACCACCTCAGACACTGCCTC  555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   465  AAGTGCCACAAAAGGAAACCTACTTGTACAATGACTGTCTCCAGGCCCGGGGCGAGGATACGGAC  464
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Qy    465 TGCAGGGAGGTGAGAGGCGGCTCCTTCAGAAAACCACCTCAGACACTGCCTC 524
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    556 AGCTGCTCCAAATGCCGAAAGGAAAATGGGGTCAGGTGGGAGAATCTCTTCTTCGACAGTGGAC 615

Qy    525 AGCTGCTCCAAATGCCGAAAGGAAAATGGGGTCAGGTGGGAGAATCTCTTCTTCGACAGTGGAC 584
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    616 CGGGACACCCGTGTGTGGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 675

Qy    585 CGGGACACCCGTGTGTGGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    676 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAAATGGGACCGGTGCCACCTCTGCCAGGAG 735

Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAAATGGGACCGGTGCCACCTCTGCCAGGAG 704
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    736 AAACAGAACACCGTGTGCCACCTGAGGACTCAGGCGACCACAG 795

Qy    705 AAACAGAACACCGTGTGCCACCTGAGGACTCAGGCGACCACAG 764
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    796 TCCTGTAGTAACTGTAAGAGAAAAGCCTGGAGTGCACGAAGTTGTGTGCCTACCCCAGATTGAG 855

Qy    765 TCCTGTAGTAACTGTAAGAGAAAAGCCTGGAGTGCACGAAGTTGTGTGCCTACCCCAGATTGAG 824
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    856 AATGTTAAGGGCACTGAGGACTCAGGCGACCACACAG 889

Qy    825 AATGTTAAGGGCACTGAGGACTCAGGCGACCACACAG 858
```

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RESULT    13

LOCUS            A19907              2176 bp      DNA          PAT          04-OCT-1994
DEFINITION       Synthetic nucleotide sequence Type I TNF receptor gene.
ACCESSION        A19907
NID              g641222
KEYWORDS         .
SOURCE           unidentified.
  ORGANISM       unidentified
                 unclassified.
REFERENCE        1 (bases 1 to 2176)
  AUTHORS        Wallach,D., Nophar,Y., Kemper,O., Engelmann,H., Brakebusch,C. and
                 Adekra,D.
  TITLE          Expression of the recombinant tumor necrosis factor binding protein
                 I (TBP-I)
  JOURNAL        Patent: EP 0439900-A 28 26-JUN-1991;
                 YEDA RESEARCH AND DEVELOPMENT COMPANY LIMITED
FEATURES         Location/Qualifiers
  source         1..2176
                 /organism="Artificial sequences"
BASE COUNT       474 a      642 c      604 g      456 t
ORIGIN

Query Match    39.5%;  Score 514;  DB 25;  Length 2176;
Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
Matches  514;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    376 GATAGTGTGTGTCCCCAAGGAGAAAATATATCCACCCTCAAAATAATTCGAATTGCTGTACC 435
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    345 GATAGTGTGTGTCCCCAAGGAGAAAATATATCCACCCTCAAAATAATTCGAATTGCTGTACC 404

Qy    436 AAGTGCCACAAAAGGAAACCTACTTGTACAAATGACATGTCCAGGCCCGGGGCCCGGGGCAGGATACGGAC 495
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    405 AAGTGCCACAAAAGGAAACCTACTTGTACAAATGACATGTCCAGGCCCGGGGCCCGGGGCAGGATACGGAC 464

Qy    496 TGCAGGGAGGTGAGAGGCGGCTCCTTCAGAAAACCACCTCAGACACTGCCTC 555
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    465 TGCAGGGAGGTGAGAGGCGGCTCCTTCAGAAAACCACCTCAGACACTGCCTC 524

Qy    556 AGCTGCTCCAAATGCCGAAAGGAAAATGGGGTCAGGTGGGAGATCTCTTCTTCGACAGTGGAC 615
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    525 AGCTGCTCCAAATGCCGAAAGGAAAATGGGGTCAGGTGGGAGATCTCTTCTTCGACAGTGGAC 584

Qy    616 CGGGACACCCGTGTGTGCGAGGAAGAACAGTACCGGCATTATTGGAGTGAAAACCTT 675
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    585 CGGGACACCCGTGTGTGCGAGGAAGAACAGTACCGGCATTATTGGAGTGAAAACCTT 644
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Db    676 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAAATGGGACCGGTGCCACCTCTGCCAGGAG 735
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAAATGGGACCGGTGCCACCTCTGCCAGGAG 704

Db    736 AAACAGAACACCGTGTGCCACCTGAGGACTCAGGCGACCACAG 795
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    705 AAACAGAACACCGTGTGCCACCTGAGGACTCAGGCGACCACAG 764

Db    796 TCCTGTAGTAACTGTAAGAGAAAAGCCTGGAGTGCACGAAGTTGTGTGCCTACCCCAGATTGAG 855
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    765 TCCTGTAGTAACTGTAAGAGAAAAGCCTGGAGTGCACGAAGTTGTGTGCCTACCCCAGATTGAG 824

Db    856 AATGTTAAGGGCACTGAGGACTCAGGCGACCACACAG 889
          |||||||||||||||||||||||||||||||||||||||||||
Qy    825 AATGTTAAGGGCACTGAGGACTCAGGCGACCACACAG 858
```

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RESULT    14

LOCUS            I26928              6889 bp      DNA          PAT          01-OCT-1996
DEFINITION       Sequence 2 from patent US 5561053.
ACCESSION        I26928
NID              g1606798
KEYWORDS         .
SOURCE           Unknown.
  ORGANISM       Unknown
                 Unclassified.
REFERENCE        1 (bases 1 to 6889)
  AUTHORS        Crowley,C.W.
  TITLE          Method for selecting high-expressing host cells
  JOURNAL        Patent: US 5561053-A 2 01-OCT-1996;
FEATURES         Location/Qualifiers
  source         1..6889
                 /organism="unknown"
BASE COUNT       1729 a      1826 c      1681 g      1653 t
ORIGIN

Query Match    39.5%;  Score 514;  DB 25;  Length 6889;
Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
Matches  514;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Db   1725 GATAGTGTGTGTCCCCAAGGAGAAAATATATCCACCCTCAAAATAATTCGAATTGCTGTACC 1784
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    345 GATAGTGTGTGTCCCCAAGGAGAAAATATATCCACCCTCAAAATAATTCGAATTGCTGTACC 404

Db   1785 AAGTGCCACAAAAGGAAACCTACTTGTACAAATGACATGTCCAGGCCCGGGGCCCGGGGCAGGATACGGAC 1844
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405 AAGTGCCACAAAAGGAAACCTACTTGTACAAATGACATGTCCAGGCCCGGGGCCCGGGGCAGGATACGGAC 464

Db   1845 TGCAGGGAGGTGAGAGGCGGCTCCTTCAGAAAACCACCTCAGACACTGCCTC 1904
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    465 TGCAGGGAGGTGAGAGGCGGCTCCTTCAGAAAACCACCTCAGACACTGCCTC 524

Db   1905 AGCTGCTCCAAATGCCGAAAGGAAAATGGGGTCAGGTGGGAGATCTCTTCTTCGACAGTGGAC 1964
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    525 AGCTGCTCCAAATGCCGAAAGGAAAATGGGGTCAGGTGGGAGATCTCTTCTTCGACAGTGGAC 584

Db   1965 CGGGACACCCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 2024
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    585 CGGGACACCCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Db   2025 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAAATGGGACCGGTGCCACCTCTGCCAGGAG 2084
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    645 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAAATGGGACCGGTGCCACCTCTGCCAGGAG 704

Db   2085 AAACAGAACACCGTGTGCCACCTGAGGACTCAGGCGACCACAG 2144
          |||||||||||||||||||||||||||||||||||||||||||
Qy    705 AAACAGAACACCGTGTGCCACCTGAGGACTCAGGCGACCACAG 764

Db   2145 TCCTGTAGTAACTGTAAGAGAAAAGCCTGGAGTGCACGAAGTTGTGTGCCTACCCCAGATTGAG 2204
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    765 TCCTGTAGTAACTGTAAGAGAAAAGCCTGGAGTGCACGAAGTTGTGTGCCTACCCCAGATTGAG 824
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Db   2205  AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 2238
           |||||||||||||||||||||||||||||||||
Qy    825  AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 858

RESULT  15
LOCUS       A20255      2061 bp    DNA             PAT       20-SEP-1995
DEFINITION  55kD receptor gene for human TNF-alpha.
ACCESSION   A20255
NID         g1247401
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2061)
  AUTHORS
  TITLE     MODIFIED HUMAN TNFALPHA (TUMOR NECROSIS FACTOR ALPHA) RECEPTOR
  JOURNAL   Patent: WO 9207076-A 23 30-APR-1992;
FEATURES             Location/Qualifiers
  source          1..2061
                  /organism="Homo sapiens"
                  /db_xref="taxon:9606"
BASE COUNT       429 a      616 c      573 g      443 t
ORIGIN

Query Match       39.0%;  Score 507;  DB 25;  Length 2061;
Best Local Similarity   99.8%;   Pred. No. 0.00e+00;
Matches   513;  Conservative   0;  Mismatches  0;  Indels   1;  Gaps   1;

Qy    275  GATAGTGTGTGTCCCCAAGGAAAAATATATCCACCCTCAAAATAAATTAAATTCGATTTGCTGTACC 334
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    345  GATAGTGTGTGTCCCCAAGGAAAAATATATCCACCCTCAAAATAAATTAAATTCGATTTGCTGTACC 404

Db    335  AAGTGCCACAAAAGGAAACCTACTTGTACAAATGACACTGTTCAGCCCGGGGGGCCAGGAATACGGAC 394
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    405  AAGTGCCACAAAAGGAAACCTACTTGTACAATGACACTGTTCAGCCCGGGGGGCCAGGAATACGGAC 464

Qy    395  TGCAGGGAGTGTGAGAGCGGGTCCCTTCAGAAAAACCACTCAGACACTGCCTC 454
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    465  TGCAGGGAGTGTGAGAGCGGGTCCCTTCAGAAAAACCACTCAGACACTGCCTC 524

Db    455  AGCTGCTCCCAAATGCCGAAAGGAAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 514
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    525  AGCTGCTCCCAAATGCCGAAAGGAAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Qy    515  CGGGGACACCGTGTGTGGGCTGCAGGAAGAAACCAGTACCGGGCAATTATTGGAGTGAAAAACCTT 574
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    585  CGGGGACACCGTGTGTGGGCTGCAGGAAGAAACCAGTACCGGGCAATTATTGGAGTGAAAAACCTT 644

Db    575  TTCCAGTGCTTCAATTGCAGCCTCTGCCCTCAATGGGGACCGTGCAC-TCTCCTGCCAGGAG 633
           ||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Qy    645  TTCCAGTGCTTCAATTGCAGCCTCTGCCCTCAATGGGGACCGTGCACCTCTCCTGCCAGGAG 704

Qy    634  AAACAGAACACCGTGTGCACCTGCCATGCAGTTTCTTCTAAGGAGAAACGAGTGTGTC 693
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    694  TCCTGTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACCAAGTTGTGCCTACCCCAGATTGAG 753

Db    705  AAACAGAACACCGTGTGCACCTGCCATGCAGTTTCTTCTTAAGAGAAAACGAGTGTGTC 764
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    765  TCCTGTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACCAAGTTGTGCCTACCCCAGATTGAG 824

Db    754  AATGTTTAAGGGCCACTGAGGACTTCAGGCCACCACAG 787
           ||||||||||||||||||||||||||||||||||||
Qy    825  AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 858
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| |  | |  __/ ___) |  _ <| |___|  _  |
|_|  |_|_|   |____/|_| \_\\____|_| |_|  (TM)
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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed May 6 15:05:10 1998; MasPar time 167.20 Seconds
           897.906 Million cell updates/sec

Tabular output not generated.

Database: n.a.

Title: >US-08-804-166-7
Description: (1-1301) from US08804166.seq
Perfect Score: 1301
N.A. Sequence: 1 CTCGAGATGGCTACAAGTAA...........CACAATAAGGATCCCCTCGAG 1301
Comp: GAGCTCTACCGGATGTCCATT..........GTGTTATTCCTAGGAGGAGCTC

Scoring table: TABLE default
                Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 159651 seqs, 57698962 bases x 2

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Statistics: Mean 9.269; Variance 5.321; scale 1.742

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	514	39.5	1334	1	Q06282	Plasmid Tumour Necros	0.00e+00
2	514	39.5	1368	8	Q49932	Lambda-derived TNF-R	0.00e+00
3	514	39.5	2062	4	Q24440	Encodes TNF-alpha R	0.00e+00
4	514	39.5	2062	3	Q20973	TNF-alpha binding pro	0.00e+00
5	514	39.5	2088	2	Q10883	30kD TNF inhibitor pr	0.00e+00
6	514	39.5	2175	15	Q10955	Encodes human 55kD TN	0.00e+00
7	514	39.5	2175	15	Q90513	p55 TNF-R gene.	0.00e+00
8	514	39.5	6889	18	T19931	DHFR/intron (WTrasSD)	0.00e+00
9	512	39.4	2141	1	Q06285	Human Tumour Necrosis	0.00e+00
10	512	39.2	2176	2	Q22215	Type I TNF receptor.	0.00e+00
11	510	39.2	2170	9	Q50870	p55 Tumour necrosis f	0.00e+00
12	478	36.7	608	4	Q24441	Encodes truncated TNF	0.00e+00
13	416	32.0	579	8	Q14800	p55 Tumour truncated	6.61e-279
14	415	31.9	836	17	T03212	Single chain gonadotr	3.64e-278
15	415	31.9	836	17	T03243	Single chain gonadotr	3.64e-278

c

ALIGNMENTS

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
16	411	31.6	575	17	T03240	Human CG beta-subunit	3.34e-275
17	383	29.4	504	4	Q24445	Encodes truncated TNF	1.75e-254
18	354	27.2	474	4	Q24442	Encodes truncated TNF	4.64e-233
19	321	24.7	743	17	T03219	Single chain gonadotr	9.76e-209
20	304	23.4	2771	31	T76770	Rat Fabpl gut-specifi	3.12e-196
21	303	23.3	2150	33	T62826	Human growth hormone	1.69e-195
22	296	22.8	336	6	Q41459	Human growth hormone	2.35e-190
23	285	21.9	426	2	N60524	Sequence encoding hum	2.78e-182
24	282	21.7	743	17	T03231	Single chain gonadotr	4.41e-180
25	282	21.7	752	17	T03231	Single chain gonadotr	4.41e-180
26	282	21.7	752	17	T03229	Single chain gonadotr	1.10e-175
27	276	21.2	744	17	T03221	Single chain gonadotr	1.10e-175
28	267	20.5	752	17	T03227	Single chain gonadotr	4.31e-169
29	259	19.9	2173	17	Q06284	Rat Tumour Necrosis F	3.07e-163
30	257	19.8	477	4	Q24444	Encodes truncated TNF	8.89e-162
31	221	17.0	462	4	Q24443	Encodes truncated TNF	1.56e-135
32	215	16.5	525	1	N03844	Bovine beta LH subuni	3.57e-131
33	213	16.4	540	1	Q03851	Porcine beta LH subun	1.01e-129
34	208	16.0	2660	4	N30032	Sequence encoding gen	4.28e-126
35	188	14.5	496	2	N60523	Sequence encoding dog	1.26e-111
36	185	14.2	611	2	O03848	Equine beta LH subuni	1.84e-109
37	132	10.1	1027	2	O10878	Partial sequence of c	1.41e-71
38	101	7.8	114	2	N60522	Sequence encoding aml	7.09e-50
39	99	7.6	138	13	Q80819	LH-beta -5 to 41 frag	1.7e-48
40	79	6.1	1047	2	Q80819	Human Natriuretic Pep	7.76e-35
41	73	5.6	651	2	O10572	Human Natriuretic Pep	2.20e-31
42	72	5.5	114	6	O34669	DNA encoding hCG beta	8.1e-30
43	71	5.5	700	2	N71239	Sequence encoding hum	1.76e-29
44	71	5.5	651	2	N60678	Sequence encoding pre	1.76e-29
45	71	5.5	3557	2	N60801	Human pro-growth horm	1.76e-29

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RESULT 1
ID    Q06282 standard; DNA; 1334 BP.
AC    Q06282;
DT    29-JAN-1991 (first entry)
DE    Plasmid Tumour Necrosis Factor-Binding Protein 15 cDNA insert.
KW    Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
OS    Homo sapiens.
KW    pTNF-BP15; ss.
FH    Key           Location/Qualifiers
FT    CDS           213..1325
FT    /product=TNF-BP
FT    /*tag=        a
PN    EP-393438-A.
PD    24-OCT-1990.
PF    06-APR-1990; 106624.
PR    21-APR-1989; DE-913101.
PR    21-JUN-1989; DE-920282.
PA    (BOEH ) BOEHRINGER INGELHEIMINT.
PI    Hauptmann R, Himmler A, Maurer-Fogy I, Stratowa C;
DR    WPI; 90-321987/43.
DR    P-PSDB; R07449.
PT    DNA encoding TNF binding protein and TNF - receptor - used in
PT    tumour treatment and to understand mechanismsm to TNF action
PS    Disclosure; Fig 1(1-3); 5ipp; German.
PT    pTNF-BP15 is one of 30 positives clones in a screened cDNA library
PT    from induced TNF-induced fibrosarcoma cells. A TNF-BP had been
CC    isolated from the urine of patients with uraemia and probes/primers
CC    were constructed from the determined amino acid sequence.
CC    To produce a vector expressing a soluble form of TNF-binding
CC    protein, this plasmid was cut with XmnI, amplified by PCR and the
CC    amplified DNA cut with BamHI and EcoRI.
CC    The resulting 0.75 kb DNA fragment was inserted into pT7/T3 alpha-19
CC    (BRL) cut with the same enzymes to recover pTNF-BP. This was cut
CC    with BamHI and EcoRI, and the recovered fragment inserted into
CC    pAD-CMVI (Q06283) to give the required plasmid pADTNF-BP.
CC    See also Q06282-Q06285.
SQ    Sequence      1334 BP;

Query Match          1334 BP;   299 A;   409 C;   342 G;   284 T;

Query Match          39.5%;   Score 514;   DB 1;   Length 1334;
```

Best Local Similarity 100.0%;   Conservative 0; Pred. No. 0.00e+00; Mismatches 0; Indels 0; Gaps 0;
Matches 514;

```
Db   333  gatagtgtgtgtcccaaggaaaatatatccaccctcaaaatcaattcgattttgctgtacc  392
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   345  GATAGTGTGTGTCCCAAGGAAAATATATCCACCCTCAAAATCAATTCGATTTTGCTGTACC  404

Db   393  aagtgccacaaaggaacctacttgtacaatgactgtccaggccgggggccaggatacggac  452
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   405  AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCGGGGGCCAGGATACGGAC  464

Db   453  tgcaggggagttgttgagagcgggtccttcacccgcttcagaaaaccactcagacactgcctc  512
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   465  TGCAGGGGAGTTGTTGAGAGCGGGTCCTTCACCCGCTTCAGAAAACCACTCAGACACTGCCTC  524

Db   513  agctgctcccaaatgccgaaaggaaatgggtcaggtcagggagatctcttcttgcacagtggac  572
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   525  AGCTGCTCCCAAATGCCGAAAGGAAATGGGTCAGGTCAGGGAGATCTCTTCTTGCACAGTGGAC  584

Db   573  cgggacacacgtgtgtggcctgcaggagaaccagtaccggccatattggagtgaaaacctt  632
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   585  CGGGACACACGTGTGTGGCCTGCAGGAGAACCAGTACCGGCCATATTGGAGTGAAAACCTT  644

Db   633  ttccagtcgtcttcaattgcagcctctcgctcaatgggaccgtgcacctcctctgccaggag  692
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   645  TTCCAGTCGTCTTCAATTGCAGCCTCTCGCTCAATGGGACCGTGCACCTCCTCTGCCAGGAG  704

Db   693  aaacagaacaccgtgtcgcacctgcaggtttctttctttaagagagaaaacagagtgtgtc  752
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   705  AAACAGAACACCGTGTCGCACCTGCAGGTTTCTTTCTTTAAGAGAGAAAACAGAGTGTGTC  764

Db   753  tcctgctagtaactgtaggacctggagtgagtgcacgaagtttgtgcctacccccagaattgag  812
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   765  TCCTGCTAGTAACTGTAGGACCTGGAGTGAGTGCACGAAGTTTGTGCCTACCCCCAGAATTGAG  824

Db   813  aatgttaagggcactgaggagactcaggcacccacag  846
          |||||||||||||||||||||||||||||||||||||
Qy   825  AATGTTAAGGGCACTGAGGAGACTCAGGCACCCACAG  858
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RESULT 2

ID   Q49932 standard; cDNA to mRNA; 1368 BP.
AC   Q49932;
DT   29-APR-1994 (first entry)
DE   Lambda-derived TNF-R cDNA.
DE   Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;
KW   IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;
KW   rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;
KW   pulmonary fibrosis; silicosis; allograft; xenograft; rejection;
KW   graft verses host disease; sepsis; inflammation; allergy;
KW   autoimmune dysfunction; ss.
OS   Homo sapiens.
OS   Lambda-gt10-7-ctnfbp.
FH   Key   Location/Qualifiers
FH
FT   CDS   1..1366
FT   /product= hTNF-R
FT   /tag= a
FT   sig_peptide   1..120
FT   /tag= b
FT   mat_peptide   121..1363
FT   /tag= c
PN   WO9319777-A.
PD   14-OCT-1993;
PF   26-MAR-1993; U02938.
PR   30-MAR-1992; US-860710.
PA   (IMMV) IMMUNEX CORP.
PI   Smith CA;
DR   WPI; 93-336592/42.
DR   P-PSDB; R42059.
PT   New fusion protein tumour necrosis factor and human interleukin-1
PT   receptor - useful in therapy, diagnosis and assays of e.g.
PT   rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.
PS   Disclosure; Page 57-59; 85pp; English.

CC   The sequences given in Q49931-32 encode human tumour necrosis factor
CC   receptor (TNF-R) and the sequences in Q49933-34 encode human
CC   interleukin-1 receptor (IL-1R). These sequences were used in the
CC   production of a fusion protein which conformed to one of the
CC   formulae:
CC   TNF-R-linker-TNF-R;
CC   IL-1R-linker-IL-1R
CC   TNF-R-linker-IL-1R or
CC   IL-1R-linker-TNF-R
CC   The linker may comprise 5-100 amino acids selected from Gly, Asp,
CC   Ser, Thr and Ala. These linkers separate the individual moieties
CC   by such a distance that each component of the fusion protein is
CC   capable of folding into the secondary or tertiary structure required
CC   for its biological activity. These fusion proteins may be used in
CC   therapy, diagnosis and assays for conditions mediated by TNF or IL-1,
CC   particularly in conditions in which both TNF and IL-1 play a causitive
CC   role. They may be used to treat cachexia, rheumatoid arthritis,
CC   diabetes, multiple sclerosis, pulmonary fibrosis and silicosis,
CC   cerebral malaria, allograft and xenograft rejection in graft verses
CC   host disease, sepsis, septic shock, inflammation, allergies and
CC   autoimmune dysfunctions.
SQ   Sequence 1368 BP;

Query Match   39.5%;   Score 514;   DB 8;   Length 1368;
Best Local Similarity 100.0%;   Conservative 0; Pred. No. 0.00e+00; Mismatches 0; Indels 0; Gaps 0;
Matches 514;

Sequence 1368 BP;   292 A;   424 C;   376 G;   276 T;

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Db   121  gatagtgtgtgtcccaaggaaaatatatccaccctcaaaatcaattcgattttgctgtacc  180
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Qy   345  GATAGTGTGTGTCCCAAGGAAAATATATCCACCCTCAAAATCAATTCGATTTTGCTGTACC  404

Db   181  aagtgccacaaaggaacctacttgtacaatgactgtccaggccgggggccaggatacggac  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   405  AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCGGGGGCCAGGATACGGAC  464

Db   241  tgcaggggagttgttgagagcgggtccttcacccgcttcagaaaaccactcagacactgcctc  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   465  TGCAGGGGAGTTGTTGAGAGCGGGTCCTTCACCCGCTTCAGAAAACCACTCAGACACTGCCTC  524

Db   301  agctgctcccaaatgccgaaaggaaatgggtcaggtcagggagatctcttcttgcacagtggac  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   525  AGCTGCTCCCAAATGCCGAAAGGAAATGGGTCAGGTCAGGGAGATCTCTTCTTGCACAGTGGAC  584

Db   361  cgggacacacgtgtgtggcctgcaggagaaccagtaccggccatattggagtgaaaacctt  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   585  CGGGACACACGTGTGTGGCCTGCAGGAGAACCAGTACCGGCCATATTGGAGTGAAAACCTT  644

Db   421  ttccagtcgtcttcaattgcagcctctcgctcaatgggaccgtgcacctcctctgccaggag  480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   645  TTCCAGTCGTCTTCAATTGCAGCCTCTCGCTCAATGGGACCGTGCACCTCCTCTGCCAGGAG  704

Db   481  aaacagaacaccgtgtcgcacctgcaggtttctttctttaagagagaaaacagagtgtgtc  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   705  AAACAGAACACCGTGTCGCACCTGCAGGTTTCTTTCTTTAAGAGAGAAAACAGAGTGTGTC  764

Db   541  tcctgctagtaactgtaggacctggagtgagtgcacgaagtttgtgcctacccccagaattgag  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   765  TCCTGCTAGTAACTGTAGGACCTGGAGTGAGTGCACGAAGTTTGTGCCTACCCCCAGAATTGAG  824

Db   601  aatgttaagggcactgaggagactcaggcacccacag  634
          |||||||||||||||||||||||||||||||||||||
Qy   825  AATGTTAAGGGCACTGAGGAGACTCAGGCACCCACAG  858
```

RESULT 3

ID   Q24440 standard; DNA; 2062 BP.
AC   Q24440;
DT   05-NOV-1992 (first entry)
DE   Encodes TNF-alpha 55kD receptor.
KW   tumour necrosis factor alpha; extracellular binding domain;
KW   treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
KW   malaria; viral meningitis; graft versus host disease;
KW   autoimmune disease; rheumatoid arthritis.
OS   Homo sapiens.

```
Key                Location/Qualifiers
FH
FT  CDS            156..1517
FT  /*tag=  a
FT  /product= human TNF-alpha
FT  mat_peptide    1265..1267
FT  /*tag=  b
FT  /note=  "3"
FT  mat_peptide    1265..1267
FT  /*tag=  c
FT  /codon= seq:"TGG", aa:Thr
FT  mat_peptide    1258..1260
FT  /*tag=  d
FT  /codon= seq:"AAG", aa:Leu
FT  mat_peptide    1433..1435
FT  /*tag=  e
FT  /codon= Seq:"GAC", aa:Asn
FT  sig_peptide    156..274
FT  /*tag=  f
PN  WO9207076-A.
PD  30-APR-1992.
PF  18-OCT-1991; G01826.
PR  18-OCT-1990; GB-022648.
PA  (CHAR-) CHARING CROSS SUNLEY RES CENT.
PI  Brennan FM, Feldmann M, Gray PW, Turner MJC;
DR  WPI: 92-167156/20.
DR  P-PSDB; R24000
PS  Claim 4: Fig 1; 43pp; English.
PT  New polypeptide capable of binding human TNF alpha - comprises
PT  first three cysteine-rich subdomains of TNF alpha receptor for
PT  treating autoimmune disease, septic shock, HIV etc.
CC  This sequence encodes human TNF-alpha 55kD receptor . A placenta cDNA
CC  library in gt10 was screened with probe Q29236. Ten hybridising clones
CC  were plaque purified and cDNA size determined by PAGE against an
CC  Eco RI digested phage DNA. The inserts of two cDNA clones were then
CC  sequenced. The coding region of the human TNF-alpha
CC  55kD receptor was isolated as an EcoRI fragment encoding 374 amino
CC  acids, and cloned into a mammalian cell expression vector, resulting
CC  in prTNFR. A derivative of the TNF-alpha receptor was produced by
CC  engineering a termination codon just prior to the transmembrane
CC  domain. PCR with primers Q29237,8 generated a 300bp
CC  restriction fragment which was cloned into prTNFR, giving prTNFRecd.
CC  DNA sequencing confirmed this contained the designed DNA sequence.
CC  The TNF-alpha receptor expression plasmids were then transfected
CC  into monkey COS-7 cells.
CC  See also Q24440-51, R24000, R24080-84, R27585, Q29236-8
SQ  Sequence     2062 BP;  429 A;   618 C;   572 G;   443 T;

Query Match        39.5%;  Score 514;  DB 4;  Length 2062;
Best Local Similarity 100.0%;
Matches    514;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Db   275 gatagtgtgtccccaaggaaaatatatccacctcaaaataattcgatttgctgtacc 334
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCTCAAAATAATTCGATTTGCTGTACC 404

Db   335 aagtgccacaaaggaacctacttgtacaatgactgtgtccaggcccgggcaggatacggac 394
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db   395 tgcaggggagtgtgagagcggggctcctccaccgcttcaggaaaacacacctgcctgcgctc 454
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   465 TGCAGGGGAGTGTGAGAGCGGGGCTCCTCCACCGCTTCAGGAAAACCACCTCAGACACTGCCTC 524

Db   455 agctgtctccaaatgccgaaatggtcaagtgtgagagatctctcttcttgcacagtggac 514
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   525 AGCTGCTCCAAATGCCGAAATGGGTCAGGTGGAGATCTCTCTTCTTGCACAGTGGAC 584

Db   515 cgggacaccgtgtgtggctgtcaggaagaccagtacgggcattattggagtgaaaacctt 574
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   585 CGGGACACCGTGTGTGGCTGTCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAAACCTT 644

Db   575 ttccagtgcttcaattgcagaccgtgaccctgccacctctccctgccaggag 634
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   645 TTCCAGTGCTTCAATTGCAGACCGTGCACCGGCTGCTGCCCTGCCTCAATGGGAACCGGTGACCCTCCTGCCAGGAG 704

Db   635 aaacagaacacccgtgtgcaacctgccagtgcaggttttcttcttcttaagaagaagaagggtgtgtc 694
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   705 AAACAGAACACCCGTGTGCAACCTGCCAGTGCAGGGTTTTCTTTTCTTAAGAAGAAGAAGAGAGTGTGTC 764

Db   695 tcctgtagtaactgtaagacaaagcctgagtgcagaagtgttgcctacccagattgag 754
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   765 TCCTGTAGTAACTGTAAGAAAAAGCCTGAGTGCAGAAGTGTTGCCTACCCCAGATTGAG 824

Db   755 aatgttaagggcactgaggaaccttcaggccacacag 788
         |||||||||||||||||||||||||||||||||||||
Qy   825 AATGTTAAGGGCACTGAGGAACTCAGGCCACACACAG 858

RESULT  4
ID   Q20973 standard; DNA; 2062 BP.
AC   Q20973;
DT   11-MAY-1992 (first entry)
DE   TNF-alpha binding protein gene.
KW   Tumour necrosis factor alpha; autoimmune diseases; cachectin; ss;
KW   extracellular domain.
OS   Homo sapiens.
FH   Key            Location/Qualifiers
FT   CDS            155..1522
FT   /*tag=  a
FT   sig_peptide    155..274
FT   /*tag=  b
FT   mat_peptide    275..1522
FT   /*tag=  c
FT   misc_feature   473..532
FT   /*tag=  d
FT   /note=  "homologous to probe Q20974"
FT   misc_feature   242..751
FT   /*tag=  e
FT   /note=  "encodes the extracellular domain of human
FT   TNF alpha receptor"
PN   GB2246569-A.
PD   05-FEB-1992.
PF   15-JUN-1990; 013410.
PR   15-JUN-1990; GB-013410.
PA   (CHAR-) CHARING CROSS SUNLE.
PI   Feldman M, Gray P, Turner M, Brennan F;
WPI: 92-043613/06.
DR   P-PSDB; R20787.
PT   New tumour necrosis factor alpha binding protein and polypeptide
PT   - useful in treating cachexia, sepsis and auto immune diseases
PT   e.g. rheumatoid arthritis
PS   Disclosure; Fig 1; 25pp; English.
CC   The sequence is that of DNA encoding tumour necrosis factor alpha
CC   binding protein which was obtd. from a human placental cDNA library
CC   in lambda gt11 using a probe (Q20974). The DNA also encodes the
CC   extracellular domain of human TNF alpha receptor and as such it is
CC   useful for treating diseases where TNF alpha is involved as a
CC   causative agent, e.g. cachexia, sepsis and autoimmune diseases,
CC   specifically rheumatoid arthritis. See also Q20974.
SQ   Sequence     2062 BP;  429 A;  616 C;  573 G;  444 T;

Query Match        39.5%;  Score 514;  DB 3;  Length 2062;
Best Local Similarity 100.0%;
Matches    514;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Db   275 gatagtgtgtccccaaggaaaatatatccacctcaaaataattcgatttgctgtacc 334
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCTCAAAATAATTCGATTTGCTGTACC 404

Db   335 aagtgccacaaaggaacctacttgtacaatgactgtgtccaggcccgggcaggatacggac 394
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTGTCCAGGCCCGGGGCAGGATACGGAC 464

Db   395 tgcaggggagtgtgagagcggggctcctccaccgcttcaggaaaacacacctgcctc 454
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   465 TGCAGGGGAGTGTGAGAGCGGGGCTCCTCCACCGCTTCAGGAAAACCACCTCAGACACTGCCTC 524
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Left column

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Db  455 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctctcttgcacagtggac 514
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Qy  525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db  515 cgggacacccgtgtgtgggctgcaggaagaaacagtaccggcgcattattgggagtgaaacctt 574
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Qy  585 CGGGACACCCGTGTGTGGGCTGCAGGAAGAAACAGTACCGGCGCATTATTGGGAGTGAAAACCTT 644

Db  575 ttccagttgcttcaattgcagcctctgcctcaatgggaccgtgcacctctctgccaggag 634
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  645 TTCCAGTTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCTGCCAGGAG 704

Db  635 aaacagaacaccgtgtgccactgcaggtttcttcttctaagagaaaacgagagtggtgtc 694
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Qy  705 AAACAGAACACCGTGTGCCACTGCAGGTTTCTTCTTCTAAGAGAAAACGAGAGTGGTGTC 764

Db  695 tcctgtagtaactgtaagaaaagcctggagtgcacgaagttgtgcctaccccccagattgag 754
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  765 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCCAGATTGAG 824

Db  755 aatgttaaggggcactgaggagactcaggcacacag 788
        ||||||||||||||||||||||||||||||||||||
Qy  825 AATGTTAAGGGGCACTGAGGAGACTCAGGCACACAG 858
```

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RESULT 5

ID   Q10883 standard; cDNA; 2088 BP.
AC   Q10883;
DT   13-MAY-1991 (first entry)
DE   30kD TNF inhibitor precursor gene in lambda-gt10-7ctnfbp.
KW   Tumour necrosis factor; inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             171..1536
FT   /*tag=  a
PN   AU905976-A
PD   24-JAN-1991.
PF   16-JUL-1990; 058976.
PR   18-JUL-1989; US-381080.
PR   11-DEC-1989; US-450329.
PR   07-FEB-1990; US-479661.
PA   (SYNE-) SYNERGEN INC.
DR   WPI; 91-073847/11.
DR   P-PSDB; R10986.
PT   Tumour necrosis factor inhibitor - for suppression of TNF-alpha
PT   and -beta, useful as therapeutic agent.
PS   Disclosure; Fig 21; 142pp; English.
CC   The sequence encodes the entire 30 kD TNF inhibitor. The clone from
CC   which the sequence was obtd. was isolated from a cDNA library
CC   prepd. from RNA form U937 cells treated with PMA/PHA. The whole
CC   gene can be inserted into expression vectors for prepn. of TNF
CC   inhibitor for use in the treatment of inflammatory and degenerative
CC   diseases.
CC   See also Q10878, Q10884 and Q10907.
SQ   Sequence 2088 BP; 439 A; 626 C; 578 G; 445 T;

Query Match              39.5%;  Score 514;  DB 2;  Length 2088;
Best Local Similarity   100.0%;
Matches   514;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Db  289 gatagtgtgtccccaaggaaatatatccaccctccaaaataattcgattgtgtacc 348
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAAATAATTGCTGTACC 404

Db  349 aagtgccacaaaggaaacctacttgttacaatataatccaccctcaaaaataatatcc 408
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  405 AAGTGCCACAAAGGAAACCTACTTGTTACAATATATCCACCCTCAAAAATAATTGCTGTACC 464

Db  409 tgcaggagagtgtgagagcggtctcctccaccgcttcagagaaaaccaccacactgcctc 468
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Qy  465 TGCAGGAGAGTGTGAGAGCGGTCTCCTTCACCGCTTCAGAGAAAAACCACCACACTGCCTC 524
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Right column

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Db  469 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctctcttgcacagtggac 528
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Qy  525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 584

Db  529 cgggacacccgtgtgtgggctgcaggaagaaacagtaccggcgcattattgggagtgaaacctt 588
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Qy  585 CGGGACACCCGTGTGTGGGCTGCAGGAAGAAACAGTACCGGCGCATTATTGGGAGTGAAAACCTT 644

Db  589 ttccagttgcttcaattgcagcctctgcctcaatgggaccgtgcacctctctgccaggag 648
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  645 TTCCAGTTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCTGCCAGGAG 704

Db  649 aaacagaacaccgtgtgccactgcaggtttcttcttctaagagaaaacgagagtggtgtc 708
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Qy  705 AAACAGAACACCGTGTGCCACTGCAGGTTTCTTCTTCTAAGAGAAAACGAGAGTGGTGTC 764

Db  709 tcctgtagtaactgtaagaaaagcctggagtgcacgaagttgtgcctaccccccagattgag 768
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Qy  765 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCCAGATTGAG 824

Db  769 aatgttaaggggcactgaggagactcaggcacacag 802
        ||||||||||||||||||||||||||||||||||||
Qy  825 AATGTTAAGGGGCACTGAGGAGACTCAGGCACACAG 858
```

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RESULT 6

ID   Q10955 standard; cDNA; 2111 BP.
AC   Q10955;
DT   24-MAY-1991 (first entry)
DE   Encodes human 55kD TNF-binding protein.
KW   Tumour Necrosis Factor; binding protein; septic shock;
KW   autoimmune glomerulonephritis; lymphokine; cytokine.
FH   Key             Location/Qualifiers
FT   sig_peptide     187..273
FT   /*tag=  a
FT   mat_peptide     274..1551
FT   /*tag=  b
PN   EP-417563-A.
PD   20-MAR-1991.
PF   31-AUG-1990; 116707.
PR   12-SEP-1989; CH-003319.
PR   08-MAR-1990; CH-000745.
PR   20-APR-1990; CH-001347.
PA   (HOFF ) HOFFMANN-LA ROCHE AG.
PI   Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;
PI   Schlaeger EJ;
DR   WPI; 91-081851/12.
DR   P-PSDB; R11082.
PT   Insoluble tumour necrosis factor binding proteins - and DNA
PT   encoding them, useful in pharmaceutical prods. and for antibody
PT   prodn.
PS   Claim 4; Fig 1; 26pp; German.
CC   Partial amino acid sequences were determined for the 55 and 75kD
CC   TNF-BPs (see R11072-R11081) and oligonucleotide primers were
CC   synthesised based on these partial sequences. The primers were used
CC   to produce a cDNA fragment for use as aprobe to screen a human
CC   placental cDNA bank constructed in lambda gt11. Positive clones were
CC   identified and sequenced. DNA constructs comprising the TNF-BP coding
CC   sequence may also contain a fragment encoding a human Ig domain.
CC   Recombinant constructs are used to transform cells to confer
CC   improved TNF-binding properties.
CC   See also Q10956.
SQ   Sequence 2111 BP; 445 A; 628 C; 588 G; 450 T;

Query Match              39.5%;  Score 514;  DB 2;  Length 2111;
Best Local Similarity   100.0%;
Matches   514;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Db  307 gatagtgtgtccccaaggaaatatatccaccctccaaaataattcgattgtgtacc 366
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAAATAATTGCTGTACC 404
```

RESULT 7

ID   Q90513 standard; DNA; 2175 BP.
AC   Q90513;
DT   19-JAN-1996 (first entry)
DE   p55 TNF-R gene.
KW   p55; tumour necrosis factor receptor; TNF-R; human; murine; chimera;
KW   epidermal growth factor receptor; EGF-R; protease; inhibitor;
KW   phorbol myristate acetate; PMA; ss.
OS   Homo sapiens.
FH   Key   Location/Qualifiers
FT   CDS   256..1623
FT   /tag= a
FT   /product- p55 TNF-R
FT   misc_signal   2143..2149
FT   /tag- b
FT   /note= "possible poly-A signal"

PI   Batkin M, Brakebusch C, Varfolomeev E, Wallach D;
PR   12-OCT-1993; IL-107268.
PF   12-OCT-1994; 075742.
PN   04-MAY-1995.
PN   AU947574-A.
PD   15-FEB-1996.
PR   28-JUL-1995; U09576.
DR   WPI; 95-19432/26.
DR   P-PSDB; R75084.
PT   New protease capable of cleaving soluble tumour necrosis factor
PT   (TNF) receptor - from cell-bound TNF- receptor, useful for
PT   antagonising deleterious effects of TNF.

PS   Disclosure; Fig 1; 40pp; English.
CC   This sequence represents human p55 tumour necrosis factor (TNF-R) DNA.
CC   Expression of this receptor is regulated by shedding of the extracellular
CC   receptor fragment. The p55 TNF-R can be shed in response to different
CC   inducing agents, e.g. phorbol myristate acetate (PMA), depending on cell
CC   type. The only region of the receptor whose structure affects the
CC   shedding response is the spacer region (see R75012) in the extracellular
CC   domain. This region is located close to a site of cleavage of the
CC   molecule, and links the Cys rich module to the transmembrane domain. The
CC   spacer region of the encoded protein was used to create the chimeras
CC   between human p55 TNF-R and murine epidermal growth factor receptor
CC   (EGF-R) that are represented by R75007-11. This spacer region was
CC   subjected to deletion mutations (R75013-25) and substitutions

Query Match   39.58; Score 514; DB 15; Length 2175;
Best Local Similarity   100.0%;
Matches   514; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   376 gatagtgtgtcccaaaggaagaaccaccggccaccgccaccttgaagtagaaactt 435
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   345 GATAGTGTGTGTCCCAAGGAAGAAAATATATCCACCCTCAAAATAATTCGAATGTGTACC 404

CC   (R75026-47); Of the spacer region, the most important residues are
CC   Asn 172, Val 173, Lys 174 and Gly 175, with Val 173 being the most
CC   important of these. The shedding of the receptor is independent of the
CC   side chain identity of these residues, with the exception of a limited
CC   dependence on the identity of Val 173. Mutations which alter the
CC   conformation of the protein adversely effect the shedding process. The
CC   mutations shown in R75013-47 were introduced in order to create an
CC   inhibitor of a protease that is capable of cleaving the soluble TNF-R
CC   from the cell bound TNF-R. Fragments of these inhibitors can be seen in
CC   R75017-9, R75025, R75033-5 and R75042-3. These protease inhibitors can
CC   be used for enhancing TNF function.

SQ   Sequence 2175 BP; 474 A; 642 C; 603 G; 456 T;

Qy   376 gatagtgtgtcccaaaggaagaaccaccggccaccgccacccttgaagtagaaactt 435
Qy   436 aagtgcccacaaaggaacctacttgtacaatgactgactgtccaagccagggatcaggac 495
Qy   496 tgcaggggagtgtgagagacggctccttccttcacgcttcagagaaaacaactcagacactgccctc 555
Qy   556 agctgcctccaaatcgccgaaaggaaaatgggtcaggttggagagatctctcttctctgcacagttggac 615
Qy   616 cgggacacgtgtgttgtggctgcaggagagaaccaccggccaccgccaccttgaagtagaaactt 675
Qy   676 ttccagtgcttcaattgcagccctctcgcctcaatggggaccgttgcaccttctcctgccaggag 735
Qy   705 AAACAGAACACCGTGTCGCACCTCCAATCGCAGG 764
Qy   727 tcctgtgtagtaactgtaagaaaagccctggagtgtcacgaagtgttgtcctacccacagattgag 786
Qy   765 TCCTGTAGTAACTGTAAGAAAACCTGGAGTGTGCACGAAGTTGTGCCTACCCAGATTGAG 824
Qy   796 tcctgtagtaactgtaagaaaagccctggagtgtcacgaagttgtcctacccacagattgag 855
Qy   825 AATGTTAAGGGCACTGAGGACTCAGGCACCACACAG 858

Db   367 aagtgcacaaaggaacctacttgtacaatgactgtccaagggccccggggaggagatacggac 426
Db   405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAAGCCCAGGGCAGGGATACGGGAC 464
Db   427 tgcaggggagtgtcagagagacgggctccttccaccgcttcagaaaacacacttcagacaagctgcctc 486
Db   465 TGCAGGGAGTGTGAGACGGGCTCCTTCACCGCTTCAGAAAAACACCCTCAGACACTGCCTC 524
Db   487 agtcgtcccaaatgccgaaaggaaatgggtcaggttgagaagatctctcttctctgcacagttggac 546
Db   525 AGTGCGTTCAAAATGCCGAAAGGAAATGGGTCAGGTGGAGAATCTCTTCTTGCACAGTGGAC 584
Db   547 cgggaccacgtgtgctgcaggagaaaaaccagtacccgggcattattggtaaaaacctt 606
Db   585 CGGGACACCGTGTGGTGCAGGAGAACCAGTACCCGGCATTATTGGTGAGTGAAAACCTT 644
Db   607 ttccagtgcttcaattgcagccctctcgcctcaatggcagacctctcctgccaggag 666
Db   645 TTCCAGTGCTTCAATTGCAGCCCTCTCGCCTCAATGGGGACCGTTGCACCTTCTCCTGCCAGGAG 704
Db   667 aaacagaacaccgtgtgcaacctgcaatcgcaggagtttcttcttctaagacagaaacgagtgtgtc 726
Db   705 AAACAGAACACCGTGTGCAACCTCCAATCGCAGGAGTTTCTTCTTCTAAGAGAAAACGAGTGTGTC 764
Db   727 tcctgtgtagtaactgtaagaaaagccctggagtgtcacgaagttgtcctacccacagattggag 786
Db   765 TCCTGTGTAGTAACTGTAAGAAAACCTGGAGTGTGCACGAAGTTGTGCCTACCCAGATTGAG 824
Db   787 aatgttaagggcactgaggactcaggcaccacag 820
Db   825 AATGTTAAGGGCACTGAGGACTCAGGCACCACACAG 858

RESULT 8

ID   T15931 standard; DNA; 6889 BP.
AC   T15931;
DT   20-JUN-1996 (first entry)
DE   DHFR/intron (WTrasSD)-TNFr-IgG dicistronic vector.
KW   Recombinant host cell; dihydrofolate reductase; selectable marker;
KW   DHFR; ras splice donor; dicistronic vector; gene expression;
KW   immunoadhesin; TNFr-IgG; tumour necrosis factor; ds.
OS   Synthetic.
PN   WO9604391-A1.
PD   15-FEB-1996.
PR   28-JUL-1995; U09576.
PR   05-AUG-1994; US-286740.
PA   (GETH) GENENTECH INC.
PI   Crowley CW;
DR   WPI; 96-129407/13.
PT   Improved process for the selection of recombinant host cells
PT   expressing high level of a desired product - uses eukaryotic host
PT   cells contg. a DNA construct comprising a selectable gene

Qy   856 aatgttaagggcactgaggactcaggcaccacag 889
         ||||||||||||||||||||||||||||||||||
Db   825 AATGTTAAGGGCACTGAGGACTCAGGCACCACACAG 858

Db   736 aaacagaacaccgtgtgcaacctgccatgcaggtttcttcttctaagagaaaacgagtgtgtc 795
Db   705 AAACAGAACACCGTGTGCAACCTGCCATGCAGGTTTCTTCTTCTAAGAGAAAACGAGTGTGTC 764
Db   796 tcctgtagtaactgtaagaaaagccctggagtgtcacgaagttgtgcctacccacagattgag 855
Db   765 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGTGCCTACCCAGATTGAG 824
Db   856 aatgttaagggcactgaggactcaggcaccacag 889
Db   825 AATGTTAAGGGCACTGAGGACTCAGGCACCACACAG 858

Example 2: Page 36-42; 137pp; English.

PS   A dicistronic vector (TI5930) comprises a regulatory region
CC   derived from the cytomegalovirus immediate-early gene, a
CC   selectable dihydrofolate reductase gene positioned within an
CC   intron having a 5' wild-type ras splice donor site, a downstream
CC   sequence coding for an immunoadhesin, TnFr-IgG, capable of binding
PS   tumour necrosis factor, and a poly-A sequence. Transfection of CHO
PT   DHFR- cells and subsequent methotrexate amplification and growth of
CC   the cells in nutrient-rich medium gave TnFr-IgG in yields of 9.5
CC   ug/ml (15-fold higher compared to conventional vector amplified
CC   pools).
SQ   Sequence 6889 BP;   1729 A;   1826 C;   1681 G;   1653 T;

Query Match
Best Local Similarity 100.0%;   Score 514;   DB 18;   Length 6889;
Matches 514;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy 1725 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataaattcgatttgtgtgtacc 1784
         |||||||||||||||||||||||||||||||||||||||||||||||||||| |||| ||||
Db   345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAAATTCGATTTGCTGTACC 404

Qy 1785 aagtgccacaaaggaacctactcttgtacaatgactgtccaggcgccgggggcaggatacggac 1844
         ||||||||||||||||||||| ||||||||||||||||||||| |||||||||||||||||||
Db   405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCCGGGGGCAGGATACGGAC 464

Qy 1845 tgcaggggagtgtgagagcggcggctcctttcacccgcttcagaaaaacaccactgcctc 1904
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   465 TGCAGGGGAGTGTGAGAGCGGCGGCTCCTTTCACCCGCTTCAGAAAAACACCACTGCCCTC 524

Qy 1905 agctgctccaaatgccgaaaaatgggtcaagtgagagtctcttcttcacagtggac 1964
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   525 AGCTGCTCCAAATGCCGAAAAGAAATGGGTCAGGTGGAGATCTCTTCTTGACAGTGGAC 584

Qy 1965 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaacctt 2024
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Qy 2025 ttccagtgctccaattgcagccgctctgcacctcctcctgccaggag 2084
         |||||||||||||||||||||||||||||||||||||||||||||||
Db   645 TTCCAGTGCTCCAATTGCAGCCGCTCTGCCACCTCCTCCTGCCAGGAG 704

Qy 2085 aaacagaacaccgtgtcacctgcatgcaggttcttctttctaagagaaaacgagtgtgtc 2144
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   705 AAACAGAACACCGTGTGCACCTGCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Qy 2145 tcctgtagtaactgtaagaaaagcctggagtcgcacgaagttgtgtcctacccccagattgag 2204
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   765 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTCGCACGAAGTTGTGTCCTACCCCCAGATTGAG 824

Qy 2205 aatgttaagggcactgaggactcaggcaccacag 2238
         ||||||||||||||||||||||||||||||||||
Db   825 AATGTTAAGGGCACTGAGGACTCAGGCCACCACAG 858

RESULT 9

ID   Q06285 standard; DNA; 2141 BP.
AC   Q06285;
DT   29-JAN-1991 (first entry)
DE   Human Tumour Necrosis Factor-Receptor cDNA insert.
KW   Tumour necrosis factor binding protein; TNF-receptor;
OS   Homo sapiens.
KW   lambdaTNF-R2; ratNF-R8; ss.
FH   Key   Location/Qualifiers
FH
FT   CDS   213..1577
FT   /*tag=   a
FT   /label=huTNF-R
PN   EP-393438-A
PD   24-OCT-1990.
PD   06-APR-1990; 106624.
PR   21-APR-1989; DE-913101.
PR   21-JUN-1989; DE-920282.
PA   (BOEH) BOEHRINGER INGELHEIM1NT.
PI   Hauptmann R, Himmler A, Maurer-Fogy I, Stratowa C;

DR   WPI; 90-321987/43.
DR   P-PSDB; R07451.
PT   DNA encoding TNF binding protein and TNF- receptor - used in
PT   tumour treatment and to understand mechanismsm to TNF action
PS   Disclosure; Fig 91(1-2); 51pp; German.
CC   raTNF-R8 (Q06284) was used to screen the HS913T cDNA library.
CC   lambdaTNF-R2 encodes the complete human TNF-R2 and was used to
CC   construct a plasmid (pADTNF-R) expressing the product the same way
CC   as pADFNF-BP (see Q06282).
CC   See also Q06282-Q06285.
SQ   Sequence 2141 BP;   455 A;   633 C;   593 G;   460 T;

Query Match
Best Local Similarity 99.8%;   Score 512;   DB 1;   Length 2141;
Matches 513;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

Qy   333 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataaattcgatttgtgtgtacc 392
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAAATTCGATTTGCTGTACC 404

Qy   393 aagtgccacaaaggaacctactcttgtacaatgactgtccaggcgccgggggcaggatacggac 452
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCCGGGGGCAGGATACGGAC 464

Qy   453 tgcaggggagtgtgagagcggcggctcctttcacccgcttcagaaaaacaccactgcctc 512
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   465 TGCAGGGGAGTGTGAGAGCGGCGGCTCCTTTCACCCGCTTCAGAAAAACACCACTGCCCTC 524

Qy   513 agctgctccaaatgccgaaaaatgggtcaagtgagagtctcttcttcacagtggac 572
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   525 AGCTGCTCCAAATGCCGAAAAGAAATGGGTCAGGTGGAGATCTCTTCTTGACAGTGGAC 584

Qy   573 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaacctt 632
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   585 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 644

Qy   633 ttccagtgctccaattgcagccgctctgcacctcctcctgccaggag 692
         |||||||||||||||||||||||||||||||||||||||||||||||
Db   645 TTCCAGTGCTCCAATTGCAGCCGCTCTGCCACCTCCTCCTGCCAGGAG 704

Qy   693 aaacagaacaccgtgtcacctgcatgcaggttcttctttctaagagaaaacgagtgtgtc 752
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   705 AAACAGAACACCGTGTGCACCTGCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 764

Qy   753 tcctgtagtaactgtaagaaaagcctggagtcgcacgaagttgtgtcctacccccagattcag 812
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   765 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTCGCACGAAGTTGTGTCCTACCCCCAGATTGAG 824

Qy   813 aatgttaagggcactgaggactcaggcaccacag 846
         ||||||||||||||||||||||||||||||||||
Db   825 AATGTTAAGGGCACTGAGGACTCAGGCCACCACAG 858

RESULT 10

ID   Q12215 standard; DNA; 2176 BP.
AC   Q12215;
DT   12-SEP-1991 (first entry)
DE   Type I TNF receptor.
KW   Tumour Necrosis Factor; TNF; binding protein; TBP-I; ss.
OS   Homo sapiens.
FH   Key   Location/Qualifiers
FH
FT   terminator   244..246
FT   /*tag=   a
FT   CDS   256..1620
FT   /*tag=   a
FT   /note=   "in-frame termination codon"
FT   /*tag=   a
FT   /product= type I TNF receptor
FT   sig_peptide   256..318
FT   /*tag=   b
FT   /product= type I TNF receptor
FT   /*tag=   b
FT   mat_peptide   319..1620
FT   /*tag=   c
FT   misc_RNA   319..864
FT   /*tag=   d

FT   /label= soluble_domain
FT   /note= "may be 2 codons shorter or a few codons
FT   longer"
FT   misc_feature   376..414
FT   /note= "TBP-I derived sequence"
FT   /tag= e
FT   misc_feature   583..627
FT   /note= "TBP-I derived sequence"
FT   /tag= f
FT   misc_feature   850..858
FT   /note= "TBP-I derived sequence"
FT   /tag= g
FT   misc_RNA   889..957
FT   /tag= h
FT   /label= transmembrane_domain
FT   repeat_unit   385..504
FT   /tag= i
FT   repeat_unit   505..633
FT   /number= 1
FT   /tag= j
FT   repeat_unit   634..756
FT   /number= 2
FT   /tag= k
FT   repeat_unit   757..858
FT   /number= 3
FT   /tag= l
FT   repeat_unit
FT   /number= 4
FT   /tag=
FT   polyA_signal   2145..2150
FT   /tag= m

PN   EP-433900-A.
PD   26-JUN-1991.
PD   13-DEC-1990; 124133.
PR   13-DEC-1989; IL-092697.
PR   12-JUL-1990; IL-095064.
PA   (YEDA) YEDA RES & DEV CO LTD.
PI   Wallach D, Nophar Y, Kemper O, Engelmann H, Brakebusch C;
PI   Aderka D;
WPI: 91-186774/26.
DR   P-PSDB; R12550.

CC   Recombinant tumour necrosis factor binding protein I - prepd. by
CC   transfecting eukaryotic cells with vector contg. deoxyribonucleic
CC   acid encoding human type I TNF receptor or soluble domain
PS   Disclosure; Fig 1(D);30pp; English.
PT   The Tumour Necrosis Factor Binding Protein I is the soluble form of
PT   type I TNF-receptor and constitutes a fragment of the cell surface
CC   form of this receptor, corresp. to its extracellular domain.
CC   There is no characteristic poly(A) addition signal near the 3' end
CC   of the cDNA. The sequence ACTAAA (tag m) may serve as an
CC   alternative to this signal, but with low efficiency.
CC   See also Q12212-15.
SQ   Sequence 2176 BP;

Query Match   39.4%;   Score 512;   DB 2;   Length 2176;
Best Local Similarity   99.8%;   Pred. No. 0.00e+00;
Matches 513;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

475 A;   644 C;   602 G;   455 T;

```
Qy  585  CGGGACACCCGTGTGTGGGCGTGCAGGAGAACCAGTACCGGCGATTATTGGAGTGAAAACCTT  644
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  676  ttccagtgcttcaattgcagcctctgccctcaagtgggacggtgcacctccctgccaggag  735
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  645  TTCCAGTGCTTCAATTGCAGCCTCTGCCCTCAAGTGGGACGGTGCACCTCCCTGCCAGGAG  704
Db  736  aaacagaacaccgtgtgcacctgccatgcagcaggttctttctaagagaagaaacgagtgtgtc  795
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  705  AAACAGAACACCGTGTGCACCTGCCATGCAGCAGGTTCTTTCTAAGAGAAGAAACGAGTGTGTC  764
Db  796  tcctgctagtaacttgaagaaagctctgggatgcacgaagttgtgctacccagaggttgag  855
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  765  TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGTTACCCCAGAGTTGAG  824
Db  856  aatgttaaggggcactgaggaactcaggcacacacag  889
         ||||||||||||||||||||||||||||||||||||
Qy  825  AATGTTAAGGGGCACTGAGGAGACTCAGGCACCACAG  858
```

RESULT   11
ID   Q50870 standard; DNA; 2170 BP.
AC   Q50870;
DT   13-MAY-1994 (first entry)
PN   EP-568925-A.
PD   10-NOV-1993.
DE   p55 Tumour necrosis factor receptor coding sequence.
KW   TNF; tumour necrosis factor; receptor; disease; autoimmunity;
KW   rheumatoid arthritis; graft rejection; graft vs. host; septic shock;
KW   effector protein; ss.
OS   Homo sapiens.

Key   Location/Qualifiers
FH
CDS   256..1623
FT   /*tag= a
FT   /product= p55 Tumour necrosis factor receptor.

DR   WPI; 93-353057/45.
DR   P-PSDB; R42197.
PA   (YEDA) YEDA RES & DEV CO LTD.
PI   Brakebusch C, Wallach D;
PR   03-MAY-1992; IL-101769.
PR   29-APR-1993; 106981.
PS   Claim 2; Figure 1; 17pp; English.

PT   Modulating activity of tumour necrosis factor receptor - using
PT   peptide(s), antibodies, etc. which interact with critical regions
PT   of receptor or effector protein, for controlling auto-immune
PT   disease, septic shock, etc.
CC   Modification of the tumour necrosis factor receptor by mutation or
CC   deletion modulates signal transduction and/or cleavage effected by
CC   the receptor. This modulation of activity can also be achieved
CC   using effector proteins which interact with the TNF receptor.
CC   Molecules which interact with the TNF receptor or the effector
CC   proteins can be used to treat or prevent diseases associated with
CC   TNF activity e.g. autoimmune disease; rheumatoid arthritis; graft
CC   rejection; graft vs. host disease or septic shock. They can also
CC   be used to treat overdoses of exogenous TNF.
SQ   Sequence 2170 BP;

Query Match   39.28%;   Score 510;   DB 9;   Length 2170;
Best Local Similarity   99.6%;   Pred. No. 0.00e+00;
Matches 512;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

474 A;   657 C;   584 G;   455 T;

```
Db  376  gatagtgtgtgtcccaaggaaaatatatccacctcaaaataattcgatttgctgtacc  435
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  345  GATAGTGTGTGTCCCAAGGAAAAATATATCCACCTCAAAATAATTCGATTTGCTGTACC  404
Db  436  aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac  495
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  405  AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC  464
Db  496  tgcagggagtgtgagagcggctccttcacccgcttcagagaaacaccactcagcctcctc  555
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  465  TGCAGGGAGTGTGAGAGCGGCTCCTTCACCCGCTTCAGAGAAACACCACTCAGCCTCCTC  524
```

Db 376 gatagtgtgtgtcccaaggaaaatatatccacctcaaaataattcgattttgctgtacc 435
Qy 345 GATAGTGTGTGTCCCAAGGAAAAATATATCCACCTCAAAATAATTCGATTTGCTGTACC 404
Db 436 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccggggcaggatacggac 495
Qy 405 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 464
Db 496 tgcagggagtgtgagagcggctccttcacccgcttcagagaaacaccactcagcctcctc 555
Qy 465 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCCGCTTCAGAGAAACACCACTCAGCCTCCTC 524

Db 556 agtcgctccaaatgccggaaaagaaatgggtcagtggagatctctcttcttgcacagtggac 615
Qy 525 AGTCGCTCCAAAATGCCGAAAAGAAATGGGTCAGTGGAGATCTCTTCTTTGCACAGTGGAC 584
Db 616 cgggacaccgtgtgtggctgcgaggaagaaccagtaccggcgattattggagtgaaaacctt 675

Db 556 agctgctgctccaaatgccgaaaggaaatggttcagttgacgtggagatctctcttgacagtggac 615
         |||||||| |||||||||||||||||||||| ||| |||||||||||| |||||||||||||||
Qy 525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGACAGTGGAC 584

Db 616 cgggacccgtgtggctgcaggaagaaccagtaccggcaccttattggtagtgaaaaacctt 675
         ||||||| ||||||||||||||||||||||||||||| ||| |||||||||||||||||||
Qy 585 CGGGACACCGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGTAGTGAAAAACCTT 644

Db 676 ttccagtgtcttcaattgcagacgcctcatgcgacctctcctgtccaggag 735
         |||||||||||||||||| || ||| ||| ||||| | ||| |||||||||
Qy 645 TTCCAGTGTCTTCAATTGCAGCCTCTGCCTCATGGGACGTCCACCTCCTGCCTCCAGGAG 704

Db 736 aaacagaacaccgtgtcgcacctgcctcgccatgcaggtttcttctcttaagagaaaacg 795
         ||||||||||||||||| ||||||||||||||||| ||| ||||||| |||||| |||||
Qy 705 AAACAGAACACCGTGTGCCACCTGCCTCGCCATGGGACCTCTCAATGGGACGTCCACCTC 764

Db 796 tcctgtagtaactgtaagaaagaggtcaccgaagtcgcacgaagttgctacccagattgag 855
         ||||||||||||||||||||| || || |||| ||| |||||||||| ||||| |||||||
Qy 765 TCCTGTAGTAACTGTAAGAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 824

Db 856 aatgttaaggcacactgaggactcaggcacacag 889
         |||||||||||| ||||||||||||||||||||||
Qy 825 AATGTTAAGGCACTGAGGACTCAGGCACACAG 858

RESULT 12
ID   Q24441 standard; DNA; 608 BP.
AC   Q24441;
DT   05-NOV-1992 (first entry)
DE   Encodes truncated TNF-alpha 55kd receptor (197 amino acids).
KW   tumour necrosis factor alpha; extracellular binding domain;
KW   treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
KW   autoimmune disease; rheumatoid arthritis.
OS   Homo sapiens.
PN   WO9207076-A.
PD   30-APR-1992.
PF   18-OCT-1991; G01826.
PR   18-OCT-1990; GB-022648.
PA   (CHAR-) CHARING CROSS SUNLEY RES CENT.
PI   Brennan FM, Feldmann M, Gray PW, Turner MJC;
DR   WPI; 92-167156/20.
DR   P-PSDB; R24080.
PT   New polypeptide capable of binding human TNF alpha - comprises
PT   first three cysteine-rich subdomains of TNF alpha receptor for
PT   treating autoimmune disease, septic shock, HIV etc.
PS   Example; Fig 7; 43pp; English.
CC   This sequence encodes the designed TNF-alpha 55kd receptor
CC   derivative, as present in pTNFRecd. This was produced as described in
CC   Q24441. This derivative lacks the 81 carboxyl terminal residues of
CC   the cytoplasmic domain. The derivative could be used in the
CC   regulation of TNF-alpha mediated responses by binding and
CC   sequestering human TNF-alpha e.g. in the treatment of pulmonary
CC   diseases, septic shock, HIV infection, malaria, viral meningitis,
CC   graft versus host disease and autoimmune diseases, esp. rheumatoid
CC   arthritis.
CC   See also Q24440-51, R24000, R24080-84, R27585, O29236-8
SQ   Sequence 608 BP;   148 A;   159 C;   165 G;   136 T;

Query Match   36.7%;
Best Local Similarity   99.8%;
Matches   479;   Conservative   0;   Mismatches   1;   Indels   0;   Gaps   0;

Db   129 gatagtgtgtgtccccaaggaaaatatatccacccaagaaatatcgattgctgtacc 188
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   345 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCAAGAAATATCGATTTGCTGTACC 404

Db   189 aagtgccacaaaggaacctacttgtccaaggccccggggcccggggccaggataccggac 248
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   405 AAGTGCCACAAAGGAACCTACTTGTACAAATGACTGTCCAGGCGGCCCGGGGCAGGATACCGGAC 464

Qy   465 TCCAGGAGTGTGAGACGGCGTCCTTCACCGGCTTCAGAAAACCACCTGACAACTGCCTC 524
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   309 agctgctccaaatgccgaaaggaaatggggtcaggtggagatctctcttgacagtggac 368

Qy   525 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGACAGTGGAC 584
          ||||||||||||||||||||||||||||| ||||||||||||||| |||||||||||||
Db   369 cgggacaccgtgtggctgcaggaagaaccagtaccggcattattggtagtgaaaaacctt 428

Qy   585 CGGGACACCGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGTAGTGAAAAACCTT 644
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   429 ttccagtgtcttcaattgcagcctctgcctcatgggacgtccacctcctgcctccaggag 488

Qy   645 TTCCAGTGTCTTCAATTGCAGCCTCTGCCTCATGGGACGTCCACCTCCTGCCTCCAGGAG 704
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   489 aaacagaacaccgtgtgccacctgcctcgccatgggacctctcaatgggacgtccacctc 548

Qy   705 AAACAGAACACCGTGTGCCACCTGCCTCGCCATGGGACCTCTCAATGGGACGTCCACCTC 764
          |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db   549 tcctgtagtaactgtaagaaagcctggagtgcacgaagttgtgcctaccccagattag 608

Qy   765 TCCTGTAGTAACTGTAAGAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 824

RESULT 13
ID   Q14800 standard; DNA; 579 BP.
AC   Q14800;
DT   11-FEB-1992 (first entry)
DE   Human chorionic gonadotropin beta subunit analogue.
KW   Glycoprotein hormone; hCGB'; fertility; immuno-castration;
KW   immuno-contragestive; vaccine; ds.
OS   Homo sapiens.
FH   Key   Location/Qualifiers
FH
FT   CDS   26..523
FT   mat_peptide   86..520
FT   /tag= a
FT   /tag= b
FT   sig_peptide   26..85
FT   /tag= c
FT   polyA_site   524..579
FT   /tag= d
FT   mutation   229
FT   /tag= e
FT   /note="c -> g"
FT   mutation   232
FT   /note="c -> g"
FT   /tag= f
FT   /tag= g"
PN   WO9116922-A.
PD   14-NOV-1991; U03162.
PF   07-MAY-1990; US-520703.
PR   08-MAY-1990; US-520703.
PA   (UYNE-) UNIV MED NEW JERSEY.
PI   Campbell RK, Moyle WR;
DR   WPI; 91-353528/48.
DR   P-PSDB; R15043.
PT   New glyco-protein hormone analogues - for inducing fertility as
PT   immuno-castration agents, for suppressing reproductive system
PT   development and as immuno-contragestive vaccines.
PS   Example 3; Fig 4a; 94pp; English.
CC   The sequence is an analogue of hCG beta subunit cDNA contg. two
CC   silent mutations which eliminate restriction sites. It was prepd.
CC   from the plasmid pKMB-hCG-beta, a construct contg. the hCG beta
CC   subunit isolated from human placenta (Fiddes and Goodman) in
CC   plasmid pKMB, a derivative of pUC18 designed to facilitate cloning
CC   of glycoprotein hormones. The sequence was used as the starting
CC   construct for many mutants. (See R15061-R15125 and R15161-R15198).
SQ   Sequence 579 BP;   205 C;   151 G;   95 T;

Query Match   32.0%;
Best Local Similarity   99.5%;
Matches   418;   Conservative   0;   Mismatches   2;   Indels   0;   Gaps   0;

Db   104 ccacggtggccgcccatcaatgccaccctggctgtggagaaggagggctgccccgtgtgc 163
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy   870 CCACGGTGCGCGCGCCATCAATGCCACCCTGGCTGTGTGGAGAGGAGGGGCTGCGCCCGTGTGC 929
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   164 atcaccgtcaacacactctgtgccggctactgccccaccatgacccgtgctgcag 223
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   930 ATCACCGTCAACACACTATGTGCCGGCTACTGCCCCACCATGACCCGCGTGCTGCAG 989

Db   224 gggtgtgtccccggccctgccttgcaaactacccggatgtgcgttcagagtcc 283
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   990 GGGGTCCTGCCGGCCCTGCCTCAGGTGGTGCGAACTACCGCGGCTTCGAGTCC 1049

Db   284 atccggtgctccctggcctgcccgccgcggggcgtggtgtccctactgccgttggctctc 343
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1050 ATCCGGCGTCCCTGGCTGCCGCGCCGGGGCGTGAACCCGTGGTCTTCTACGCCGTGGCTCTC 1109

Db   344 agctgtcaatgtgcactctgccgccgcgcagcacaactgactgcggggtccccaaggaccac 403
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1110 AGCTGTCAATGTGCACTCTGCCGCCGCAGCACCACTGACTGCGGGGTCCCCAAGGACCAC 1169

Db   404 ccttgacctgtgatgaccccccgcttccaggactccctcttcctcaaaggcccctcccccc 463
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1170 CCCTTGACCTGTGATGACCCCCCGCTTCCAGGACTCCCTCTTCCTCAAAGGCCCCTCCCCCC 1229

Db   464 agcctccaagcccatcccgactcccggggacacccgaatccctccacaataa 523
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1230 AGCCTTCCAAGCCCATCCCGACTCCCGGGGCGCCCTCCGGACACCCGAATCCCTCCACAATAA 1289

RESULT 14

ID   T03212 standard; cDNA; 836 BP.
AC   T03212;
DT   26-APR-1996 (first entry)
DE   Single chain gonadotropin analogue 1 coding sequence.
KW   Single chain gonadotropin; human chorionic gonadotropin; hCG;
KW   alpha; beta; subunit; analogue; glycoprotein hormone; fertility;
KW   inhibit; stimulate; increase; lutropin; luteinising hormone; LH;
KW   follicle stimulating hormone; FSH; vaccine; contraceptive; ds.
OS   Synthetic.
FH   Key   Location/Qualifiers
FT   CDS   33..830
FT   /tag= a
FT   /transl_except= pos:240..242, aa:Arg
FT   sig_peptide   33..92
FT   /tag= b
FT   mat_peptide   93..827
FT   /tag= c
FT   /label= Analogue_1
FT   /note= "nucleotides 93..527 encode amino acids
FT   1-145 of hCG beta-subunit; nucleotides
FT   528..551 encode a (Gly-Ser)4 linker and
FT   nucleotides 552..827 encode amino acids
FT   1-92 of gonadotropin alpha-subunit"
FT   misc_feature   1..26
FT   /tag= d
FT   /label= sticky_end
FT   /note= "single-strand overhang. The complementary
FT   strand also has a single-strand overhang at
FT   its 5'-end; the sequence of the overhang is
FT   5'-TCCGGATTAGCTTGAGATGGATCC-3'"
PN   WO9522340-A1.
PD   24-AUG-1995.
PF   17-FEB-1995; U02067.
PR   18-FEB-1994; US-199382.
PA   (SENS-) SENSI-TEST.
PI   Moyle WR;
PT   Methods for altering fertility in mammals, esp. humans - e.g.
PT   stimulating fertility by reducing the activity and/or levels of
PT   circulating glyco:protein hormones having lutropin activity
PS   Example 12; Fig 6; 10pp; English.
DR   WPI; 95-302553/39.
DR   P-PSDB; R86247.

CC   Analogue 1 (human CG-beta(1-145)-linker-human CG-alpha(1-92)) is a
CC   specific example of a single chain gonadotropin having a chorionic
CC   gonadotropin (CG) beta-subunit at the N-terminus and a CG alpha-

---

CC   subunit at the C-terminus, joined by a linker of 1-16 amino acids.
CC   The analogue has luteinising hormone (lutropin) activity and is
CC   useful for inducing ovulation and increasing male fertility.
CC   The sequences coding for analogue 1 were cloned from a human
CC   placental cDNA library using strand overlap extension PCR.
SQ   Sequence 836 BP; 166 A; 282 C; 222 G; 166 T;

Query Match   31.9%; Score 415; DB 17; Length 836;
Best Local Similarity 99.8%; Pred. No. 3.64e-278;
Matches 416; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy   111 ccacggtgcgcgcccatcaatgccacccctggctgtgtggagaggaggggctgcgcccgtgtgc 170
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   870 CCACGGTGCGCGCGCCATCAATGCCACCCCTGGCTGTGTGGAGAGGAGGGGCTGCGCCCGTGTGC 929

Qy   171 atcaccgtcaacacacactctgtgccggctactgccccaccatgacccgtggctgctgcag 230
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   930 ATCACCGTCAACACACTATGTGCCGGCTACTGCCCCACCATGACCCGCGTGCTGCAG 989

Qy   231 gggtgtcctgccggccctgcctcaggtggtgtcaactaccgcggcttcgagtcc 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   990 GGGGTCCTGCCGGCCCTGCCTCAGGTGGTGCGAACTACCGCGGCTTCGAGTCC 1049

Qy   291 atccggcgtcccctggctgccgcgccggggcgtgaacccgtggtcttctacgccgtggctctc 350
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1050 ATCCGGCGTCCCTGGCTGCCGCGCCGGGGCGTGAACCCGTGGTCTTCTACGCCGTGGCTCTC 1109

Qy   351 agctgtcaatgtgcactctgccgccgcgcagcacaactgactgcggggtccccaaggaccac 410
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1110 AGCTGTCAATGTGCACTCTGCCGCCGCAGCACCACTGACTGCGGGGTCCCCAAGGACCAC 1169

Qy   411 ccttgacctgtgatgaccccccgcttccaggactccctcttcctcaaaggcccctcccccc 470
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1170 CCCTTGACCTGTGATGAGCCCCCGCTTCCTCTTCCTCAAAGGCCCCTCCCCCC 1229

Qy   471 agcctccaagcccatcccgactcccggggacacccgaatccctccaccccaa 527
              |||||||||||||||||||||||||||||||||||||| |||
Db 1230 AGCCTTCCAAGCCCATCCCGACTCCCGGGGCGCCCTCCGGACACCCGAATCCCTCCACA 1286

RESULT 15

ID   T03243 standard; cDNA; 836 BP.
AC   T03243;
DT   08-MAY-1996 (first entry)
DE   Single chain gonadotropin analogue 1a coding sequence.
KW   Single chain gonadotropin; human chorionic gonadotropin; hCG;
KW   alpha; beta; subunit; analogue; glycoprotein hormone; fertility;
KW   inhibit; stimulate; increase; lutropin; luteinising hormone; LH;
KW   follicle stimulating hormone; FSH; vaccine; contraceptive; ds.
OS   Synthetic.
FH   Key   Location/Qualifiers
FT   CDS   33..830
FT   /tag= a
FT   /transl_except= pos:240..242, aa:Arg
FT   sig_peptide   33..92
FT   /tag= b
FT   mat_peptide   93..827
FT   /tag= c
FT   /label= Analogue_1a
FT   /note= "nucleotides 93..527 encode amino acids
FT   1-145 of hCG beta-subunit; nucleotides
FT   528..551 encode a (Gly-Ser)4 linker and
FT   nucleotides 552..827 encode amino acids
FT   1-92 of gonadotropin alpha-subunit lacking
FT   the glycosylation sites at amino acid
FT   positions 52 and 78"
FT   misc_difference 705..707
FT   /tag= d
FT   /note= "wild-type Asn 52 codon has been changed to a
FT   Gln codon to remove a glycosylation site"
FT   misc_difference 783..785
FT   /tag= e
FT   /note= "wild-type Asn 78 codon has been changed to a

```
FT                Gln codon to remove a glycosylation site"
FT   misc_feature  1..26
FT                /*tag= f
FT                /label= sticky_end
FT                /note= "single-strand overhang. The complementary
FT                strand also has a single-strand overhang at
FT                its 5'-end; the sequence of the overhang is
FT                5'-TCGGATTAGCTTGAGAGGATCC-3'."
PN   WO9522340-A1.
PD   24-AUG-1995.
PF   17-FEB-1995; U02067.
PR   17-FEB-1995; U02067.
PR   18-FEB-1994; US-199382.
PA   (SENS-) SENSI-TEST.
PI   Moyle WR;
DR   WPI; 95-302553/39.
DR   P-PSDB; R86259.
PS   Example 23; Fig 18; 102pp; English.
PT   Methods for altering fertility in mammals, esp. humans - e.g.
PT   stimulating fertility by reducing the activity and/or levels of
PT   circulating glyco:protein hormones having lutropin activity
CC   Analogue 1a (human CG-beta(1-145)-linker-human CG-alpha(1-92)[N530,
CC   N78Q]) is a specific example of a single chain gonadotropin having
CC   a chorionic gonadotropin (CG) beta-subunit at the N-terminus and a
CC   CG alpha-subunit at the C-terminus, joined by a linker of 1-16 amino
CC   acids. The analogue 1a was derived from analogue 1 by removing the
CC   two glycosylation sites from the alpha-subunit. The analogue has
CC   anti-luteinising hormone (lutropin) activity and can be used for
CC   facilitating ovulation, terminating pregnancy and reducing androgen
CC   secretion. The present sequence codes for analogue 1a.
SQ   Sequence 836 BP;
```

Query Match   31.9%; Score 415; DB 17; Length 836;
Best Local Similarity 99.8%; Pred. No. 3.64e-278;
Matches 416; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy  111 ccacggtgcgcgcccatcaatgccacccctggcctgtgggaggaagggagggctgccccgtgtgtgc 170
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  870 CCACGGTGCGCGCCCATCAATGCCACCCTGGCTGTGGGAGGAAGGGACGGCTGCCCCGTGTGC 929

Qy  171 atcaccgtcaacacacaccatctgtgccggctactgcccccaccacccatgacccggtgctgcag 230
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  930 ATCACCGTCAAACACACCATCTGTGCCGGCTACTGCCCCACCACCCGGTGCTGCAG 989

Qy  231 ggggtcctgccggccctgcctcaggtggtgtgctcaactaccggatgtgcgcttccgagtcc 290
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  990 GGGGTCCTGCCGGCCCCTGCCTTCAGGTGGTGTGCAACTACCGGATGTGCGCCTTCGAGTCC 1049

Qy  291 atccggctctccctggctgcccgcgccgcagcaccactgactgcggggggtcccaaggaccac 350
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1050 ATCCGGCTCTCCCTGGCTGCCGCGCCGCGGCCGTGAACCCCGTGGTCTCCTACGGCCGTGGCTCTC 1109

Qy  351 agctgtcaatgtgcactctgccgccgccagcaccactgactgcgggggtcccaaggaccac 410
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1110 AGCTGTCAATGTGCACTCTGCCGCGCGCCGCAGCACCACTGACTGCGGGGGTCCCAAGGACCAC 1169

Qy  411 ccctggacctgtgatgaccccgcttccaggacctcctcttccctcaaaggcccctccccc 470
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1170 CCCTTGACCTGTGATGACCCCGGCTTCCAGGACTCCTCTTCCCTCAAAAGGCCCCTCCCCC 1229

Qy  471 agccttccaagcccatcccgactcccgggccctcgggacaacccgatctcccccaa 527
        ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db 1230 AGCCTTCCAAGCCCATCCCGACTCCCGGGCCCTCGGGACACCCGATTCCTCCACA 1286
```

```
**********************************************************
                        MPSRCH (TM)
**********************************************************
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   Distribution rights by Oxford Molecular Ltd
**********************************************************
```

MPsrch_nn   n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed May 6 14:44:44 1998; MasPar time 1191.25 Seconds
                                      1327.720 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-7
Description: (1-1301) from US08804166.seq
Perfect Score: 1301
N.A. Sequence: 1 CTCGAGATGGCTACAGGTAA...............CACAATAAGGATCCCTCGAG 1301
Comp: GAGCTCTACCGATGTCCATT...............GTGTTATTCCTAGGGAGCTC

Scoring table: TABLE default
                Gap 6

Nmatch   STD : Dbase 0; Query 0

Searched: 1610801 seqs, 607859669 bases x 2

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database: embl-est
   1:em_est1 2:em_est2 3:em_est3 4:em_est4 5:em_est5
   6:em_est6 7:em_est8 8:em_gss 9:em_est13

Database: genbank-est
   10:gb_est1 11:gb_est2 12:gb_est3 13:gb_est4 14:gb_est5
   15:gb_est6 16:gb_est7 17:gb_est8 18:gb_est9 19:gb_est10
   20:gb_est11 21:gb_sts 22:gb_gss 23:gb_est12 24:gb_est13
   25:gb_est14 26:gb_est15 27:gb_est16 28:gb_est17
   29:gb_est18 30:gb_est19 31:gb_est20

Statistics: Mean 11.285; Variance 2.123; scale 5.317

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

| | Result No. | Score | % Match | Query Length | DB | ID | Description | Pred. No. |
|---|---|---|---|---|---|---|---|---|
| c | 1 | 397 | 30.5 | 601 | 13 | N32759 | yw91b05.s1 Homo sapien | 0.00e+00 |
| c | 2 | 391 | 30.1 | 537 | 13 | N30276 | yw69d04.s1 Homo sapien | 0.00e+00 |
| c | 3 | 387 | 29.7 | 564 | 13 | N32604 | yw95d03.s1 Homo sapien | 0.00e+00 |
| c | 4 | 385 | 29.6 | 548 | 13 | N30036 | yw80b11.s1 Homo sapien | 0.00e+00 |
| c | 5 | 383 | 29.4 | 593 | 13 | N25730 | yw78b03.s1 Homo sapien | 0.00e+00 |
| c | 6 | 379 | 29.1 | 442 | 13 | N32233 | yw81f08.s1 Homo sapien | 0.00e+00 |
| c | 7 | 379 | 29.1 | 473 | 13 | N27302 | yw71f12.s1 Homo sapien | 0.00e+00 |
| c | 8 | 379 | 29.1 | 566 | 13 | N30831 | yw70b04.s1 Homo sapien | 0.00e+00 |
| c | 9 | 377 | 29.0 | 563 | 13 | N31955 | yw89a07.s1 Homo sapien | 0.00e+00 |
| c | 10 | 377 | 29.0 | 479 | 13 | N30684 | yw77h04.s1 Homo sapien | 0.00e+00 |
| c | 11 | 376 | 28.7 | 473 | 25 | AA400910 | zt71h09.s1 Soares test | 0.00e+00 |
| c | 12 | 371 | 28.5 | 446 | 13 | N31616 | yw84a02.s1 Homo sapien | 0.00e+00 |
| c | 13 | 367 | 28.2 | 526 | 28 | AA644163 | af62d08.s1 Soares NhHM | 0.00e+00 |
| c | 14 | 356 | 27.4 | 400 | 25 | AA232905 | zr46c04.s1 Soares NhHM | 0.00e+00 |
| c | 15 | 351 | 27.0 | 419 | 16 | H95374 | yw60b03.s1 Soares plac | 0.00e+00 |
| c | 16 | 350 | 26.9 | 531 | 16 | W71989 | zd66b03.s1 Soares feta | 0.00e+00 |
| c | 17 | 335 | 25.7 | 403 | 13 | N26397 | yw76g11.s1 Homo sapien | 0.00e+00 |
| c | 18 | 331 | 25.4 | 441 | 13 | N30741 | yw74b04.s1 Homo sapien | 0.00e+00 |
| c | 19 | 322 | 24.8 | 422 | 11 | R23214 | yh28a03.s1 Homo sapien | 0.00e+00 |
| c | 20 | 319 | 24.5 | 404 | 13 | R30833 | yw70b08.s1 Homo sapien | 0.00e+00 |
| c | 21 | 319 | 24.5 | 515 | 11 | N30608 | yw72c07.s1 Homo sapien | 0.00e+00 |
| c | 22 | 317 | 24.4 | 386 | 13 | N30822 | yw65h07.s1 Homo sapien | 0.00e+00 |
| c | 23 | 315 | 24.2 | 367 | 11 | R68815 | yl43c05.s1 Homo sapien | 0.00e+00 |
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| c | 25 | 305 | 23.4 | 367 | 16 | H94446 | yw55f02.s1 Soares plac | 0.00e+00 |
| c | 26 | 300 | 23.1 | 352 | 13 | H87664 | yw17e05.s1 Homo sapien | 0.00e+00 |
| c | 27 | 298 | 22.9 | 380 | 13 | N30290 | yw56f05.s1 Homo sapien | 0.00e+00 |
| c | 28 | 297 | 22.8 | 526 | 25 | AA393716 | zt71h09.r1 Soares test | 0.00e+00 |
| c | 29 | 295 | 22.7 | 427 | 13 | N27111 | yw75h12.s1 Homo sapien | 0.00e+00 |
| c | 30 | 293 | 22.5 | 386 | 13 | H94451 | yw55g08.s1 Soares plac | 0.00e+00 |
| c | 31 | 285 | 21.9 | 319 | 13 | H87631 | yw17e12.s1 Homo sapien | 0.00e+00 |
| c | 32 | 280 | 21.5 | 329 | 13 | H87156 | yw15b04.s1 Homo sapien | 0.00e+00 |
| c | 33 | 276 | 21.2 | 311 | 10 | T47334 | yh10e11.s1 Homo sapien | 0.00e+00 |
| c | 34 | 273 | 21.0 | 284 | 13 | H93656 | yw5a11.s1 Homo sapien | 0.00e+00 |
| c | 35 | 268 | 20.6 | 303 | 13 | H86993 | yw15b10.s1 Homo sapien | 0.00e+00 |
| c | 36 | 259 | 19.9 | 310 | 10 | T90191 | yw38g09.s1 Homo sapien | 0.00e+00 |
| c | 37 | 266 | 19.9 | 266 | 13 | H93668 | yw55c12.s1 Homo sapien | 0.00e+00 |
| c | 38 | 251 | 19.3 | 251 | 19 | ES934462 | ES934462 Embryo, 6 wee | 0.00e+00 |
| c | 39 | 245 | 18.8 | 278 | 10 | T49170 | yb09g02.r1 Homo sapien | 0.00e+00 |
| c | 40 | 240 | 18.4 | 519 | 23 | C18044 | Human placenta cDNA 5' | 0.00e+00 |
| c | 41 | 235 | 18.1 | 248 | 16 | H95381 | yw60d07.s1 Soares plac | 0.00e+00 |
| c | 42 | 230 | 17.7 | 342 | 16 | T29543 | ES783815 Homo sapiens | 0.00e+00 |
| c | 43 | 224 | 17.2 | 244 | 16 | H94107 | yw58h09.s1 Soares plac | 0.00e+00 |
| c | 44 | 224 | 17.2 | 360 | 14 | HSC22B021 | H. sapiens partial cDN | 0.00e+00 |
| c | 45 | 219 | 16.8 | 255 | 11 | R63352 | y107h10.s1 Homo sapien | 0.00e+00 |

ALIGNMENTS

```
RESULT  1
LOCUS       N32759    601 bp    mRNA          EST        10-JAN-1996
DEFINITION  yw91b05.s1 Homo sapiens cDNA clone 259569 3' similar to gb:J00117
            CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
ACCESSION   N32759
NID         g1153158
KEYWORDS    EST.
SOURCE      human clone=259569 primer=ml3 -40 forward library=Soares placenta
            8to9weeks 2NbHP8to9W vector=pT7T3D (Pharmacia) with a modified
            polylinker host=DH10B (ampicillin resistant) Rsite1=Not I
            Rsite2=Eco RI two placenta: one from 8 weeks and another from 9
            weeks post conception. 1st strand cDNA was primed with a Not I -
            oligo(dT) primer
            [5'-TGTTACCAATCTGAAGTGGGAGCGGCGCGCGCGATTTTTTTTTTTTTTTTTT-3'],
            double-stranded cDNA was size selected, ligated to Eco RI adapters
            (Pharmacia), digested with Not I and cloned into the Not I and Eco
            RI sites of a modified pT7T3 vector (Pharmacia). Library
            constructed by Bento Soares and M. Fatima Bonaldo.
ORGANISM    Homo sapiens
            Eukaryotae; Metazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 601)
REFERENCE
AUTHORS     Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
TITLE       The WashU-Merck EST Project
JOURNAL     Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washu-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
```

REFERENCE   1 (bases 1 to 537)
ORGANISM   Homo sapiens
   Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
   Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Osteichthyes;
   Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
   Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

DEFINITION   yw69d04.s1 Homo sapiens cDNA clone 257479 3' similar to gb:J00117
   CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
ACCESSION   N30276
NID   g1148796
KEYWORDS   EST.
SOURCE   human clone=257479 primer=m13 -40 forward library=Soares placenta
   8to9weeks 2NDHPBto9W vector=pT7T3D (Pharmacia) with a modified
   polylinker host=DH10B (ampicillin resistant) Rsite1=Not I
   Rsite2=Eco RI two placentae: one from 8 weeks and another from 9
   weeks post conception. 1st strand cDNA was primed with a Not I -
   oligo(dT) primer
   [5'-TGTTACCAATCTGAAGTAGGAATGGAGCAGCGGCGGCGGCGATTTTTTTTTTTTTTTTT-3'],
   double-stranded cDNA was size selected, ligated to Eco RI adapters
   (Pharmacia), digested with Not I and cloned into the Not I and Eco
   RI sites of a modified pT7T3 vector (Pharmacia). Library
   constructed by Bento Soares and M. Fatima Bonaldo.

RESULT   2
LOCUS   N30276   537 bp   mRNA   EST   05-JAN-1996

Query Match   30.5%;   Score 397;   DB 13;   Length 601;
Best Local Similarity   97.9%;   Pred. No. 0.00e+00;
Matches   411;   Conservative   0;   Mismatches   8;   Indels   1;   Gaps   1;

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Db    17 TTATTGTGGGAGGAATCGGGGTGGTGTCCGAGGGCGCCCGGGAGTCGGGGAGTCGGGGAGGCCTTGGAAGGCT  76
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Cp  1289 TTATTGTGGGAGGAATCGGGGTGTGTCCGAGGGCGCCCGGGAGTCGGGGAGTCGGGGAGGCCTTGGAAGGCT 1230

Db    77 GGGGGGAGGGAGGGGCCTTTGAGGAAGAGGAGTCTCGGAAGCGGGGGGTCATCACAGGTCAAGGG  136
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp  1229 GGGGGGAGGGAGGGGCCTTTGAGGAAGAGGAGTCTCGGAAGCGGGGGTCATCACAGGTCAAGG 1170

Db   137 GTGGGTCCTTGGGCACCCC--GCAGTCAGTGGGTGCTGCGGCGGCCAGAGTCGCACATTGACAGCT  195
         ||||||||||||||||||   |||||||||||||||||||||||||||||||||||||||||||||
Cp  1169 GTGGTCCTTGGGCACCCCCGCAGTCAGTGGGTGCTGCGGCGGCCAGAGTCGCACATTGACAGCT 1110

Db   196 GAGAGCCACACGGCGCTAGGAGAACCACGGGGGTTCACGCCGCCGCGCGGGCGGCCAGAGGAGCCCGGAT  255
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp  1109 GAGAGCCACACGGCGCGTAGGAGAACCACGGGGGTTCACGCCGCCGCGCGGGCGGCCAGAGGAGCCCGGAT 1050

Db   256 GGACTCGGAAGCGCACATCGCGGTAGTTGCACCACCACCTGAGCGGCCAGGACCCC  315
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp  1049 GGACTCGGAAGCGCACATCGCGGTAGTTGCACCACCACCTGAGCGGCCAGGACCCC  990

Db   316 TTGCAGCGACGCGGGTCATGGTGGGGCAGTAGGGGGGCAGTAGGGGCACAGAGGTGAT  375
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp   989 CTGCGACGCGGGGTCATGGTGGGGCAGTAGGCCGGCACAGAGGTGGGTGGTGTTGACGGTGAT  930

Db   376 GCACACGGGGCACCCCTCCTTCTCCACAGCCCAGGTGCCGCATTGAATGGGGCGGCCACCGTGG  435
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Cp   929 GCACACGGGGCAGCCCTCCTTCTTCCACAGCCCAGGTGCCGCATTGAATGGGGCGGCCACCGTGG  870
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REFERENCE   1 (bases 1 to 537)

AUTHORS   Hillier,L., Clark,N., Dubuque,T., Ellston,K., Hawkins,M.,
   Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
   Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
   Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
   Wilson,R.

   Email: est@watson.wustl.edu
   The WashU-Merck EST Project
TITLE   The WashU-Merck EST Project
JOURNAL   Unpublished (1995)
COMMENT

   Contact: Wilson RK
   WashU-Merck EST Project
   Washington University School of Medicine
   4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
   Tel: 314 286 1800
   Fax: 314 286 1810
   Email: est@watson.wustl.edu
   High quality sequence stops: 313
   Source: IMAGE Consortium, LLNL
   This clone is available royalty-free through LLNL ; contact the
   IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES
   source   Location/Qualifiers
     1..537
     /organism="Homo sapiens"
     /clone="257479"
   mRNA   <1..>537
BASE COUNT   98 a   145 c   201 g   90 t   3 others
ORIGIN

Query Match   30.1%;   Score 391;   DB 13;   Length 537;
Best Local Similarity   96.2%;   Pred. No. 0.00e+00;
Matches   426;   Conservative   0;   Mismatches   13;   Indels   4;   Gaps   4;

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Db    17 TTATTGTGGGAGGAATCGGGGTGTGTCCGAGGGCGCCCGGGAGTCGGGGAGTCGGGGAGGCCTTGGAAGGCT  76
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Cp  1289 TTATTGTGGGAGGAATCGGGGTGTGTCCGAGGGCGCCCGGGAGTCGGGGAGTCGGGGAGGCCTTGGAAGGCT 1230

Db    77 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGAAGCGGGGGGTCATCACAGGTCAAGGG  136
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Cp  1229 GGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGG 1170

Db   137 GTGGTCCTTGGGCACCCC--GCAGTCAGTAGTGGTGCTGCGGCGCAGAGTCGCACATTGACAGCT  195
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Cp  1169 GTGGTCCTTGGGACCCCCCGCCAGTCAGTGGTGCTGCGGCGCAGAGTCGCACATTGACAGCT 1110

Db   196 GAGAGCCACGGCGTTAGGAGGACCACGGGGGTTCACGCCGCCGCGG-CAGCCAGGGGAGCCGGA  254
         |||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Cp  1109 GAGAGCCACGGCGT-AGGAGGACCACGGGGGTTCACGCCGCCGCGGGCCGCGGCCAGGGAGCCGGA 1051

Db   255 TGGACTCGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGCGGCCAGGACCC  314
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp  1050 TGGACTCGGAAGCGCACATCGCGGTAGTTGCACACCACCTGAGCGGCCAGGACCC  991

Db   315 CCCTGCCAGCACGCGGGGTCATGGTGGGGGCAGTAACCGGCACAGAGGTGTGTTGACGGTG  374
         |||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp   990 CC-TGCCAGCACGCGGGTCATGGTGGGGGCAGTAGCCGGCACAGAGGTGGTGGTGTTGACGGTG  932

Db   375 ATGGACACGGGGCAGCCCTCCTTCTCCACAGCCAGGTGCCGCATTGAATGATGGGGGGCGGCCANCGT  434
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Cp   931 ATGCCACACGGGGCAGCCCTCCTTCTTCCACAGCCAGGTGGCATTGAATGGGGCGGCCACCGT  872

Db   435 GGCNAAGCCGGCTCCTTGGATGCC  457
         ||   ||| | ||| |||| ||||
Cp   871 GGACCAGCCACCAGCTGTGGTGCC  849
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REFERENCE   1 (bases 1 to 537)

   Email: est@watson.wustl.edu
   High quality sequence stops: 387
   Source: IMAGE Consortium, LLNL
   This clone is available royalty-free through LLNL ; contact the
   IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES
   source   Location/Qualifiers
     1..601
     /organism="Homo sapiens"
     /clone="259569"
   mRNA   <1..>601
BASE COUNT   112 a   154 c   219 g   110 t   6 others
ORIGIN

RESULT   3
LOCUS   N32604   564 bp   mRNA   EST   10-JAN-1996

DEFINITION   yw95d03.s1 Homo sapiens cDNA clone 259973 3' similar to gb:J00117
   CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
ACCESSION   N32604
NID   g1153003
KEYWORDS   EST.
SOURCE   human clone=259973 primer=m13 -40 forward library=Soares placenta

Cp   930 TGCACACGGGGCGGCAGCCCTCCTTCTCCACAGCACCAGGGTGGCATTGATGGGGCGGCACCGTG 871
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   435 GCCNA 439
           |||||
Cp   870 GACCA 866

RESULT 4

LOCUS   N30036   548 bp   mRNA   EST   05-JAN-1996
DEFINITION   yw80b11.s1 Homo sapiens cDNA clone 258525 3' similar to gb:J00117
             CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
ACCESSION   N30036
NID   g1148556
KEYWORDS   EST.
SOURCE   human clone=258525 primer=rm13 -40 forward library=Soares placenta
             8to9weeks 2NDHP8to9W vector=pT7T3D (Pharmacia) with a modified
             polylinker host=DH10B (ampicillin resistant) Rsite1=Not I
             Rsite2=Eco RI two placentae: one from 8 weeks and another from 9
             weeks post conception. 1st strand cDNA was primed with a Not I -
             oligo(dT) primer
             [5'-TGTTACCAATCTGAAGTGGGGACGCGGCCGCGGAATTTTTTTTTTTTTTTTTT-3'],
             double-stranded cDNA was size selected, ligated to Eco RI adapters
             (Pharmacia), digested with Not I and cloned into the Not I and Eco
             RI sites of a modified pT7T3 vector (Pharmacia). Library
             constructed by Bento Soares and M. Fatima Bonaldo.
ORGANISM   Homo sapiens
             Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
             Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
             Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
             Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 548)
AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
             Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
             Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
             Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
             Wilson,R.
TITLE   The WashU-Merck EST Project
JOURNAL   Unpublished (1995)
COMMENT   Contact: Wilson RK
             WashU-Merck EST Project
             Washington University School of Medicine
             4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
             Tel: 314 286 1800
             Fax: 314 286 1810
             Email: est@watson.wustl.edu
             High quality sequence stops: 333
             Source: IMAGE Consortium, LLNL
             This clone is available royalty-free through LLNL ; contact the
             IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES   Location/Qualifiers
     source   1..548
                     /organism="Homo sapiens"
                     /clone="258525"
     mRNA   <1..>548
BASE COUNT   99 a   143 c   206 g   93 t   7 others
ORIGIN

Query Match   29.6%; Score 385; DB 13; Length 548;
Best Local Similarity 97.8%; Pred. No. 0.00e+00;
Matches 413; Conservative 0; Mismatches 6; Indels 4; Gaps 4;

Db   18   TTATTGTGTGGGAGGATCGGGGTGTCGGAGGGCCCCGGAGCAGTCGGGGATGGGCTTGGAAGGCT 77
            || ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Cp   1289   TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGAGTCGGGGATGGGCTTGGAAGGCT 1230
FEATURES
     source   1..548
                     /organism="Homo sapiens"
                     /clone="258525"
Db   78   GGGGGAGGGGCCTTTGAGGAAGAAGGAGTTCCTGGAAGCGGGGGGTCATCACAGGTCAAGG 137
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp   1229   GGGGGAGGGGCCTTTGAGGAAGAAGGAGTTCCTGGAAGCGGGGGGTCATCACAGGTCAAGG 1170
Db   138   GTGGTCCTTGGGACCCC -GCAGTCAGTGGTTGCTTGCCGGCGGCAGAGTGCACATTGACACAGCT 196
            ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db   138   GTGGTCCTTGGGACCCC -GCAGTCAGTGGTTGCTTGCCGGCGGCAGAGTGCACATTGACACAGCT 196

Cp   930 TGCACACGGGGCGGCAGCCCTCCTTCTCCACAGCACCAGGGTGGCATTGATGGGGCGGCACCGTG 871
Db   435 GCCNA 439
Cp   870 GACCA 866

LOCUS   8to9weeks 2NDHP8to9W vector=pT7T3D (Pharmacia) with a modified
             polylinker host=DH10B (ampicillin resistant) Rsite1=Not I
             Rsite2=Eco RI two placentae: one from 8 weeks and another from 9
             weeks post conception. 1st strand cDNA was primed with a Not I -
             oligo(dT) primer
             [5'-TGTTACCAATCTGAAGTGGGGACGCGGCCGCGGAATTTTTTTTTTTTTTTTTT-3'],
             double-stranded cDNA was size selected, ligated to the Not I and Eco
             RI sites of a modified pT7T3 vector (Pharmacia). Library
             constructed by Bento Soares and M. Fatima Bonaldo.
ORGANISM   Homo sapiens
             Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
             Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
             Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
             Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 564)
AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
             Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
             Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
             Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
             Wilson,R.
TITLE   The WashU-Merck EST Project
JOURNAL   Unpublished (1995)
COMMENT   Contact: Wilson RK
             WashU-Merck EST Project
             Washington University School of Medicine
             4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
             Tel: 314 286 1800
             Fax: 314 286 1810
             Email: est@watson.wustl.edu
             High quality sequence stops: 364
             Source: IMAGE Consortium, LLNL
             This clone is available royalty-free through LLNL ; contact the
             IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES   Location/Qualifiers
     source   1..564
                     /organism="Homo sapiens"
                     /clone="259973"
     mRNA   <1..>564
BASE COUNT   103 a   148 c   206 g   99 t   8 others
ORIGIN

Query Match   29.7%; Score 387; DB 13; Length 564;
Best Local Similarity 97.2%; Pred. No. 0.00e+00;
Matches 413; Conservative 0; Mismatches 9; Indels 3; Gaps 3;

Db   17   TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGAGTCGGGGATGGGCTTGGAAGGCT 76
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Cp   1289   TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGAGTCGGGGATGGGCTTGGAAGGCT 1230
Db   77   GGGGGAGGGGCCTTTGAGGAAGAAGGAGTCCTGGAAGCGGGGGGTCATCACAGGTCAAGG 136
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp   1229   GGGGGAGGGGCCTTTGAGGAAGAAGGAGTCCTGGAAGCGGGGGGTCATCACAGGTCAAGG 1170
Db   137   GTGGTCCTTGGGACCCC--GCAGTCAGTGGTGTCTGTGCGGCCGGCAGAGTGCACATTGACAGCT 195
            ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Cp   1169   GTGGTCCTTGGGGACCCCCGCAGTCAGTGGTGGTGCTGCGGCGGCAGAGTGCACATTGACACT 1110
Db   196   GAGAGCCACGGCGTAGGAGAGACCACGGGGGTTCACGCCCGCCAGCCAAAGGGAGCCCGGAT 255
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp   1109   GAGAGCCACGGCGTAGGAGACCACGGGTTCACGCCCGCCAGCCGAGCCCGGAT 1050
Db   256   GGACTCGAAGCCCACATCGCGGCGTAGTTGCACCACCTGAGCCGCGCCAAGACCCC 315
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Cp   1049   GGACTCGAAGCCCACATCGCGGCGTAGTTGCACCACCTGAGCCGCGCCAGGACCCC 990
Db   316   CTTGCAGCACGCGGGGGTCATGGTGGGGCAGTAGC -GGCACAGAGTGGTGGTTGACGGTGA 374
            ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Cp   989   CT-GCAGCACGCGGGGTCATGGTGGGGCAGTAGCCGCGGCACAGAGTGGTGGTTGACGGTGA 931
Db   375   TGCACACGGGGCGGCCTCCTTCTCTCACAGCACCAGGGTGGCATTGATGGGGCGGCACCGTG 434
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 5

LOCUS   N29730   593 bp   mRNA   EST   05-JAN-1996
DEFINITION   yw78h03.s1 Homo sapiens cDNA clone 258389 3' similar to gb:J00117
             CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
ACCESSION   N29730
NID   g1148250
KEYWORDS   EST.
SOURCE   human clone=258389 primer=m13 -40 forward library=Soares placenta
             8to9weeks 2NbHP8to9W vector=pT7T3D (Pharmacia) with a modified
             polylinker host=DH10B (ampicillin resistant) Rsite1=Not I
             Rsite2=Eco RI two placentae: one from 8 weeks and another from 9
             weeks post conception. 1st strand cDNA was primed with a Not I -
             oligo(dT) primer
             [5'-TGTTACCAATCTGAAGTGGGAGCGGCGCCGCGGATTTTTTTTTTTTTTTTTTT-3'],
             double-stranded cDNA was size selected, ligated to Eco RI adapters
             (Pharmacia), digested with Not I and cloned into the Not I and Eco
             RI sites of a modified pT7T3 vector (Pharmacia). Library
             constructed by Bento Soares and M. Fatima Bonaldo.
ORGANISM   Homo sapiens
             Eukaryotae; Metazoa; Bilateria; Coelomata;
             Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
             Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
             Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 593)
AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
             Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
             Parsons,J., Rifkin,L., Rohling,T., Soares,M., Tan,F.,
             Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
             Wilson,R.
TITLE   The WashU-Merck EST Project
JOURNAL   Unpublished (1995)
COMMENT   Contact: Wilson RK
             WashU-Merck EST Project
             Washington University School of Medicine
             4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
             Tel: 314 286 1800
             Fax: 314 286 1810
             Email: est@watson.wustl.edu
             High quality sequence stops: 368
             Source: IMAGE Consortium, LLNL
             This clone is available royalty-free through LLNL ; contact the
             IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES   Location/Qualifiers
     source   1..593
                     /organism="Homo sapiens"
                     /clone="258389"

BASE COUNT   109 a   151 c   216 g   111 t   6 others

ORIGIN
Query Match   29.4%;   Score 383;   DB 13;   Length 593;
Best Local Similarity   95.3%;   Pred. No. 0.00e+00;
Matches 422;   Conservative   0;   Mismatches 17;   Indels 4;   Gaps 4;

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  1289 TTATTGTGGGAGGGAGGATCGGGGTGTCCGAGGGCCCCGGAGGTCGGGGATGGGGAAGGCT 1230

Cp   78 GGGGGGAGGGGGCCTTTGAGGAGGAGGAGGTCCTGGAAGAGGGGGGGGTCATCACAGGTCAAGGG 137
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  1229 GGGGGGAGGGGGCCTTTGAGGAGGAGGAGTCCTGGAAGAGGGGGGGTCATCACAGGTCAAGGG 1170

Db   138 GTGGTCCTTGGGACCCC-GCAGTCAGTGGTGTCGCGGGGGGCAGTTGCACATTGACAGCT 196
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
  1169 GTGGTCCTTGGGACCCCGCAGTCAGTGGTGTCGCGGGGGGCAGTTGCACATTGACAGCT 1110

Cp   197 GAGAGCCACGGCGTAGGAGACCACGGGGTTCACGCCGCCGGNG-CAGCCAGGAGCGGAT 255
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
  1109 GAGAGCCACGGCGTAGGAGACCACGGGGTTCACGCCGCCGGGGCAGCCAGGAGCGGAT 1050

Db   256 GGACTCGAAGGCACACATCGCGGTAGTTGCACACCACCTGAGGCAGCAGGGGCAGGACCAC 315
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
  1049 GGACTCGAAGGCACACATCGCGGTAGTTGCACACCACCTGAGGCAGCAGGGGCAGGACCCC 990

Cp   316 CTGCAGCCACGCGGGTCATGGGTTGGGGCCAGTAGCCGCGGCACAGATGGTGGTGTTGACGGTGA 375
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
   989 CTGCAGCCACGCGGGTCATGGT-GGGCGCAGTAGCCGCGGCACAGATGGTGGTGTTGACGGTGA 931

Db   376 TGCACACGGGGCGCAGCCCTCCTTCCTTCCACAGCCCANGGTTGCATTGATGGGGCGCACCGT 435
          |||||||||||||||||||||| |||||||||||||||||||||||||||||
   930 TGCACACGGGGCGCAGCCCTCCTTCCTTCCACAGCCCAGGGT-GGCATTGATGGGGCGCACCGT 872

Cp   436 GGCCAAGCGGCGTCCTTGGGATGCC 458
         ||||||||||||||||||||||||
   871 GGCCAGCAGCACCAGCTGTGGTGCC 849

RESULT 6

LOCUS   N32233   442 bp   mRNA   EST   10-JAN-1996
DEFINITION   yw81f08.s1 Homo sapiens cDNA clone 258663 3' similar to gb:J00117
             CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
ACCESSION   N32233
NID   g1152632
KEYWORDS   EST.
SOURCE   human clone=258663 primer=m13 -40 forward library=Soares placenta
             8to9weeks 2NbHP8to9W vector=pT7T3D (Pharmacia) with a modified
             polylinker host=DH10B (ampicillin resistant) Rsite1=Not I
             Rsite2=Eco RI two placentae: one from 8 weeks and another from 9
             weeks post conception. 1st strand cDNA was primed with a Not I -
             oligo(dT) primer
             [5'-TGTTACCAATCTGAAGTGGGAGCGGCGCCGCGGATTTTTTTTTTTTTTTTTTT-3'],
             double-stranded cDNA was size selected, ligated to Eco RI adapters
             (Pharmacia), digested with Not I and cloned into the Not I and Eco
             RI sites of a modified pT7T3 vector (Pharmacia). Library
             constructed by Bento Soares and M. Fatima Bonaldo.
ORGANISM   Homo sapiens
             Eukaryotae; Metazoa; Bilateria; Coelomata;
             Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
             Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
             Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 442)
AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
             Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
             Parsons,J., Rifkin,L., Rohling,T., Soares,M., Tan,F.,
             Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
             Wilson,R.
TITLE   The WashU-Merck EST Project
JOURNAL   Unpublished (1995)
COMMENT   Contact: Wilson RK

RESULT 7

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LOCUS       N27302      473 bp   mRNA      EST      29-DEC-1995
DEFINITION  yw71f12.s1 Homo sapiens cDNA clone 257711 3' similar to gb:J00117
            CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
ACCESSION   N27302
NID         g1141650
KEYWORDS    EST.
SOURCE      human clone=257711 primer=m13 -40 forward library=Soares placenta
            8to9weeks 2NbHP8to9w vector=pT7T3D (Pharmacia) with a modified
            polylinker host=DH10B (ampicillin resistant) Rsite1=Not I
            Rsite2=Eco RI two placentae: one from 8 weeks and another from 9
            weeks post conception. 1st strand cDNA was primed with a Not I -
            oligo(dT) primer
            [5'-TGTTACCAATCTGAAGTGGGAGCCGCCGCGGCCGCGAGTTTTTTTTTTTTTTTTTTTT-3'],
            double-stranded cDNA was size selected, ligated to Eco RI adapters
            (Pharmacia), digested with Not I and cloned into the Not I and Eco
            RI sites of a modified pT7T3 vector (Pharmacia). Library
            constructed by Bento Soares and M. Fatima Bonaldo.
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 473):
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 364
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES             Location/Qualifiers
     source          1..442
                     /organism="Homo sapiens"
                     /clone="258663"
     mRNA            <1..>442
BASE COUNT     85 a    110 c    174 g     68 t      5 others
ORIGIN
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Query Match 29.1%; Score 379; DB 13; Length 442;
Best Local Similarity 94.6%; Pred. No. 0.00e+00;
Matches 402; Conservative 0; Mismatches 22; Indels 1; Gaps 1;

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Db   17 TTATTGTGGGAGGAATCGGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGACTTGGAAGGCT   76
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Cp 1289 TTATTGTGGGAGGATCGGGGGTGTCCGAGGGCCCCGGGAGTCGGGATGGGACTTGGAAGGCT 1230

Db   77 GGGGGAGGGGCCTTTGAGGAAGAAGAGAGTCCTGGAAGCGCGGGGGTCATCACAGGTCAAGGG  136
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp 1229 GGGGGAGGGGCCTTTGAGGAAGAAGAGAGTCCTGGAAGCGCGGGGGTCATCACAGGTCAAGGG 1170

Db  137 GTGGGTGCTTGGGACCCCGCCAAGTCAGTTGGTTGCTGCGGCGGCAGAGTGCACATTGACAGC  196
          |||| |||||||||||||||||  |||||  ||||||||||||||||||||||||||||||||
Cp 1169 GTGGTCCTTGGGACCCCGCCAGTCAGT CGTTGCTGCGGCGGCAGAGTGCACATTGACAGC 1111

Db  197 TGAGAGGCCACGGCGTAGGAGACCACGGGGTTCACGCGCGGCAGGGAGGCCGGA  256
          |||||||||||||||||||||||||||||||||||||| |||||||||||||||
Cp 1110 TGAGAGGCCACGGCGTAGGAGACCACGGGGTTCACGCGCGGCAGGGAGGCCGGA 1051

Db  257 TGGACTCGAAGGCCACATCGCGCGGTAGTTGTTCACACCACCTGAGGCGCAGGGCGNCAAGACACAC  316
          |||||||||||||||||||| |||||||| | |||||||||  ||||||||||||   ||  |
Cp 1050 TGGACTCGAAGGCCACATCGCGGTAGTTGTGCACACCACCTTGAGGCGCAGGGACC  991

Db  317 CCTGGCACGCACGCGGGTCATGTTGGTGTGGGGGCAGTAACCGCACAGAATGGTGTGGTTGTTGACGGTNA  376
          |||| ||| |||||||||||| |||   ||||||||||| ||||||||||||||| |||||||||||| ||
Cp  990 CCTGCAGCAGCGCGGGTCATGGTGGGGCAGTAGCCGCACAGAATGGTGGTTGTTGACGGTGA  931

Db  377 TGCACACGGGGCAGCCCTCCTTTCTCCACAGCCAGGGTGGCATTGGGGCGGCGCANCGTG  436
          |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Cp  930 TGCACACGGGGCAGCCCTCCTTTCTCCACAGCCAGGGTGGCATTGGGGCGGCGCACCGTG  871

Db  437 GCCCA  441
          | ||
Cp  870 GACCA  866
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RESULT 8

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LOCUS       N30831      566 bp   mRNA      EST      05-JAN-1996
DEFINITION
ORGANISM    constructed by Bento Soares and M. Fatima Bonaldo.
            Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 473):
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 225
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES             Location/Qualifiers
     source          1..473
                     /organism="Homo sapiens"
                     /clone="257711"
     mRNA            <1..>473
BASE COUNT     87 a    122 c    182 g     76 t      6 others
ORIGIN
```

Query Match 29.1%; Score 379; DB 13; Length 473;
Best Local Similarity 95.5%; Pred. No. 0.00e+00;
Matches 402; Conservative 0; Mismatches 17; Indels 2; Gaps 2;

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Db   18 TTATTGTGGGAGGATCGGGGGTGTCCGAGGGCCCCCGGGAGTCGGGANGGGACTTGGAAGGCT   77
          |||||||||||||||||||||||||||||||||||| ||||||||||| |||||||||||||
Cp 1289 TTATTGTGGGAGGATCGGGGGTGTCCGAGGGCCCCCGGGAGTCGGGATGGGACTTGGAAGGCT 1230

Db   78 GGGGGAGGGGCCTTTGAGGAAGAAGAGAGAGTCCTGGAAGRTCCTGGAAGTCATCACAGGTCAAGGG  137
          |||||||||||||||||||||||||||||||||||||||||
Cp 1229 GGGGGAGGGGCCTTTGAGGAAGAAGAGAGTCCTGGAAGCGCGGGGGTCATCACAGGTCAAGGG 1170

Db  138 GTGGGTCCTTGGGACCCCGCCAGTCAGTGGTTGGTGCTGCGGCGGCAGAGTGCACATTGACAGCT  197
          |||| |||||||||||||||||||||||| |  ||||||||||||||||||||||||||||||||
Cp 1169 GTGGTCCTTGGGACCCCGCCAGTCAGTGGTCGTTGCTGCGGCGGCAGAGTGCACATTGACAGCT 1110

Db  198 GAGAGCCCACGGCGTAGGAGGACCACGGGGTTCACGCGCGGG-CAGCCAGGGANCCGGAT  256
          ||||||||||||||||||||||||||||||||||||||||||  ||||||||| ||||||
Cp 1109 GAGAGCCCACGGCGTAGGAGGACCACGGGGTTCACGCGCGGGCAGCCAGGGAGCCGGAT 1050

Db  257 GGACTCGAANCGCACATCGCGGGTAGGGGTAGTTGCACACCACACCTGAGGCGCAGGGCGGGGGACACCACC  316
          |||||||||| ||||||||||||||||  |||||||||||||  ||||||||||||||| |||  |
Cp 1049 GGACTCGAAGCGCACATCGCGGGTAGTTGCACACCACCTGAGGCGCAGGGCCGGCGCAGGACCCC  990

Db  317 TTGCAGCACACGCGGGTCATGGTGGGGCGGCAGTANCCGGGCACAGATAGGTGGTGGTTNACGGTGA  376
           |||||||||||||||||||||||||||| ||||| ||||  ||||||||||||||||| ||||||
Cp  989 CTGCAGCACACGCGGGTCATGGTGGGGCAGTAGCCGG-CACAGATAGGTGGTGGTTGACGGTGA  931

Db  377 TGCACGGGGCAGCCCNCCTTCTCCACACCACCAGGGTGGCATTGANTGGGCGGCGCACCGTN  436
          ||||| |||||||||| ||| |||||||||      |||||||||| ||||||||||||||||
Cp  930 TGCACACGGGGCAGCCCTCCTTCTCCACAGGTGGCATTGAGTGGGCGGCGCACCGTG  871

Db  437 G  437
          |
Cp  870 G  870
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DEFINITION   yw70b04.s1 Homo sapiens cDNA clone 257551 3' similar to gb:J00117
             CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
ACCESSION   N30831
NID   g1149351
KEYWORDS   EST.
SOURCE   human clone-257551 primer=m13 -40 forward library=Soares placenta
             8to9weeks 2NbHP8to9W vector=pT7T3D (Pharmacia) with a modified
             polylinker host=DH10B (ampicillin resistant) Rsite1=Not I
             Rsite2=Eco RI two placentae: one from 8 weeks and another from 9
             weeks post conception. 1st strand cDNA was primed with a Not I -
             oligo(dT) primer
             [5'-TGTTACCAATCTGAAGTGGGAGACGGCGCGCCGATTTTTTTTTTTTTTTTT-3'],
             double-stranded cDNA was size selected, ligated to Eco RI adapters
             (Pharmacia), digested with Not I and cloned into the Not I and Eco
             RI sites of a modified pT7T3 vector (Pharmacia). Library
             constructed by Bento Soares and M. Fatima Bonaldo.
ORGANISM   Homo sapiens
             Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
             Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
             Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
             Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 566)
AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
             Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
             Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
             Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
             Wilson,R.
TITLE   The WashU-Merck EST Project
JOURNAL   Unpublished (1995)
COMMENT   Contact: Wilson RK
             WashU-Merck EST Project
             Washington University School of Medicine
             4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
             Tel: 314 286 1800
             Fax: 314 286 1810
             Email: est@watson.wustl.edu
             High quality sequence stops: 400
             Source: IMAGE Consortium, LLNL
             This clone is available royalty-free through LLNL ; contact the
             IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES   Location/Qualifiers
     source   1..566
                     /organism="Homo sapiens"
                     /clone="257551"
BASE COUNT   103 a   148 c   209 g   100 t   6 others
ORIGIN

Query Match   29.1%; Score 379; DB 13; Length 566;
Best Local Similarity   96.7%; Pred. No. 0.00e+00;
Matches   408; Conservative   0; Mismatches   11; Indels   3; Gaps   3;

Db   17 TTATTGTGGGAGGATCGGGGTGTCCAGGGACCCGGGGATGGGCAGTAGGGTCACAGATGGTGGGTGGTGTTGACGGTG   93
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Cp   1289 TTATTGTGGGAGGATCGGGGTGTCCGAGGGACCCGGGGATGGGCAGTAGGGTCGGGAAGGCT 1230

Db   77 GGGGGGAGGGGGGCCTTTGAGGAAGAGAGAGAGTCCTGGAAGCGGGGAGTCGGGAT... 136
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Cp 1229 GGGGGAGGGGGGCCTTTGAGGAAGAGAGAGCGGGGGTCATCACAGTCAAGGG 1170

Db   137 GTGGTCCTTGGG-CCCCCGCGAGTCAGTGGTCGTGCTCGCGCAGAGTCACATTGACAGCT 195
         |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Cp 1169 GTGGTCCTTGGGACCCCCGCAGTCAGTGGTCGTGCTCGCGCAGAGTCACATTGACAGCT 1110

Db   196 GAGAGGCACGGCTTAGGAGAGACCACCGGGGTTCACGCGCCGCGCGCAACCANGGGAGGCGGA 255
         ||||||||||||||||||||||||||||||||||||| |||||||||||||
Cp 1109 GAGAGCCACGGCGGTAGGAGACCACCGGGGTTCACGCGCCGCGCGCCAGCCA-GGGAGCCGGA 1051

Db   256 TGGACTCGGAACGCAAATCGCGGGTAGTTGCACACCACACCTGAGGCAGGAGCGGCGCCAGACCC 315
         ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Cp 1050 TGGACTCGGAACGCACAATCGCGGG-TAGTTGCACACCACACCTGAGGCAGGGCGGCCAGACC 992

DEFINITION   yw89a07.s1 Homo sapiens cDNA clone 259380 3' similar to gb:J00117
             CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
RESULT 9
LOCUS   N31955   563 bp   mRNA   EST   10-JAN-1996
ACCESSION   N31955
NID   g1152354
KEYWORDS   EST.
SOURCE   human clone=259380 primer=m13 -40 forward library=Soares placenta
             8to9weeks 2NbHP8to9W vector=pT7T3D (Pharmacia) with a modified
             polylinker host=DH10B (ampicillin resistant) Rsite1=Not I
             Rsite2=Eco RI two placentae: one from 8 weeks and another from 9
             weeks post conception. 1st strand cDNA was primed with a Not I -
             oligo(dT) primer
             [5'-TGTTACCAATCTGAAGTGGGAGACGGCGCGCCGATTTTTTTTTTTTTTTTT-3'],
             double-stranded cDNA was size selected, ligated to Eco RI adapters
             (Pharmacia), digested with Not I and cloned into the Not I and Eco
             RI sites of a modified pT7T3 vector (Pharmacia). Library
             constructed by Bento Soares and M. Fatima Bonaldo.
ORGANISM   Homo sapiens
             Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
             Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
             Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
             Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 563)
AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
             Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
             Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
             Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
             Wilson,R.
TITLE   The WashU-Merck EST Project
JOURNAL   Unpublished (1995)
COMMENT   Contact: Wilson RK
             WashU-Merck EST Project
             Washington University School of Medicine
             4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
             Tel: 314 286 1800
             Fax: 314 286 1810
             Email: est@watson.wustl.edu
             High quality sequence stops: 335
             Source: IMAGE Consortium, LLNL
             This clone is available royalty-free through LLNL ; contact the
             IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES   Location/Qualifiers
     source   1..563
                     /organism="Homo sapiens"
                     /clone="259380"
BASE COUNT   101 a   148 c   208 g   103 t   3 others
ORIGIN

Query Match   29.0%; Score 377; DB 13; Length 563;
Best Local Similarity   97.4%; Pred. No. 0.00e+00;
Matches   418; Conservative   0; Mismatches   5; Indels   6; Gaps   6;

Db   17 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCGGGGATGGGGTCGGGAGAGTCGGGGGGAGGGGGGCTTGGAAGGCT 76
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Cp 1289 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCGGGGATGGGGTCGGGAGAGTCGGGGGGGATGGGGCTTGGAAGGCT 1230

RESULT 10

```
LOCUS       N30684      479 bp    mRNA            EST       05-JAN-1996
DEFINITION  yw77h04.s1 Homo sapiens cDNA clone 258295 3' similar to gb:J00117
            CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
ACCESSION   N30684
NID         g1149204
KEYWORDS    EST.
SOURCE      human clone=258295 primer=ml3 -40 forward library=Soares placenta
            8to9weeks 2NbHP8to9W vector=pT7T3D (Pharmacia) with a modified
            polylinker host=DH10B (ampicillin resistant) Rsite1=Not I
            Rsite2=Eco RI two placentae: one from 8 weeks and another from 9
            weeks post conception. 1st strand cDNA was primed with a Not I -
            oligo(dT) primer
            [5'-TGTTACCAATCTGAAGTGGGACGGCCGCGANTTTTTTTTTTTTTTTTTT-3'],
            double-stranded cDNA was size selected, ligated to Eco RI adapters
            (Pharmacia), digested with Not I and cloned into the Not I and Eco
            RI sites of a modified pT7T3 vector (Pharmacia). Library
            constructed by Bento Soares and M. Fatima Bonaldo.
ORGANISM    Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 479)
AUTHORS     Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
TITLE       The WashU-Merck EST Project
JOURNAL     Unpublished (1995)
COMMENT     Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 333
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
```

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Db    77 GGGGGGAGGGGGCCTTTGAGGAAGGAGAAGGAGGAGAGGAGAAGGGGGGGGTCATCACAGGTCAAGGG   136
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Cp  1229 GGGGGGAGGGGGCCTTTGAGGAAGGAGAGGAGAGGAGAGGAGAAGGGGGGGGTCATCACAGGTCAAGGG  1170

Db   137 GTGGTCCTTGGGACCCC-GCAGTCAGTTGGTGCTGCGGCGCAGAGTGCACATTGACAGC   195
         |||||| |||||||||| ||||||||||||||||||||||||||||||||||||||||
Cp  1169 GTGGTCCTTGGGACCCCCGCAGTCAGT-GGTGCTGCGGCGCAGAGTGCACATTGACAGC  1111

Db   196 TGAGAGCCACGGCGTTAGGAGACCACGGGGT-TCACGCGGGGACCCG   255
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Cp  1110 TGAGAGCCACGGCGT-AGGAGACCACGGGGTTCACCCA-CGGAGCCG  1170

Db   256 GATGGACTCGAAGCGCACATCCGGTAGTTGCACACCACCTGAGGCAGGGC-GGCAAGAC   314
         |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Cp  1052 GATGGACTCGAAGCGCACATCCGGTAGTTGCACACCACCTGAGGCAGGGCCGGCAAGAC  1053

Db   315 CCC-TGCAGCACGCGGGTCATGGTGGGGCCGCAGTAGCCCGGCACAGATAGGTGGGTGTTGACCGT   373
         ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp   992 CCCCTGCAGCACGCGGGTCATGGTGGGGCCGCAGTAGCCCGGCACAGATGGTGGGTGTTGACCGT    933

Db   374 GATGCACACGGGGCAGCGCCTCCTTCTCCACACACCAGGGTGGGCATTGATTGAGGGGGCCACCG   433
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Cp   932 GATGCACACGGGGCAGCGCCTCCTTCTCCACAGCCAGGGTGGGCATTGATGGGGGGCCACCG      873

Db   434 TGGCCAAGC  442
         ||| | |||
Cp   872 TGGACCAGC  864
```

RESULT 11

```
FEATURES             Location/Qualifiers
     source          1..479
                     /organism="Homo sapiens"
                     /clone="258295"
BASE COUNT     86 a    122 c    184 g     79 t      8 others
ORIGIN
Query Match      28.9%;  Score 376;  DB 13;  Length 479;
Best Local Similarity   96.0%;  Pred. No. 0.00e+00;
Matches   403;  Conservative   0;  Mismatches 14;  Indels   3;  Gaps   3;

LOCUS       AA400910    473 bp    mRNA            EST       12-AUG-1997
DEFINITION  zt71h09.s1 Soares testis NHT Homo sapiens cDNA clone 727841 3'
            similar to gb:J00117 CHORIOGONADOTROPIN BETA CHAIN PRECURSOR
            (HUMAN);.
ACCESSION   AA400910
NID         g2054783
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
            Homo.
REFERENCE   1  (bases 1 to 473)
AUTHORS     Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
            Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
            White,Y., Wylie,T., Waterston,R. and Wilson,R.
TITLE       WashU-Merck EST Project 1997
JOURNAL     Unpublished (1997)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 640   Std Error: 0.00
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Db    17 TTATTGTGGGAGGAATCGGGGTGTCCGAGGGCCCCGGGGCCGAGTCGGGGGAATGGGGCTTGGAAGGGCT    76
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Cp  1289 TTATTGTGGGAGGAATCGGGGTGTCCGGAGGGCCCCGGGGCCGAGTTGGGGGAATGGGGCTTGGAAGGGCT  1230

Db    77 GGGGGGAGGGGGCCTTTGAGGAAGGAGAGGAGGTCCGGGCACACAGATGGTGGGTGTTGNATTCACAGGTCAAGGG   136
         |||||||||||||||||||||||||||| |||| ||||||||||||||||||||||||| ||||||||||||||||
Cp  1229 GGGGGGAGGGGGCCTTTGAGGAAGGAGAGGAGAGGGGGCACAGATGGTGGGTGTTGGGTCATCACAGGTCAAGGG  1170

Db   137 GTGGTCCTTGGGACCCC-GCAGTCAGTGGTGGTGCTGCGGCGCAGAGTGCACATTGACAGCT   195
         |||||| ||||||||| |||||||||| ||||||||||||||||||||||||||||||||
Cp  1169 GTGGTCCTTGGGACCCCCGCAGTCAGTGGTGCTGCGGCGCAGAGTGCACATTGACAGCT    1110

Db   196 GAGAGCCACGGCNTAGGAGACCACGGGGTTCAGGCGGCAGGGGCCACGG   255
         |||||||||||| |||||||||||||||||||||||| |||||||||||
Cp  1109 GAGAGCCACGGCGTAGGAGACCACGGGGTTCAGGCGCCCAGGGAGCCGGAT  1050

Db   256 GGACTCGAAGCGCACATCCGGTAGTTGCACACCACCTGAGGCAGGGC-GGCAGACCCCC   314
         |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Cp  1049 GGACTCGAAGCGCACATCCGGTAGTTGCACACCACCTGAGGCAGGGCCGGCAGACCCC    990

Db   315 TTGCAGCACGCGGGTCATGGTGGGGCCGCAGTAGCCCGGCACAGATGGTGGGTGTTGACGGTGAT   374
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Cp   989 CTGCAGCACGCGGGTCATGGTGGGGCCGCAGTAGCCCGGCACAGATGGTGGGTGTTGACGGTGAT    930

Db   375 GCACACGGGGCAGCGCCTCCTTCTCCACAGCCANGGGTGGNATTCGATGGGGGGCCACNTTG   434
         |||||||||||||||||||||||||| |||||| ||||| |||||||||||||||||||
Cp   929 GCACACGGGGCAGCGCCTCCTTCTCCACAGCCA-GGGTGGCATTGATGGGGGGCCACCGTG    871
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```
RESULT 12

LOCUS       N31616        446 bp    mRNA            10-JAN-1996
DEFINITION  yw84a02.s1 Homo sapiens cDNA clone 258890 3' similar to gb:J00117
            CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
ACCESSION   N31616
NID         g1152015
KEYWORDS    EST.
SOURCE      human.
DEFINITION  human clone=258890 primer=m13 -40 forward library=Soares placenta
            8to9weeks 2NbHP8to9W vector=pT7T3D (Pharmacia) with a modified
            polylinker host=DH10B (ampicillin resistant) Rsite1=Not I
            Rsite2=Eco RI two placentas: one from 8 weeks and another from 9
            weeks post conception. 1st strand cDNA was primed with a Not I -
            oligo(dT) primer
```

FEATURES
source   Location/Qualifiers
          1..473
          /organism="Homo sapiens"
          /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
          polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
          was prepared from mRNA obtained from Clontech
          Laboratories, Inc., and primed with a Not I - oligo(dT)
          primer [5'-
          TGTTACCAATCTGAAGTGGGAGCGGCGCCGCGCCAATTTTTTTTTTTTTTTT-3'].
          Double-stranded cDNA was ligated to Eco RI adaptors
          (Pharmacia), digested with Not I and cloned into the Not I
          and Eco RI sites of the modified pT7T3 vector. Library
          went through one round of normalization to Cot5, and was
          constructed by Bento Soares and M. Fatima Bonaldo."
          /db_xref="taxon:9606"
          /clone="727841"
          /clone_lib="Soares testis NHT"
          /sex="male"
          /lab_host="DH10B"
          /clone="DH10B"
mRNA   complement(<1..>473)
          /db_xref=GDB:5924752"

BASE COUNT   120 c   190 g   78 t   1 others
ORIGIN

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Query Match          28.7%;   Score 373;  DB 25;  Length 473;
Best Local Similarity  97.8%;  Pred. No. 0.00e+00;
Matches  406;  Conservative  0;  Mismatches  4;  Indels  5;  Gaps  5;

Db    20 TTATTGTGGGAGGATCGGGGTGTCTCGAGGGGGGGGGGGGGGATGGGGTTGGAAGGCT 79
         |||||||||||||||||| |||| |||||||                  ||||||||||
Cp  1289 TTATTGTGGGAGGATCGGGGTGTCCGAGGGGGGGGGGATGGGGTTGGAAGGCT 1230

Db    80 GGGGGGAGGGGGCCTTTGAGGAAGAGAGAGGCCTGGAAGGGGCCCGGGAGTCGGGAGTCGGGAT CAAGGG 139
         |||||||||||||||||||||||||||||||||||||||||||||
Cp  1229 GGGGGGAGGGGGCCTTTGAGGAAGAGAGAGTCCATCACAGGTCAAGGG 1170

Db   140 GTGGGTCCTTGGGACCCC-GCAGTCAGTGGTGCTGGGGCGGCACGTGCACATTGACAGCT 198
         |||||||||||||||   || |||||||||||||||||||||||||||||||
Cp  1169 GTGGGTCCTTGGGACCCCGCAGTCAGTGGTGCTGCGGCGCGAGAGTGCACATTGACAGCT 1110

Db   199 GAGAGGCCACGGGCGTAGGAGAGACCACGGGGTTCACGCGGCGCGGG-CAGCCAGGGAGGCCGGAT 257
         |||||||||||||||||||||||||||||||||||||
Cp  1109 GAGAGCCACGGGGTTAGGAGACCACGGGGTTCACGCGCGCGGG 1050

Db   258 GGACTCGAAGCGCACATCGCGCGTAGGTGCACACCACCTGAGGCAGGGGCCCGGCGCGGGN CAG-ACCCC 316
         |||||||||||||||||||||| | |||| | |||||
Cp  1049 GGACTCGAAGCGCACATCGCGCGTAGGTTGCACACCACCTGAGGCAGGGGCCCGGCGCGGGAT 990

Db   317 -TGCAGCACGCGGGTCATGTGGGGCCAGTAGC--GGCACAGATGGTGGGTGGTGGTGTTGACGGTGAT 374
         ||||||||||||||||||||||||||||||||||||||||||
Cp   989 CTGCAGCACGCGGGTCATGGTGGGGCCAGTAGCCGGCACAGATGGTGGTGTTGACGGTGAT 930

Db   375 GCACACGGGGCCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGAIGGGGCGGGCAC 429
         |||||||||||||||||||||||||||||||||||||||||||||||
Cp   929 GCACACGGGGCCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGAIGGGGCGGGCAC 875
```

COMMENT   Contact: Wilson RK
            Washu-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 329
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
TITLE   The WashU-Merck EST Project
JOURNAL   Unpublished (1995)

REFERENCE   1 (bases 1 to 446)
AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
ORGANISM   Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
SOURCE   Homo sapiens
            [5'-TGTTACCAATCTGAAGTGGGAGCGGCGCCGCGCCAATTTTTTTTTTTTTTTT-3'],
            double-stranded cDNA was size selected, ligated to Eco RI adaptors
            (Pharmacia), digested with Not I and cloned into the Not I and Eco
            RI sites of a modified pT7T3 vector (Pharmacia). Library
            constructed by Bento Soares and M. Fatima Bonaldo.

FEATURES
source   Location/Qualifiers
            1..446
            /organism="Homo sapiens"
            /clone="258890"

BASE COUNT   82 a   108 c   170 g   71 t   15 others
ORIGIN

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Query Match          28.5%;   Score 371;  DB 13;  Length 446;
Best Local Similarity  94.8%;  Pred. No. 0.00e+00;
Matches  399;  Conservative  0;  Mismatches  18;  Indels  4;  Gaps  4;

Db    17 TTANTGTGGGANGANTNGGGGGTTTNCGANGGCCCCGGGANTNNNNATGGACTTGGNAGGCT 76
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Cp  1289 TTATTGTGGGAGGATCGGGGTGTCCGAGGGGGGGGGGATGGGGTTGGAAGGCT 1230

Db    77 GGGGGGAGGGGGCCTTTNAGGAAGAGAGAGAGTCCTGGAANCCGGGGTCATCACAGGTCAAGGG 136
         ||||||||||||||| ||||||||||  | ||||||||||||||
Cp  1229 GGGGGGAGGGGGCCTTTGAGGAAGAGAGAGTCCATCACAGGTCAAGGG 1170

Db   137 GTGGTCCTTGGGACCCC--GCAGTCAGTGGTGTGCTGCGGCGCAGAGTGCACATTNACAGCT 195
         ||||||||||||||||   |||||||||||||| |||| ||||||||||||||||
Cp  1169 GTGGGTCCTTGGGACCCCGCAGTCAGTGGTGCTGCGGCGCGAGAGTGCACATTGACAGCT 1110

Db   196 GAGAGCCACGCGGTAGGAGAGACCACGGGGTTCACGCGCGCGGG-CAGCCAGGGAGCCCGGAT 254
         ||||| ||||| |||||||||||||||||||||||||||||| ||||||||||||||||
Cp  1109 GAGAGCCACGGGGTTAGGAGACCACGGGGTTCACGCGCGCGGG-CAGCCAGGGAGCCGGAT 1050

Db   255 GGACTCGAAGCGCACATCGCGCGTAGGTTGCACACCACCTGAGGCAGGGGCCGGCGCGGGAT 313
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp  1049 GGACTCGAAGCGCACATCGCGCGTAGGTTGCACACCACCTGAGGCAGGGGCCCGGCGCGGGAT 990

Db   314 TTGCAGCACGCGGGTCATGGTGGGGCCAGTAACCGGCACAGATGGTGGTGTTGACGGTGAT 373
         ||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Cp   989 CTGCAGCACGCGGGTCATGGTGGGGCCAGTAGCCGGCACAGATGGTGGTGTTGACGGTGAT 930

Db   374 GCACACGGGGCAGCCCTCCTTCTCCACAGCCAGGGTGGCATTGANGCGGCGCGCACCGTG 433
         |||||||||| |||||||||||||||||||||||||||||| || ||||||  |||||
Cp   929 GCACACGGGGCCAGCCCTCCTTCTCCACAGCCAGGGTGGCATT-GATGGGGCGGCGCACCGTG 871

Db   434 G 434
         |
Cp   870 G 870
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RESULT 13

LOCUS   AA644163   526 bp   mRNA   EST   27-OCT-1997

DEFINITION af62d08.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 1046607 3'
            similar to gb:J00117 CHORIOGONADOTROPIN BETA CHAIN PRECURSOR
            (HUMAN);.

ACCESSION   AA644163
NID   g2569381
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.

REFERENCE   1 (bases 1 to 526)
AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
            Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
            Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
TITLE   WashU-NCI human EST Project
JOURNAL   Unpublished (1997)

COMMENT   Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 335.

FEATURES   Location/Qualifiers
     source   1..526
                     /organism="Homo sapiens"
                     /note="Organ: mixed (see below); Vector: pT7T3D-Pac
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; Equal amounts of plasmid DNA from three
                     normalized libraries (melanocyte 2NbHM, pregnant uterus
                     NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
                     were made in vitro. Following HAP purification, this DNA
                     was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from pools of
                     5,000 clones made from the same 3 libraries. The pools
                     consisted of I.M.A.G.E. clones 260232-265223,
                     340488-345479, and 484488-489479."
                     /db_xref="taxon:9606"
                     /clone="1046607"
                     /clone_lib="Soares NhHMPu S1"
                     /tissue_type="Pooled human melanocyte, fetal heart, and
                     pregnant uterus"
                     /lab_host="DH10B"

BASE COUNT   100 a   140 c   201 g   85 t
ORIGIN

Query Match   28.2%;   Score 367; DB 28; Length 526;
Best Local Similarity 97.1%;   Pred. No. 0.00e+00;
Matches   409;   Conservative   0;   Mismatches 6;   Indels 6;   Gaps 6;

Db   16 TTAATTGTGGGAGGATCGGGGTGTCCGAGGGGCCCCGGGAGTCGGGGATGGACTTGGAAGGCT 75
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp   1289 TTATTGTGGGAGGATCGGGGTGTCCGAGGGCCCCGGGAGTCGGGGATGGGCTTGGAAGGCT 1230

Db   76 GGCAGGAGGGGGCCTTAAGGAAGAGGAGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGGG 135
            || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp   1229 GGGGGGAGGGGGCCTTTCAGGAAGAGGAGAGTCCTGGAAGCGGGGGTCATCACAGGTCAAGG 1170

Db   136 GTGGTCCTTTGGGACCCCGGACACGTCAGTCGTGCTGCGCGGCGCAGAGTCGCACATTGACAGCT 195
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp   1169 GTGGTCCTTGGGACCCCGCAGTCAGTGGTGCTGCGCGGCGCAGAGTCGCACATTGACAGCT 1110

Db   196 GAGAGCCACGCGCGTAGGAGAGACCACGGGGTTCACGCCGCGCGCGG-CAGCCAGGAGGAGCCGGGAT 254
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp   1109 GAGAGCCACGCGCGTAGGAGAGACCACGGGGTTCACGCCGCGGGGGG-GGCAGGACCCC 1050

Db   255 GGGACTCGGAAGCGCACATGCGGTAGTTGCACACCACCTGAGGGAGGGG-GGCAGGACCCC 313
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp   1049 GGACTCGGAAGCGCACATCCCGGTAGTTGCACACCACCTGAGCAGGAGGGGCCGCAGGACCCC 990

Db   314 -TGGCAGGCACGGCGGGGTCAtTGGTGGGGCAGTAGC-GGCACAGAGATGGTGGTCGTTGGGTTGACGGTGAT 371
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp   989 CTCCAGCACGCGGGGGGTCAtGGTGGGCCAGTAGCCGCCACAGATGGTGGTGGTTGACGGTGAT 930

Db   372 GGCACACGGGGCAGCCCCTCCTTCTCCACAGCCACGAGGGTGGCATTGATGGGGCGG-ACCGTG 430
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cp   929 G-CACACGGGGCAGCCCCTCCTTCTCCACAGCCACGAGGGTGGCATTGATGGATGCGGGGCGG 871

Db   431 G 431
            |
Cp   870 G 870

RESULT 14

LOCUS   AA232905   400 bp   mRNA   EST   06-AUG-1997

DEFINITION zr46c04.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 666438 3'
            similar to gb:J00117 CHORIOGONADOTROPIN BETA CHAIN PRECURSOR
            (HUMAN);.

ACCESSION   AA232905
NID   g1855917
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
            Homo.

REFERENCE   1 (bases 1 to 400)
AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
            Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
            White,Y., Wylie,T., Waterston,R. and Wilson,R.
TITLE   WashU-Merck EST Project 1997
JOURNAL   Unpublished (1997)

COMMENT   Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 834   Std Error: 0.00
            Seq primer: -41m13 fwd. ET from Amersham
            High quality sequence stop: 361.

FEATURES   Location/Qualifiers
     source   1..400
                     /organism="Homo sapiens"
                     /note="Organ: mixed (see below); Vector: pT7T3D-Pac
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; Equal amounts of plasmid DNA from three
                     normalized libraries (melanocyte 2NbHM, pregnant uterus
                     NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
                     were made in vitro. Following HAP purification, this DNA
                     was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from pools of
                     5,000 clones made from the same 3 libraries. The pools
                     consisted of I.M.A.G.E. clones 260232-265223,
                     340488-345479, and 484488-489479."
                     /db_xref="taxon:9606"
                     /clone="666438"
                     /clone_lib="Soares NhHMPu S1"
                     /tissue_type="Pooled human melanocyte, fetal heart, and
                     pregnant uterus"
                     /lab_host="DH10B"

Left column

RESULT 15

LOCUS	H95374	419 bp	mRNA	EST	25-NOV-1996

DEFINITION   yw60b03.s1 Soares placenta 8to9weeks 2NbHP8to9W Homo sapiens cDNA clone 255589 3' similar to gb:J00117 CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.
ACCESSION   H95374
NID   g1103007
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
    Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
    Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 419)
AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
    Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
    Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
    Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
    Wilson,R.
TITLE   The WashU-Merck EST Project
JOURNAL   Unpublished (1995)
COMMENT   Contact: Wilson RK
    WashU-Merck EST Project
    Washington University School of Medicine
    4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
    Tel: 314 286 1800
    Fax: 314 286 1810
    Email: est@watson.wustl.edu
    High quality sequence stops: 297
    Source: IMAGE Consortium, LLNL
    This clone is available royalty-free through LLNL; contact the
    IMAGE Consortium (info@image.llnl.gov) for further information.
    Insert Length: 1014   Std Error: 0.00
    Seq primer: Promega -21m13.

mRNA

BASE COUNT	74 a	98 c	165 g	63 t

ORIGIN

complement(<1..>400)
/db_xref="GDB:5428470"

Query Match   27.4%; Score 356; DB 25; Length 400;
Best Local Similarity 97.4%; Pred. No. 0.00e+00;
Matches 376; Conservative 0; Mismatches 8; Indels 2; Gaps 2;

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Db   17 TTATTGTGGGAGGATCGGGGGTGTCCGAGGCGCCCCGGGAGTCGGGGATCGGGGTTGGAAGG     76
        ||||||||||||||||||||||||||||||| ||||||||||||||||||| ||||||||
Cp 1289 TTATTGTGGGAGGATCGGGGGTGTCCGAGGCGGGGGGAGTCGGGGATCGGGGCTTGGAAGGCT 1230

Db   77 GGGGGGGAGGATGGCCTTTGAGGAAGAGGAGTGCCTGGAAGAGGAGGGGGGTCATCACAGGTCAAGGG    136
        |||||| |||  ||||||||||||||||||| |||||||||||| |||||||||||||||||||||
Cp 1229 GGGGGGGAGGGGCCTTTGAGGAAGAGGAGTCCTGGAAGAGGAGGGGGGTCATCACAGGTCAAGGG   1170

Db  137 GTGGTGGTCCTTGGGACACCCCCAGTCAGTGTGTGCTCCGGGGTGCTGCGCGCCAGGAGGCACATTGACAGCT    196
        ||||| |||||||||| ||||||||||||||          ||||| |||||| |||||||||||||||||||
Cp 1169 GTGGTCCTTGGGACCCCCCAGTCAGTGGTTGCTGCGCGCGCGCGCCAGGAGTGCACATTGACAGCT      1110

Db  197 GAGAGCCCACGGCGTAGGAGGACCACGGGGGTTCACGCCGCGGCAGCCCAGGGAGCCGGAT    256
        |||||||||||||||||||| ||||||||| ||||||||||||||||||||||||||||||
Cp 1109 GAGAGCCCACGGCGTAGGAGACCACGGGGTTCACGCCGCGGCAGCCCAGGGAGCCGGAT    1050

Db  257 GGGACTCGAAGCGCACATCCGCGGGTAGTTGCACACCACCTGAGGCCAGGCACGGGCAGGCCGGTCAG-AGCCC    315
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| | |||  ||
Cp 1049 GGGACTCGAAGCGCACATCCGCGGGTAGTTGCACACCACCTGAGGCCAGGCACGGGCAGGCCGGGCAGGCGGGACCCC  990

Db  316 CTGCAGCAGCGCGGGGTCATGGTGGGGCAGTAGC--GGCACAGANTGGTGGTTGGTGTGTTGGACGGTGAT    374
        ||||||||  |||||||||||||||||||||||||  | |||||||||||||||||||||||||||||||
Cp  989 CTGCAGCACCGCGGGGTCATGGTGGGGCCAGTAGCCGCACACAGATGGTGGTTGGTGTGTTGGACGGTGAT    930

Db  375 GCACACGGGGCGGGCCAGCCCTCCTTCTCCA    400
        |||||||||| | |||||||||||||| |||
Cp  929 GCACACGGGGGCAGCGCCCTCCTTCTCTCTCA    904
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Right column

FEATURES   Location/Qualifiers
source   1..419
    /organism="Homo sapiens"
    /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
    modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
    strand cDNA was primed with a Not I - oligo(dT) primer [5'
    TGTTACCAATCTGAGTGGGACGGGCGGCCGCGATTTTTTTTTTTTTTTTT 3'],
    double-stranded cDNA was size selected, ligated to Eco RI
    adapters (Pharmacia), digested with Not I and cloned into
    the Not I and Eco RI sites of a modified pT7T3 vector
    (Pharmacia). Library constructed by Bento Soares and
    M.Fatima Bonaldo."
    /db_xref="taxon:9606"
    /clone="255589"
    /clone_lib="Soares placenta 8to9weeks 2NbHP8to9w"
    /dev_stage="two placentae: one from 8 weeks and another
    from 9 weeks post conception"
    /lab_host="DH10B (ampicillin resistant)"

mRNA   complement(<1..>419)

BASE COUNT	73 a	109 c	168 g	63 t	6 others

ORIGIN

Query Match   27.0%; Score 351; DB 16; Length 419;
Best Local Similarity 95.6%; Pred. No. 0.00e+00;
Matches 390; Conservative 0; Mismatches 13; Indels 5; Gaps 5;

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Db    1 CCGAGGGCCCCCGGGGAGTGCGTGGGAGGGGGGATGGACTTGGAAGGCTGGGGGGGGG     60
        |||||||||||||||||| ||||||  ||||||||||| |||||||||||||||||
Cp 1266 CCGAGGGCCCCCGGGGAGTCGGGGGGATGGGGCTTGGAAGGCTGGGGGGGGGGGGG   1207

Db   61 AGGAGGCCTGAAAGCGGGGGGTCATCACAGGTCAAGGGGGTCAAGGGGTGTCCTTGGG    120
        |||| ||||||||| |||||||||||||||||||||||||||||||||||||||
Cp 1206 AGGAGTCCTGGAAGCGGGGGGTCATCACAGGTCAAGGGGTGTGTCCTTGGGACCCCCGCAGT   1147

Db  121 CAGTGGTGCTTCCGGCGCCGCNGAGTGCACATTGACAGCTGAGAGGCCACGGGGTTAGGAGACCA    180
        ||||||||| |||||||||||| |||| ||||||||||||||||| |||||||||||||||||
Cp 1146 CAGTGGTGCTTCGCGGCGCCGCAGAGTGCACATTGACAGCTGAGAGGCCACGGGGCGTAGGAGACCA   1087

Db  181 CGGGGTTCACGCCGCGGNGGCCAGCCCAGGGAGCCGGAGGGACTCGAAGCGCACATCGCGGT    240
        |||||||||||||||| |||||||||||||||||||| |||||||||||||||||||| |||
Cp 1086 CGGGGTTCACGCCGCGGCAGCCCAGGGAGCCGGATGGGACTCGAAGCGCACGTCGCGGT   1027

Db  241 TAGTTGCACACCACCTGAGGCAGGCAGCGGGCGCCAGGACNCCCCGTGCAGCGACGCGGGGTCATGG    300
        ||||||||||||||||||||||||||||||||||| |||||| |||||||||||||||||||||||
Cp 1026 -AGTTGCACACCACCTGAGGCAGGCAGGGAC-CCCCTCCAGCACGGGGT-CATGG    970

Db  301 TGGGGCAGTAGGCNCACAGATGGTGGTGTTGTTGAGGTGTGTTGGACGGTGGTTGACGGTGGCCAAGC    360
        |||||||||||| ||||||||||||| ||||||||| ||| ||||||||||||||||||||||||||
Cp  969 TGGGGCAGTAGCCGCACAGATGGTGGTTGTTGTTGACGGTGTTGACGGTGATCCACACGGGGGGCCAGCCCTCCT   910

Db  361 TNCTCCACAGCCAGGTGGCTTTGAGTTGGGGGGGGCAGGCGGCCGCGTGGCCCAAGC    408
        | ||||||||||||| ||||||||||||||||||||||||||||||||
Cp  909 T-CTCCACAGCCAGGGTGGCATTGAT-GGGGCGGCCGCGGCACCGTGGACCAGC    864
```

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*****************************************************************
*****************************************************************
**                                                             **
**        M P S R C H                                          **
**                                              (TM)           **
**                                                             **
*****************************************************************
*****************************************************************

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MPsrch_pp    protein - protein database search, using Smith-Waterman algorithm

Run on:          Wed May  6 09:06:59 1998;   MasPar time 10.23 Seconds
                                              491.010 Million cell updates/sec

Tabular output not generated.

Title:        >US-08-804-166-8
Description:  (1-336) from US08804166.pep
Perfect Score: 2541
Sequence:     1 SRTSLLAFGLLCLPWLQEG.........PSLPSPSRLPGPSDPPILPQ 336

Scoring table:  PAM 150
                Gap 11

Searched:     120837 seqs, 14945562 residues

Post-processing:  Minimum Match 0%
                  Listing first 45 summaries

Database:     a-geneseq31
              1:part1  2:part2  3:part3  4:part4  5:part5  6:part6  7:part7
              8:part8  9:part9 10:part10 11:part11 12:part12 13:part13
             14:part14 15:part15 16:part16 17:part17 18:part18
             19:part19 20:part20 21:part21 22:part22 23:part23
             24:part24 25:part25 26:part26

Statistics:   Mean 32.744;  Variance 136.204;  scale 0.240

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                            SUMMARIES

Result                    Query
No.   Score   %   Match Length DB  ID       Description              Pred. No.

  1   2541  100.0   336   26 W33360  TBP(20-190)/hCG-beta       2.22e-245
  2   2022   79.5   307   26 W33358  TBP(20-161)/hCG-beta       7.11e-192
  3   1505   59.2   285   26 W33359  TBP(20-190)/hCG-alpha      8.93e-139
  4   1322   52.0   371    2 R07449  Tumour Necrosis Facto      4.69e-120
  5   1321   52.0   451   13 R70107  TNF-R-GBP 130 fusion       5.93e-120
  6   1322   52.0   455   14 R24000  TNF-alpha 55kD recept      4.69e-120
  7   1322   52.0   455    4 R75084  p55 TNF-R.                 4.69e-120
  8   1322   52.0   455    4 R20787  TNF-alpha binding pro      4.69e-120
  9   1322   52.0   455    2 R42059  Lambda derived TNF-R.      4.69e-120
 10   1322   52.0   455    2 R10986  30kD TNF inhibitor pr      4.69e-120
 11   1321   52.0   455   13 R11082  Human 55kD TNF-bindin      4.69e-120
 12   1321   52.0   900   13 R70103  TNF-R-GBP 130 fusion       5.93e-120
 13   1319   51.9   309   13 R70108  TNF-R-GBPH fusion pro      9.50e-120
 14   1319   51.9   455   13 R07451  Human Tumour Necrosis      9.50e-120
 15   1319   51.9   547   13 R70104  TNF-R-GBP 130 fusion       9.50e-120
 16   1319   51.9  1604   13 R70105  TNF-R-GBPH fusion pro      9.50e-120
 17   1317   51.8  1245   13 R70106  TNF-R-Pl.                  9.50e-120
 18   1313   51.7   433    8 R51032  Mutant p55 tumour nec      3.89e-119
 19   1313   51.7   443    8 R51033  Mutant p55 tumour nec      3.89e-119
 20   1313   51.7   455    8 R42197  p55 Tumour necrosis f      3.89e-119
 21   1313   51.7   455    8 R51034  Mutant p55 tumour nec      3.89e-119
 22   1308   51.5   455    3 R12550  Type I TNF receptor.       1.26e-118
 23   1291   50.8   256   26 W33357  TBP(20-161)/hCG-alpha      6.87e-117
 24   1263   49.7   161    5 R27496  Native 30 kD TNF inhi      4.96e-114
 25   1252   49.3   884   13 R70109  TNF-R-GBP 130 fusion       6.57e-113
 26   1030   40.5   199    4 R24080  Truncated TNF-alpha 5      8.37e-90
 27   1030   40.5   145    6 R15043  Human chorionic gonad      6.60e-90
 28   1025   40.3   145    3 R30999  Human chorionic gonad      2.37e-90
 29   1022   40.2   145   15 R15174  hCG methionine substi      1.69e-89
 30   1022   40.2   145    3 R15171  hCG methionine substi      1.69e-89
 31   1021   40.2   145    3 R15120  hCG/hLH chimera, A5.       2.13e-89
 32   1021   40.2   265   15 R86247  Single chain gonadotr      2.13e-89
 33   1021   40.2   265   15 R86259  Partially deglycosyla      2.13e-89
 34   1020   40.1   145   25 R31200  Human chorionic gonad      2.69e-89
 35   1020   40.1   145    3 R15117  hCG/hLH chimera, A3a.      2.69e-89
 36   1020   40.1   145    3 R15169  hCG methionine substi      2.69e-89
 37   1018   40.1   181   15 R15173  hCG histidine substit      4.30e-89
 38   1016   40.0   145    3 R86258  Human CG beta-subunit      6.86e-89
 39   1015   39.9   145    3 R27681  Chorionic gonadotroph      8.67e-89
 40   1015   39.9   145   15 R15177  hCG histidine substit      8.67e-89
 41   1014   39.9   145   24 R27688  Chorionic gonadotroph      1.09e-88
 42   1013   39.9   145    3 R15103  hCG/hLH chimera, D7.       1.38e-88
 43   1013   39.9   145   15 R15170  hCG methionine substi      1.38e-88
 44   1013   39.9   145    3 W27687  Chorionic gonadotroph      1.38e-88
 45   1013   39.9   145   24 W27682  Chorionic gonadotroph      1.38e-88

                            ALIGNMENTS

RESULT      1
ID   W33360 standard; Protein; 336 AA.
AC   W33360;
DT   19-MAR-1998  (first entry)
DE   TBP(20-190)/hCG-beta fusion protein.
KW   Fusion protein; thrombopoietin; TPO; human chorionic gonadotrophin;
KW   beta subunit; hCG-beta.
OS   Homo sapiens.
PN   WO9730161-A1.
PD   21-AUG-1997;
PF   20-FEB-1997; U02315.
PF   20-FEB-1996; US-011936.
PR   (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
PA   Campbell RK, Chappel SC, Jameson BA;
PI   Campbell RK, Chappel SC, Jameson BA;
DR   WPI; 97-425036/39.
DR   N-PSDB; T94022.
PT   Hybrid dimeric protein comprising two co-expressed units - each
PT   based on receptor or ligand and a subunit of a heterodimeric
PT   hormone, especially FSH, for inducing follicular maturation
PS   Example; Pages 39-40; 60pp; English.
PT   A novel fusion protein comprises 2 dimer forming co-expressed amino
CC   acid sequences, each consisting of a homodimeric or heterodimeric
CC   receptor chain or ligand, with ligand-receptor binding activity,
CC   bound directly or via a peptide linker to a subunit of a
CC   heterodimeric protein hormone capable of forming a heterodimer with
CC   the hormone's other subunits. The fusion protein, e.g. the
CC   thrombopoietin (TPO)/human chorionic gonadotrophin-beta subunit
CC   (hCG-beta) fusion protein denoted by the present sequence,
CC   significantly increases the biological activity of the hormone
CC   component, reducing the requirement for hormone itself and the
CC   number of injections needed.
SQ   Sequence  336 AA;

Query Match          100.0%;  Score 2541;  DB 26;  Length 336;
Best Local Similarity 100.0%;  Pred. No. 2.22e-245;
Matches  336;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy     1 srtsllafgllclpwlqegssadsvcpqgkyihpqnnsicctkchkgtylyndcpgpggd 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 srtsllafgllclpwlqegssadsvcpqgkyihpqnnsicctkchkgtylyndcpgpggd 60

Qy    61 tdcrecesgsftasenhlrhclscskcrkemgqvelssctvdrdtvcgcrknqyrhywse 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 tdcrecesgsftasenhlrhclscskcrkemgqvelssctvdrdtvcgcrknqyrhywse 120
```

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Qy    61  TDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSE 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  nlfqcfncslclngtvhlscqekqntvctchagfflrenecvscsnckkslectklclpq 180

Qy   121  NLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||:|||||||
Db   181  ienvkgtedsgttagagprcrpinatlavekegcpvcitvnttlcagycptmtrvlggvl 240

Qy   181  IENVKGTEDSGTTAGAGPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVL 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  palpqvvcnyrdvrfesirlpgccprgvnpvvsyavalscqcalcrrsttdcggpkdhplt 300

Qy   241  PALPQVVCNYRDVRFESIRLPGCCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  cddprfqdsssskappslpspsrlpgpsdtpilpq 336

Qy   301  CDDPRFQDSSSSKAPPSLPSPSRLPGPSDTPILPQ 336
```

RESULT 2

```
ID    W33358 standard; Protein; 307 AA.
AC    W33358;
DT    19-MAR-1998 (first entry)
DE    TBP(20-161)/hCG-beta fusion protein.
KW    Fusion protein; thrombopoletin; TPO; human chorionic gonadotrophin;
KW    beta subunit; hCG-beta.
OS    Homo sapiens.
FH    Key                     Location/Qualifiers
FT    CDS                     279..1202
FT                            /*tag= a
PN    WO9730161-A1.
PD    21-AUG-1997;
PF    20-FEB-1997; U02315.
PF    20-FEB-1996; US-011936.
PA    (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
PI    Campbell RK, Chappel SC, Jameson BA;
DR    WPI; 97-425036/39.
DR    N-PSDB; T94408.
PT    Hybrid dimeric protein comprising two co-expressed units - each
PT    based on receptor or ligand and a subunit of a heterodimeric
PT    hormone, especially FSH, for inducing follicular maturation
PS    Example; Pages 34-35; 60pp; English.
CC    A novel fusion protein comprises 2 dimer forming co-expressed amino
CC    acid sequences, each consisting of a homodimeric or heterodimeric
CC    receptor chain or ligand, with ligand-receptor binding activity,
CC    bound directly or via a peptide linker to a subunit of a
CC    heterodimeric protein hormone capable of forming a heterodimer with
CC    the hormone's other subunits. The fusion protein, e.g. the
CC    thrombopoletin (TPO)/human chorionic gonadotrophin-beta subunit
CC    (hCG-beta) fusion protein denoted by the present sequence,
CC    significantly increases the biological activity of the hormone
CC    component, reducing the requirement for hormone itself and the
CC    number of injections needed.
SQ    Sequence    307 AA;
```

Query Match   79.6%; Score 2022; DB 26; Length 307;
Best Local Similarity 91.4%; Pred. No. 7.11e-192;
Matches 307; Conservative 0; Mismatches 0; Indels 29; Gaps 1;

```
Qy     1  srtsillaflgllclpwlqegsadsvcpqgykyihpqnnslcctkchkqtylyndcppgqd 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  SRTSLLAFGLLCLPWLQEGSADSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQD 60

Qy    61  tdcrecesgsftasenhlrhclscskcrkemgqveissctvdrdtvcgcrknqyrhywse 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  TDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSE 120

Qy   121  nlfqcfncslclngtvhlscqekqntvctchagfflrenecvsc------------ 164
              ||||||||||||||||||||||||||||||||||||||||||||
Db   121  NLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQ 180

Qy   165  ----------agagprcrpinatlavekegcpvcitvnttlcagycptmtrvlggvl 211
                         ||||||||||||||||||||||||||||||||||||||||||||
Db   165  -----------agagprcrpinatlavekegcpvcitvnttlcagycptmtrvlggvl 211
```

```
Qy   181  IENVKGTEDSGTTAGAGPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVL 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   212  palpqvvcnyrdvrfesirlpgccprgvnpvvsyavalscqcalcrrsttdcggpkdhplt 271

Qy   241  PALPQVVCNYRDVRFESIRLPGCCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   272  cddprfqdsssskappslpspsrlpgpsdtpilpq 307

Qy   301  CDDPRFQDSSSSKAPPSLPSPSRLPGPSDTPILPQ 336
```

RESULT 3

```
ID    W33359 standard; Protein; 285 AA.
AC    W33359;
DT    19-MAR-1998 (first entry)
DE    TBP(20-190)/hCG-alpha fusion protein.
KW    Fusion protein; thrombopoletin; TPO; human chorionic gonadotrophin;
KW    alpha subunit; hCG-alpha.
OS    Homo sapiens.
PN    WO9730161-A1.
PD    21-AUG-1997;
PF    20-FEB-1997; U02315.
PF    20-FEB-1996; US-011936.
PA    (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
PI    Campbell RK, Chappel SC, Jameson BA;
DR    WPI; 97-425036/39.
DR    N-PSDB; T94021.
PT    Hybrid dimeric protein comprising two co-expressed units - each
PT    based on receptor or ligand and a subunit of a heterodimeric
PT    hormone, especially FSH, for inducing follicular maturation
PS    Example; Pages 37-38; 60pp; English.
CC    A novel fusion protein comprises 2 dimer forming co-expressed amino
CC    acid sequences, each consisting of a homodimeric or heterodimeric
CC    receptor chain or ligand, with ligand-receptor binding activity,
CC    bound directly or via a peptide linker to a subunit of a
CC    heterodimeric protein hormone capable of forming a heterodimer with
CC    the hormone's other subunits. The fusion protein, e.g. the
CC    thrombopoletin (TPO)/human chorionic gonadotrophin-alpha subunit
CC    (hCG-alpha) fusion protein denoted by the present sequence,
CC    significantly increases the biological activity of the hormone
CC    component, reducing the requirement for hormone itself and the
CC    number of injections needed.
SQ    Sequence    285 AA;
```

Query Match   59.2%; Score 1505; DB 26; Length 285;
Best Local Similarity 98.0%; Pred. No. 8.93e-139;
Matches 196; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```
Qy     1  srtsillaflgllclpwlqegsadsvcpqgykyihpqnnslcctkchkqtylyndcppgqd 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  SRTSLLAFGLLCLPWLQEGSADSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQD 60

Qy    61  tdcrecesgsftasenhlrhclscskcrkemgqveissctvdrdtvcgcrknqyrhywse 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  TDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSE 120

Qy   121  nlfqcfncslclngtvhlscqekqntvctchagfflrenecvscsnckkslectklclpq 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  NLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQ 180

Qy   181  ienvkgtedsgttagaappgc 200
              |||||||||||||:|||||:|
Db   181  IENVKGTEDSGTTAGAGPRC 200
```

RESULT 4

```
ID    R07449 standard; protein; 371 AA.
AC    R07449;
DT    29-JAN-1991 (first entry)
DE    Tumour Necrosis Factor-Binding Protein from pTNF-BP15 cDNA.
KW    Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
KW    pTNF-BP15; infectious disease; parasitic disease; cachexia;
KW    autoimmune disease; shock.
```

OS   Homo sapiens.
PN   EP-393438-A.
PD   24-OCT-1990.
PD   06-APR-1990; 106624.
PD   21-APR-1989; DE-913101.
PR   21-JUN-1989; DE-920282.
PA   (BOEH) BOEHRINGER INGELHEIM INT.
PI   Hauptmann R, Himmler A, Maurer-Fogy I, Stratowa C;
DR   WPI; 90-321987/43.
DR   N-PSDB; Q06282.
PT   DNA encoding TNF binding protein and TNF- receptor - used in
PT   tumour treatment and to understand mechanism to TNF action
PS   Disclosure; Fig 1(1-3); 51pp; German.
CC   Clone pTNF-BP15 was used to construct pADTNF-BP, for transfection of
CC   e.g. COS7 cells. The expressed proteins are useful
CC   prophylactically and therapeutically to control disorders which
CC   involve the damaging effects of TNF-alpha or -beta (e.g. infectious or
CC   parasitic diseases, shock, cachexia, autoimmune diseases, adult
CC   respiratory distress syndrome etc., or side effects of treatment with
CC   TNG-alpha). They can also be used as diagnostic reagents for
CC   assaying TNF and in study of TNF-receptor interactions.
CC   See also Q06282-Q06285.
SQ   Sequence 371 AA;

Query Match   52.0%; Score 1322; DB 2; Length 371;
Best Local Similarity 100.0%; Pred. No. 4.69e-120;
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db   41 dsvcpggkyihpqnnsicctkchkgtylyndcpgpggqtdcrecesgsftasenhlrhcl 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGGQDTDCRECESGSFTASENHLRHCL 82

Db 101 scskcrkemgqveissctvdrdtvccgrknqyrhywsenlfgcfncslclngtvhlscqe 160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   83 SCSKCRKEMGQVEISSCTVDRDTVCCGRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db 161 kqntvctchagfflrenecvscsnckkslectklclpglenvkgtedsgtt 211
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 193

RESULT 5
ID   R70107 standard; Protein; 451 AA.
AC   R70107;
DT   10-NOV-1995 (first entry)
DE   TNF-R-GBP 130 fusion protein.
KW   Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;
KW   red blood cell; cytokine receptor; glycophorin binding peptide 130;
KW   GBP 130; GBPH; glycophorin binding peptide homologue; glycophorin A.
OS   Chimeric Homo sapiens.
OS   Chimeric Plasmodium falciparum.
PN   WO9506737-A.
PD   09-MAR-1995.
PD   01-SEP-1994; G01900.
PF   03-SEP-1993; GB-018350.
PR   23-AUG-1994; GB-017021.
PA   (PREN/) PRENDERGAST K F.
PI   Prendergast KF;
DR   WPI; 95-115452/15.
PT   New hybrid peptide(s) for binding cytokine(s) - comprising a
PT   malaria parasite peptide capable of binding a red blood cell and
PT   a receptor peptide.
PS   Example A. Page 53-54. 93pp; English.
CC   Hybrid peptides for binding cytokines, comprising a malaria parasite
CC   (Plasmodium falciparum) peptide (capable of binding to a red blood
CC   cell (RBC)), and a receptor peptide are claimed. R70103-25 are examples
CC   of these hybrid peptides. R70107 is a fusion of tumour necrosis factor
CC   receptor (in accordance with H Loetscher et al Cell, Vol. 61, 351-359)
CC   and glycophorin binding protein (GBP) 130. The use of cytokine
CC   receptors not normally found on RBCs means that the cytokine can bind
CC   harmlessly to the RBC without deleterious effect. The RBC protects the
CC   hybrid peptides from excretion from the kidney, and due to steric
CC   hindrance prevents the cytokines binding to a receptor in another cell.

CC   GBP 130 or GBPH (GBP homologue) are the prefd. malaria parasite peptides
CC   used, others include EBA 175 (175 kDa erythrocyte binding antigen),
CC   PfMSA (pre major merozoite surface antigen) and the Duffy binding
CC   receptor molecule (eg. exhibited by Plasmodium vivax). These peptides
CC   bind to pref. glycophorin A, B and C, sialo glycoproteins, found on
CC   the surface of RBCs. The hybrid peptides are thus used to lower
CC   the levels of free cytokines in the circulation to reduce pathological
CC   damage.
SQ   Sequence 451 AA;

Query Match   52.0%; Score 1321; DB 13; Length 451;
Best Local Similarity 99.4%; Pred. No. 5.93e-120;
Matches 171; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db   20 dsvcpggkyihpqnnsicctkchkgtylyndcpgpggqtdcrecesgsftasenhlrhcl 79
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGGQDTDCRECESGSFTASENHLRHCL 82

Db   80 scskcrkemgqveissctvdrdtvccgrknqyrhywsenlfgcfncslclngtvhlscqe 139
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   83 SCSKCRKEMGQVEISSCTVDRDTVCCGRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db 140 kqntvctchagfflrenecvscsnckkslectklclpglenvkgtedsgtna 191
         |||||||||||||||||||||||||||||||||||||||||||||||||| |
Qy 143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTTA 194

RESULT 6
ID   R24000 standard; Protein; 455 AA.
AC   R24000;
DT   05-NOV-1992 (first entry)
DE   TNF-alpha 55kD receptor.
DE   tumour necrosis factor alpha; extracellular binding domain;
KW   treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
KW   malaria; viral meningitis; graft versus host disease;
KW   autoimmune disease; rheumatoid arthritis.
OS   Homo sapiens.
FH   Key   Location/Qualifiers
FT   peptide   1..40
FT   /label= signal peptide
FT   modified_site 54..56
FT   /label= "potential"
FT   /note= N linked glycosylation site
FT   modified_site 145..147
FT   /label= "potential"
FT   /note= N linked glycosylation site
FT   modified_site 151..153
FT   /label= "potential"
FT   /note= N linked glycosylation site
FT   domain   212..234
FT   /label= transmembrane domain
PN   WO9207076-A.
PD   30-APR-1992.
PD   18-OCT-1991; G01826.
PF   18-OCT-1990; GB-022648.
PA   (CHAR-) CHARING CROSS SUNLEY RES CENT.
PA   Brennan FM, Feldmann M, Gray PW, Turner MJC;
PI   Brennan FM, Feldmann M, Gray PW, Turner MJC;
DR   WPI; 92-167156/20.
DR   N-PSDB; Q24440.
PT   New polypeptide capable of binding human TNF alpha - comprises
PT   first three cysteine-rich subdomains of TNF alpha receptor for
PT   treating autoimmune disease, septic shock, HIV etc.
PS   Example; Fig 1; 43pp; English.
CC   This sequence was deduced from human TNF-alpha cDNA isolated as in
CC   Q24440. The first 35 amino acids are generally quite hydrophobic
CC   and probably represent a signal sequence. Residues 35-40 are highly
CC   charged (DREKR) and this is not normally found in secretory
CC   signal sequences. It is possible the receptor is processed by
CC   proteolysis after residue 40 which contains a dibasic cleavage site
CC   (KR). Hydropathy analysis of this sequence predicts a single
CC   transmembrane domain of 23 amino acids, dividing the sequence into
CC   an extracellular domain of 171 residues and a cytoplasmic domain of
CC   221 residues. The sequence contains a large number of cysteine

RESULT 7

```
ID   R75084 standard; Protein; 455 AA.
AC   R75084;
DT   19-JAN-1996 (first entry)
DE   p55; TNF-R.
KW   p55; tumour necrosis factor receptor; TNF-R; human; murine; chimera;
KW   epidermal growth factor receptor; EGF-R; protease; inhibitor;
KW   phorbol myristate acetate; PMA.
OS   Homo sapiens.
FH   Key           Location/Qualifiers
FT   peptide       41..53
FT                 /note= "N terminus of soluble p55 TNF-R"
FT   modified_site 54..56
FT                 /note= "glycosylation site"
FT   modified_site 145..147
FT                 /note= "glycosylation site"
FT   modified_site 161..163
FT                 /note= "glycosylation site"
FT   peptide       193..210
FT                 /note= "peptide used in creation of chimeras"
FT   region        198..210
FT                 /note= "spacer region"
FT   misc_difference 201
FT                 /note= "major C terminus for soluble p55 TNF-R"
FT   misc_difference 202
FT                 /note= "essential for shedding reaction"
FT   misc_difference 203
FT                 /note= "minor C terminus for soluble p55 TNF-R"
FT   region        212..234
FT                 /note= "transmembrane region"
PN   AG947574 2-A.
PD   04-MAY-1995.
PF   11-OCT-1994; 075742.
PR   12-OCT-1993; IL-107268.
PA   (YEDA ) YEDA RES & DEV CO LTD.
PI   Watkin M, Brakebusch C, Varfolomeev E, Wallach D;
DR   WPI; 95-19434/26.
DR   N-PSDB; Q90513.
PT   New protease capable of cleaving soluble tumour necrosis factor
PT   (TNF) receptor - from cell-bound TNF-receptor, useful for
PT   antagonising deleterious effects of TNF.
PS   Disclosure; Fig 1; 40pp; English.
CC   This sequence represents human p55 tumour necrosis factor
CC   receptor fragment. The p55 TNF-R can be shed in response to different
CC   Inducing agents, e.g. phorbol myristate acetate (PMA), depending on cell
CC   type. The only region of the receptor whose structure affects the
CC   shedding response is the spacer region (see R75012) in the extracellular
CC   residues, the arrangement of which is similar to that of other cell
CC   surface proteins, suggesting the TNF-alpha receptor is structurally
CC   related to a family of receptors.
CC   NOTE:- Residues 371,2 given in the sequence as T,L, are encoded by
CC   TGG (W) and AAG (K).
CC   See also Q24440-51, R24000, R24080-84, R27585, Q29236-8
SQ   Sequence   455 AA;
```

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Query Match    52.0%;  Score 1322;  DB 4;  Length 455;
Best Local Similarity 100.0%;  Pred. No. 4.69e-120;
Matches   171;  Conservative   0;  Mismatches  0;  Indels  0;  Gaps  0;

Db   41  dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
         |||||||||||||||||||||||||||||||||||||||||||||||||
Qy   23  DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db   101 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
         |||||||||||||||||||||||||||||||||||||||||||||||||
Qy   83  SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db   161 kqntvctchagfflrenecvscsnckkslectklclpqienvkgtedsgtt 211
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 193
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RESULT 8

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ID   R20787 standard; Protein; 455 AA.
AC   R20787;
DT   11-MAY-1992 (first entry)
DE   TNF-alpha binding protein.
KW   Tumour necrosis factor alpha; autoimmune diseases; cachectin;
KW   extracellular domain.
OS   Homo sapiens.
FH   Key           Location/Qualifiers
FT   peptide       1..40
FT                 /note= "signal peptide"
FT   peptide       41..455
FT                 /note= "mature peptide"
FT   domain        30..199
FT                 /note= "extracellular domain"
FT   domain        212..234
FT                 /note= "transmembrane domain"
FT   modified_site 145..147
FT                 /note= "potential N-glycosylation site"
FT   modified_site 151..153
FT                 /note= "potential N-glycosylation site"
PN   GB2246569-A.
PD   05-FEB-1992.
PF   15-JUN-1990; 013410.
PR   15-JUN-1990; GB-013410.
PA   (CHAR-) CHARING CROSS SUNLE.
PI   Feldman M, Gray P, Turner M, Brennan F;
DR   WPI; 92-043613/06.
DR   N-PSDB; Q20973.
PT   New tumour necrosis factor alpha binding protein and polypeptide
PT   - useful in treating cachexia, sepsis and auto immune diseases
PT   e.g. rheumatoid arthritis
PS   Disclosure; Fig 1; 25pp; English.
CC   The amino acid sequence is that of tumour necrosis factor alpha
CC   binding protein which contains the extracellular domain of human TNF
CC   alpha receptor. It is soluble and can be used in the regulation of
CC   TNF-mediated responses by binding and sequestering the cytokine. It
CC   domain. This region is located close to a site of cleavage of the
CC   molecule, and links the Cys rich module to the transmembrane domain. The
CC   spacer region of the encoded protein was used to create the chimeras
CC   between human p55 TNF-R and murine epidermal growth factor receptor
CC   (EGF-R) that are represented by sequence R75007-11. This spacer region was
CC   subjected to deletion mutations (R75013-25) and substitutions
CC   (R75026-47). Of the spacer region, the most important residues are
CC   Asn 172, Val 173, Lys 174 and Gly 175, with Val 173 being the most
CC   important of these. The shedding of the receptor is independent of the
CC   side chain identity of these residues, with the exception of a limited
CC   dependence on the identity of Val 173. Mutations which alter the
CC   conformation of the protein adversely effect the shedding process.
CC   The mutations shown in R75013-47 were introduced in order to create an
CC   inhibitor of a protease that is capable of cleaving the soluble TNF-R
CC   from the cell bound TNF-R. Fragments of these inhibitors can be seen in
CC   R75017-9, R75025, R75033-5 and R75042-3. These protease inhibitors can
CC   be used for enhancing TNF function.
SQ   Sequence   455 AA;
```

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Query Match    52.0%;  Score 1322;  DB 14;  Length 455;
Best Local Similarity 100.0%;  Pred. No. 4.69e-120;
Matches   171;  Conservative   0;  Mismatches  0;  Indels  0;  Gaps  0;

Db   41  dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
         |||||||||||||||||||||||||||||||||||||||||||||||||
Qy   23  DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db   101 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
         |||||||||||||||||||||||||||||||||||||||||||||||||
Qy   83  SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db   161 kqntvctchagfflrenecvscsnckkslectklclpqienvkgtedsgtt 211
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 193
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Left column

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CC    can therefore be used therapeutically to treat disorders such as
CC    cachexia, sepsis and autoimmune diseases, specifically rheumatoid
CC    arthritis.
SQ    Sequence    455 AA;

Query Match    52.0%;    Score 1322;    DB 4;    Length 455;
Best Local Similarity 100.0%;    Pred. No. 4.69e-120;
Matches    171;    Conservative    0;    Mismatches    0;    Indels    0;    Gaps    0;

Qy    41 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Qy   101 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Qy   161 kqntvctchagfflrenecvscsnckkslectklclpqienvkgtedsgtt 211
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 193
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RESULT    9
ID    R42059 standard; Protein; 455 AA.
AC    R42059;
DT    29-APR-1994 (first entry)
DE    Lambda derived TNF-R.
KW    Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;
KW    IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;
KW    rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;
KW    pulmonary fibrosis; silicosis; allograft; xenograft; rejection;
KW    graft verses host disease; sepsis; inflammation; allergy;
OS    Homo sapiens.
OS    Lambda-gt10-7ctnfbp.
FH    Key          Location/Qualifiers
FT    peptide      1..40
FT                 /note= "Signal peptide"
FT                 41..455
FT                 /note= "Mature hTNF-R"
                   protein
PN    WO9319777-A.
PD    14-OCT-1993.
PF    26-MAR-1993; U02938.
PR    30-MAR-1992; US-860710.
PA    (IMMV ) IMMUNEX CORP.
PI    Smith CA;
DR    WPI; 93-335592/42.
DR    N-PSDB; Q49932.
PT    New fusion protein tumour necrosis factor and human interleukin-1
PT    receptor - useful in therapy, diagnosis and assays of e.g.
PT    rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.
PS    Disclosure; Page 57-59; 85pp; English.
CC    The sequences given in R42058-59 represent human tumour necrosis
CC    factor receptor (TNF-R) and the sequences in R42060-61 represent
CC    human interleukin-1 receptor (IL-1R). These sequences were used in
CC    the production of a fusion protein which conformed to one of the
CC    formulae:
CC    TNF-R-linker-TNF-R-linker-IL-1R
CC    IL-1R-linker-TNF-R-linker-IL-1R or
CC    TNF-R-linker-TNF-R
CC    The linker may comprise 5-100 amino acids selected from Gly, Asp,
CC    Ser, Thr and Ala. These linkers separate the individual moieties
CC    by such a distance that each component of the fusion protein is
CC    capable of folding into the secondary or tertiary structure required
CC    for its biological activity. These fusion proteins may be used in
CC    therapy, diagnosis and assays for conditions mediated by TNF or IL-1,
CC    particularly in conditions in which both TNF and IL-1 play a causitive
CC    role. They may be used to treat cachexia, rheumatoid arthritis,
CC    diabetes, multiple sclerosis, pulmonary fibrosis and silicosis,
CC    cerebral malaria, allograft and xenograft rejection in graft verses
CC    host disease, sepsis, septic shock, inflammation, allergies and
CC    autoimmune dysfunctions.
SQ    Sequence    455 AA;
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Right column

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Query Match    52.0%;    Score 1322;    DB 8;    Length 455;
Best Local Similarity 100.0%;    Pred. No. 4.69e-120;
Matches    171;    Conservative    0;    Mismatches    0;    Indels    0;    Gaps    0;

Qy    41 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgqdtdcrecesgsftasenhlrhcl 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Qy   101 scskcrkemgqveissctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Qy   161 kqntvctchagfflrenecvscsnckkslectklclpqienvkgtedsgtt 211
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 193
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RESULT    10
ID    R10986 standard; Protein; 455 AA.
AC    R10986;
DT    13-MAY-1991 (first entry)
DE    30kD TNF inhibitor precursor.
KW    Tumour necrosis factor; inhibitor.
OS    Homo sapiens.
FH    Key          Location/Qualifiers
FT    cleavage_site 40..41
FT                 note=" cleavage gives active protein "
PN    AU9058976-A.
PD    24-JAN-1991.
PF    16-JUL-1990; 058976.
PF    18-JUL-1989; US-381080.
PR    11-DEC-1989; US-450329.
PR    07-FEB-1990; US-475661.
PR    07-FEB-1990; US-475661.
PA    (SYNE-) SYNERGEN INC.
DR    WPI; 91-073847/11.
DR    N-PSDB; Q10883.
PT    Tumour necrosis factor inhibitor - for suppression of TNF-alpha
PT    and -beta, useful as therapeutic agent.
PS    Disclosure; Fig 21; 142pp; English.
CC    The sequence comprises the entire 30 kD TNF inhibitor. The clone
CC    from which the sequence was deduced was isolated from a cDNA
CC    library prepd. from U937 cells treated with PMA/PHA.
CC    The whole gene can be inserted into expression vectors for prepn.
CC    of TNF inhibitor for use in the treatment of inflammatory and
CC    degenerative diseases. The active protein is claimed (Claim 8).
CC    See also R10984 and R11001.
SQ    Sequence    455 AA;

RESULT    11
ID    R11082 standard; Protein; 455 AA.
AC    R11082;
DT    24-MAY-1991 (first entry)
DE    Human 55kD TNF-binding protein.
KW    Tumour Necrosis Factor; binding proteins; septic shock;
KW    autoimmune glomerulonephritis; lymphokine; cytokine.
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FH   Key              Location/Qualifiers
FT   modified_site    54
FT   modified_site    /label= putative N-glycosylation site
FT   modified_site    145
FT   modified_site    /label= putative N-glycosylation site
FT   modified_site    151
FT   modified_site    /label= putative N-glycosylation site
FT   modified_site    270
FT   modified_site    /label= putative N-glycosylation site
FT   region           212..230
FT   region           /label= transmembrane region
FT   peptide          1..28
FT   peptide          /label= signal peptide
PN   EP-417563-A.
PD   20-MAR-1991.
PF   31-AUG-1990; 116707.
PR   12-SEP-1989; CH-003319.
PR   08-MAR-1990; CH-0007346.
PR   20-APR-1990; CH-001347.
PA   (HOFF ) HOFFMANN-LA ROCHE AG.
PI   Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;
PI   Schlaeger EJ;
DR   WPI; 91-081851/12.
DR   N-PSDB; Q10955.
PT   Insoluble tumour necrosis factor binding proteins - and DNA
PT   encoding them, useful in pharmaceutical prods. and for antibody
PT   prodn.
PS   Claim 1; Fig 1; 26pp; German.
CC   Partial amino acid sequences were determined for the 55 and 75kD
CC   TNF-BPs (see R11072-R11081) and oligonucleotide primers were
CC   synthesised based on these partial sequences. The primers were used
CC   to produce a cDNA fragment for use as aprobe to screen a human
CC   placental cDNA bank constructed in lambda gt11. Positive clones were
CC   identified and sequenced. DNA constructs comprising the TNF-BP coding
CC   sequence may also contain a fragment encoding a human Ig domain.
CC   Recombinant constructs are used to transform cells to confer
CC   improved TNF-binding properties.
CC   See also Q10956.
SQ   Sequence    455 AA;

Query Match    52.0%;  Score 1322;  DB 2;  Length 455;
Best Local Similarity 100.0%;  Pred. No. 4.69e-120;
Matches 171;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Db   41  dsvcpggkyihpqnnsicctkchkgtylyndcpgppqgdtdcrecesgsftasenhlrhcl 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   23  dsvcpgpgkyihpqnnsicctkchkgtylyndcpgppqgdtdcrecesgsftasenhlrhcl 82

Db  101  scskcrkemgqveisscvdrdtvcgrknqyrhywsenlfqcfncslclngtvhlscqe 160
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   83  scskcrkemgqveisscvdrdtvcgrknqyrhywsenlfqcfncslclngtvhlscqe 142

Db  161  kqntvctchagfflrenecvscsnckkslectklclpqienvkgtedsgtt 211
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  143  kqntvctchagfflrenecvscsnckkslectklclpqienvkgtedsgtt 193

RESULT 12
ID   R70103 standard; Protein; 900 AA.
AC   R70103;
DT   02-NOV-1995  (first entry)
DE   TNF-R-GBP 130 fusion protein.
KW   Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;
KW   red blood cell; cytokine receptor; glycophorin binding peptide 130;
KW   GBP 130; GBPH; glycophorin binding peptide homologue; glycophorin A.
KW   tumour necrosis factor receptor; TNF-R.
OS   Chimeric Homo sapiens.
OS   Chimeric Plasmodium falciparum.
WO9506737-A.
PD   09-MAR-1995.
PF   01-SEP-1994; G01900.
PR   03-SEP-1993; GB-018350.
PR   23-AUG-1994; GB-017021.
PA   (PREN/) PRENDERGAST K F.
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PI   Prendergast KF;
DR   WPI; 95-115452/15.
PT   New hybrid peptide(s) for binding cytokine(s) - comprising a
PT   malaria parasite peptide capable of binding to a red blood cell and
PT   a receptor peptide.
PS   Example A; Page 46-47; 93pp; English.
CC   Hybrid peptides for binding cytokines, comprising a malaria parasite
CC   (Plasmodium falciparum) peptide (capable of binding to a red blood
CC   cell (RBC)) and a receptor peptide. R70103 is a fusion of tumour necrosis
CC   of these hybrid peptides. R70103-25 are examples
CC   receptor (in accordance with H Loetscher et al Cell, Vol. 61, 351-359)
CC   and glycophorin binding protein (GBP) 130. The use of cytokine
CC   receptors not normally found on RBCs means that the cytokine can bind
CC   harmlessly to the RBC without deleterious effect. The RBC protects the
CC   hybrid peptides from excretion from the kidney, and due to steric
CC   hindrance prevents the cytokines binding to a receptor in another cell.
CC   GBP 130 or GBPH (GBP homologue) are the prefd. malaria parasite peptides
CC   used, others include EBA 175 (175 kDa erythrocyte binding antigen),
CC   PMMSA (pre major merozoite surface antigen) and the Duffy binding
CC   receptor molecule (eg. exhibited by Plasmodium vivax). These peptides
CC   bind to pref. glycophorin A, B and C, sialo glycoproteins, found on
CC   the surface of RBCs. The hybrid peptides are thus used to lower
CC   the levels of free cytokines in the circulation to reduce pathological
CC   damage.
SQ   Sequence    900 AA;

Query Match    52.0%;  Score 1321;  DB 13;  Length 900;
Best Local Similarity 99.4%;  Pred. No. 5.93e-120;
Matches 171;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

Db   20  dsvcpggkyihpqnnsicctkchkgtylyndcpgppqgdtdcrecesgsftasenhlrhcl 79
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   23  dsvcpgpgkyihpqnnsicctkchkgtylyndcpgppqgdtdcrecesgsftasenhlrhcl 82

Db   80  scskcrkemgqveisscvdrdtvcgrknqyrhywsenlfqcfncslclngtvhlscqe 139
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   83  scskcrkemgqveisscvdrdtvcgrknqyrhywsenlfqcfncslclngtvhlscqe 142

Db  140  kqntvctchagfflrenecvscsnckkslectklclpqienvkgtedsgtna 191
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  143  kqntvctchagfflrenecvscsnckkslectklclpqienvkgtedsgtt 194

RESULT 13
ID   R70108 standard; Protein; 309 AA.
AC   R70108;
DT   10-NOV-1995  (first entry)
DE   TNF-R-GBPH fusion protein.
KW   Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;
KW   red blood cell; cytokine receptor; glycophorin binding peptide 130;
KW   GBP 130; GBPH; glycophorin binding peptide homologue; glycophorin A;
KW   tumour necrosis factor receptor; TNF-R.
OS   Chimeric Homo sapiens.
OS   Chimeric Plasmodium falciparum.
FH   Key              Location/Qualifiers
FT   misc_difference  230..269
FT                    /label= repeat_region
FT                    /note= "can be repeated n times, where n is a real
FT                    number"
WO9506737-A.
PD   09-MAR-1995.
PF   01-SEP-1994; G01900.
PR   03-SEP-1993; GB-018350.
PR   23-AUG-1994; GB-017021.
PA   (PREN/) PRENDERGAST K F.
DR   WPI; 95-115452/15.
PI   Prendergast KF;
PT   New hybrid peptide(s) for binding cytokine(s) - comprising a
PT   malaria parasite peptide capable of binding a red blood cell and
PT   a receptor peptide.
PS   Example A; Page 54-55; 93pp; English.
CC   Hybrid peptides for binding cytokines, comprising a malaria parasite
CC   (Plasmodium falciparum) peptide (capable of binding to a red blood
```

CC   cell (RBC) and a receptor peptide are claimed. R70103-25 are examples
CC   of these hybrid peptides. R70108 is a fusion of tumour necrosis factor
CC   receptor (in accordance with H Loetscher et al Cell, Vol. 61, 351-359)
CC   and glycophorin binding protein (GBP) homologue (GBPH). The
CC   use of cytokine receptors not normally found on RBCs means that the
CC   cytokine can bind harmlessly to the RBC without deleterious effect.
CC   The RBC protects the hybrid peptides from excretion from the kidney, and
CC   due to steric hindrance prevents the cytokines binding to a receptor in
CC   another cell. GBP 130 or GBPH are the pref'd. malaria parasite peptides
CC   used, others include EBA 175 (175 kDa erythrocyte binding antigen), PMMSA
CC   (pre major merozoite surface antigen) and the Duffy binding receptor
CC   molecule (eg. exhibited by Plasmodium vivax). These peptides bind to
CC   pref. glycophorin A, B and C, sialo glycoproteins, found on the surface
CC   of RBCs. The hybrid peptides are thus used to lower the levels of free
CC   cytokines in the circulation to reduce pathological damage.
SQ   Sequence   309 AA;

Query Match   51.9%; Score 1319; DB 13; Length 309;
Best Local Similarity   99.4%; Pred. No. 9.50e-120;
Matches 170; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Qy   20 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgsqdtdcrecessgsftasenhlrhcl 79
           ||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db   23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGSQDTDCRECESSGSFTASENHLRHCL 82

Qy   80 scskcrkemgqvelssctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 139
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   83 SCSKCRKEMGQVELSSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Qy   140 kqntvctchagfflrenecvscsnckkslectklclpqienvkgtedsgts 190
           ||||||||||||||||||||||||||||||||||||||||||||||:|||||
Db   143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 193

RESULT 14
ID   R07451 standard; protein; 455 AA.
AC   R07451;
DT   29-JAN-1991 (first entry)
DE   Human Tumour Necrosis Factor-Receptor from lambdaTNF-R2 cDNA insert.
KW   Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
KW   infectious disease; parasitic disease; cachexia;
KW   autoimmune disease; shock; lambdaTNF-R2; raTNF-R8.
OS   Homo sapiens.
PN   EP-393438-A.
PD   24-OCT-1990.
PF   06-APR-1990; 106624.
PR   21-APR-1989; DE-913101.
PR   21-JUN-1989; DE-920282.
PA   (BOEH) BOEHRINGER INGELHEIMINT.
PI   Hauptmann R, Himmler A, Maurer-Fogy I, Stratowa C;
PT   DNA encoding TNF binding protein and TNF- receptor - used in
PT   tumour treatment and to understand mechanismsm to TNF action
PS   Disclosure: Fig 91(1-2); 51pp; German.
PR   raTNF-R8 (Q06284) was used to screen the HS913T cDNA library.
PR   LambdaTNF-R2 encodes the complete human TNF-R2 and was used to
PR   construct a plasmid (pADINF-R) expressing the product the same way
PR   as pADTNF-BP (see Q06282). The expressed proteins are useful
PR   prophylactically and therapeutically to control disorders which
PR   involve the damaging effects of TNF-alpha or -beta (e.g. infectious or
PR   parasitic diseases, shock, cachexia, autoimmune diseases, adult
PR   respiratory distress syndrome etc., or side effects of treatment with
PR   TNG-alpha). They can also be used as diagnostic reagents for
PR   assaying TNF and in study of TNF-receptor interactions.
DR   WPI: 90-321987/43.
DR   N-PSDB: Q06285.
SEE   also Q06282-Q06285.

Query Match   51.9%; Score 1319; DB 2; Length 455;
Best Local Similarity   99.4%; Pred. No. 9.50e-120;
Matches 170; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Db   41 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgsqdtdcrecessgsftasenhlrhcl 100

RESULT 15
ID   R70104 standard; Protein; 547 AA.
AC   R70104;
DT   02-NOV-1995 (first entry)
DE   TNF-R-GBPH fusion protein.
KW   Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;
KW   red blood cell; cytokine receptor; glycophorin binding peptide 130;
KW   GBP 130; GBPH; glycophorin binding peptide homologue; glycophorin A;
KW   tumour necrosis factor receptor; TNF-R.
OS   Chimeric Homo sapiens.
OS   Chimeric Plasmodium falciparum.
PN   WO9506737-A.
PD   09-MAR-1995.
PF   01-SEP-1994; G01900.
PR   03-SEP-1993; GB-018350.
PR   23-AUG-1994; GB-017021.
PA   (PREN/) PRENDERGAST K F.
PI   Prendergast KF;
DR   WPI: 95-115452/15.
PT   New hybrid peptide(s) for binding cytokine(s) - comprising a
PT   malaria parasite peptide capable of binding a red blood cell and
PT   a receptor peptide.
PS   Example A; Page 47-48; 93pp; English.
CC   Hybrid peptides for binding cytokines, comprising a malaria parasite
CC   (Plasmodium falciparum) peptide (capable of binding to a red blood
CC   cell (RBC) and a receptor peptide are claimed. R70104 is a fusion of
CC   of these hybrid peptides. R70104 is a fusion of tumour necrosis factor
CC   receptor (in accordance with H Loetscher et al Cell, Vol. 61, 351-359)
CC   and glycophorin binding protein (GBP) homologue (GBPH). The use of
CC   cytokine receptors not normally found on RBCs means that the
CC   cytokine can bind harmlessly to the RBC without deleterious effect.
CC   The RBC protects the hybrid peptides from excretion from the kidney, and
CC   due to steric hindrance prevents the cytokines binding to a receptor in
CC   another cell. GBP 130 or GBPH are the pref'd. malaria parasite peptides
CC   used, others include EBA 175 (175 kDa erythrocyte binding antigen), PMMSA
CC   (pre major merozoite surface antigen) and the Duffy binding receptor
CC   molecule (eg. exhibited by Plasmodium vivax). These peptides bind to
CC   pref. glycophorin A, B and C, sialo glycoproteins, found on the surface
CC   of RBCs. The hybrid peptides are thus used to lower the levels of free
CC   cytokines in the circulation to reduce pathological damage.
SQ   Sequence   547 AA;

Query Match   51.9%; Score 1319; DB 13; Length 547;
Best Local Similarity   99.4%; Pred. No. 9.50e-120;
Matches 170; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Qy   20 dsvcpqgkyihpqnnsicctkchkgtylyndcpgpgsqdtdcrecessgsftasenhlrhcl 79
           ||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db   23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGSQDTDCRECESSGSFTASENHLRHCL 82

Qy   80 scskcrkemgqvelssctvdrdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqe 139
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   83 SCSKCRKEMGQVELSSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Qy   140 kqntvctchagfflrenecvscsnckkslectklclpqienvkgtedsgts 190
           ||||||||||||||||||||||||||||||||||||||||||||||:|||||
Db   143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 193

Search completed: Wed May 6 09:09:10 1998
Job time : 131 secs.

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| |\/| || |_) |\__ \| |_) || |   | |_| |
| |  | ||  __/ |___/|  _ < | |___|  _  |
|_|  |_||_|   |____/|_| \_\ \____|_| |_|   (TM)
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***************************************************************
*                                                             *
*  Release 3.0.5AA John F. Collins, Biocomputing Research Unit.*
*  Copyright (c) 1993-1997  University of Edinburgh, U.K.      *
*  Distribution rights by Oxford Molecular Ltd                *
*                                                             *
***************************************************************
```

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 6 09:05:45 1998; MasPar time 14.61 Seconds
                                          839.893 Million cell updates/sec

Tabular output not generated.

Title:
Description: >US-08-804-166-8
                (1-336) from US08804166.pep
Perfect Score: 2541
Sequence: 1 SRTSLLAFGLLCLPWLQEG...........PSLPSPSRLPGPSDPPILPQ 336

Scoring table: PAM 150
                Gap 11

Searched: 120446 seqs, 36531193 residues

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database: pir56
                1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 42.414; Variance 82.038; scale 0.517

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1322	52.0	455	1	GQHUT1	tumor necrosis factor receptor	9.45e-253
2	1257	49.5	160	5	1EXTA	tumor necrosis factor	1.30e-238
3	1238	48.7	158	5	1EXTB	tumor necrosis factor	1.74e-234
4	1121	44.1	142	5	INCFB	tumor necrosis factor	4.07e-209
5	1105	43.5	139	5	1TNRR	tumor necrosis factor	1.18e-205
6	1098	43.2	140	5	INCFA	tumor necrosis factor	3.86e-204
7	1030	40.5	145	2	I37412	beta-gonadotropin - h	1.88e-189
8	1030	40.5	165	1	KTHUB	choriogonadotropin be	1.88e-189
9	1028	40.5	461	2	JC4302	tumor necrosis factor	5.08e-189
10	1024	40.3	145	2	I37231	beta-gonadotropin - h	3.70e-188
11	960	37.8	454	1	GOMST1	tumor necrosis factor	2.26e-174
12	960	37.8	454	2	I57826	tumor necrosis factor	2.26e-174
13	944	37.2	461	1	GORTT1	tumor necrosis factor	5.21e-171
14	857	33.7	165	1	KTBAB	choriogonadotropin be	2.82e-152
15	803	31.6	110	5	1XULB	chorionic gonadotropin be	9.67e-141
16	803	31.6	110	5	1HCNB	chorionic gonadotropin	9.67e-141
17	803	31.6	110	5	1HRPB	chorionic gonadotropi	9.67e-141
18	740	29.1	121	5	I37994	chorionic gonadotropi	2.46e-127
19	740	27.9	115	1	UTBOB	beta-LH - human (frag	9.18e-121
20	709	27.9	115	1	UTHUB	lutropin beta chain	9.18e-121
21	614	24.2	141	1	UTBOB	lutropin beta chain p	9.77e-101
22	613	24.1	169	1	146949	luteinizing hormone be	1.58e-100
23	596	23.5	119	2	A61465	lutropin beta chain -	5.78e-97
24	598	23.5	141	1	UTPGB	lutropin beta chain p	2.20e-97
25	597	23.5	141	1	UTRTB	lutropin beta chain -	3.57e-97
26	595	23.4	118	2	PN0139	lutropin beta chain -	9.36e-97
27	594	23.4	141	2	UTSHB	lutropin beta chain p	1.52e-96
28	587	23.1	138	2	S00512	lutropin beta chain -	1.42e-95
29	585	23.0	118	2	PN0141	lutropin beta chain p	1.16e-94
30	582	22.9	141	2	JC4527	luteinizing hormone b	4.90e-94
31	430	16.9	144	1	UTCAB	gonadotropin beta cha	1.20e-62
32	427	16.8	141	1	B60626	gonadotropin beta cha	4.90e-62
33	426	16.8	146	2	S16763	gonadotropin beta cha	7.29e-62
34	420	16.5	119	2	S09344	gonadotropin beta cha	1.29e-60
35	416	16.4	142	2	C36179	gonadotropin II beta	8.39e-60
36	411	16.2	142	2	I11232	gonadotropin II beta	8.65e-59
37	407	16.0	113	2	I51242	gonadotropin II beta	5.58e-58
38	405	15.9	112	2	S21196	gonadotropin II beta	1.42e-57
39	403	15.9	140	2	A48166	gonadotropin II beta	3.59e-57
40	398	15.7	142	2	A25800	gonadotropin II beta	3.68e-56
41	388	15.3	142	2	I50143	gonadotropin beta cha	3.81e-54
42	368	14.5	156	2	A61091	luteinizing hormone b	3.92e-50
43	366	14.5	158	2	I51242	lutropin beta chain p	9.84e-50
44	361	14.2	147	2	I50994	gonadotropin II beta	9.80e-49
45	352	13.9	159	2	I51373	luteinizing hormone b	6.08e-47

RESULT ENTRY   1   ALIGNMENTS

RESULT   1
ENTRY   GQHUT1   #type complete
TITLE   tumor necrosis factor receptor type 1 precursor - human ALTERNATE_NAM
CONTAINS   tumor necrosis factor receptor alpha inhibitor; tumor necrosis factor
               binding protein 1 (TNF blocking factor)
ORGANISM   #formal_name Homo sapiens #common_name man
DATE   30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
               24-Oct-1997
ACCESSIONS   A38208; A34899; A36555; C36555; A38281; S12057;
               JT0758; A60231; A38258; A60594; A35010; JC2404
REFERENCE   A38208
   #authors   Fuchs, P.; Strehl, S.; Dworzak, M.; Himmler, A.; Ambros, P.F.
   #journal   Genomics (1992) 13:219-224
   #title   Structure of the human TNF receptor 1 (p60) gene (TNFR1) and
               localization to chromosome 12p13.
   #accession A38208
      ##molecule_type DNA
      ##residues 1-455 ##label FUC
      ##cross-references GB:M75864; GB:M75865; GB:M75866; NID:g339750
REFERENCE   A34899
   #authors   Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus,
               M.; Tabuchi, H.; Lesslauer, W.
   #journal   Cell (1990) 61:351-359
   #title   Molecular cloning and expression of the human 55 kd tumor
               necrosis factor receptor.
   #accession A34899
      ##molecule_type mRNA
      ##residues 1-455 ##label LOE
      ##cross-references GB:M58286; GB:M33480; NID:g339753; PID:g339754
      ##experimental_source placenta
      ##note   part of this sequence, including the amino end of the
                 mature protein, confirmed by protein sequencing
REFERENCE   A34900
   #authors   Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.;
               Wong, G.H.W.; Gatanaga, T.; Granger, G.A.; Lentz, R.; Raab,
               H.; Kohr, W.J.; Goeddel, D.V.
   #journal   Cell (1990) 61:361-370
   #title   Molecular cloning and expression of a receptor for human
               tumor necrosis factor.
   #accession A34900
      ##molecule_type mRNA
      ##residues 1-455 ##label SCH
      ##cross-references GB:M33294; NID:g339744; PID:g339745

REFERENCE
#authors Himmler, A.; Maurer-Fogy, I.; Kronke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.; Olsson, I.; Hauptmann, R.; Stratowa, C.; Adolf, G.R.
#journal DNA Cell Biol. (1990) 9:705-715
#title Molecular cloning and expression of human and rat tumor necrosis factor receptor chain (p60) and its soluble derivative, tumor necrosis factor receptor-binding protein.
#cross-references MUID:91090841
#accession A36555
##molecule_type mRNA
##residues 1-455 ##label HIM
##cross-references GB:M63121; NID:g339755; PID:g339756
#accession C36555
##molecule_type protein
##residues 30-38;41-53,'X',55-79,'XX',82-94,'NK',/XX',100-104; 107-128;162-167,'X',169-201 ##label HI2
##note the purified protein, called tumor necrosis factor binding protein, is a soluble derivative of the receptor

REFERENCE
#authors Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann, M.
#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:7380-7384
#title Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of recombinant soluble TNF-binding protein.
#cross-references MUID:91017509
#accession A38281
##molecule_type mRNA
##residues 1-455 ##label GRA
##cross-references GB:M37764
##note the authors translated the codon TGG for residue 371 as Thr, the AAG for residue 372 as Leu, and GAC for residue 427 as Asn

REFERENCE
#authors S12057
Nophar, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang, R.; Aderka, D.; Holtmann, H.; Wallach, D.
#journal EMBO J. (1990) 9:3269-3278
#title Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the type I TNF-R, cloned using amino acid sequence data of its soluble form, encodes both the cell surface and a soluble form of the receptor.
#cross-references MUID:91060021
#accession S12057
##molecule_type mRNA
##residues 1-455 ##label NOP
##cross-references EMBL:X55313; NID:g37223; PID:g37224
##note parts of soluble TNF binding protein 1, including its amino and carboxyl ends, were confirmed by protein sequencing

REFERENCE
#authors JT0758
Kemper, O.; Wallach, D.
#gene (1993) 134:209-216
#journal Cloning and partial characterization of the promoter for the human p55 tumor necrosis factor (TNF) receptor.
#title
#accession JT0758
##molecule_type DNA
##residues 1-13 ##label KEM

REFERENCE
#authors A60231
Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.
#journal Eur. J. Immunol. (1990) 20:1167-1174
#title Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequence and evidence for anti-inflammatory and immunomodulatory activities.
#cross-references MUID:90292116
#accession A60231
##molecule_type protein
##residues 41-43,'X',45-53,'X',55-57 ##label SEC

REFERENCE
#authors A38258
Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci III, J.A.; Jeffes, E.W.B.; Lentz, R.; Tomich, J.; Yamamoto, R.S.; Granger, G.A.

#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:8781-8784
#title Purification and characterization of an inhibitor (soluble tumor necrosis factor receptor) for tumor necrosis factor and lymphotoxin obtained from the serum ultrafiltrates of human cancer patients.
#cross-references MUID:91062364
#accession A38258
##molecule_type protein
##residues 41-60 ##label GAT
##experimental_source cancer patient serum

REFERENCE
#authors A60594
Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thysell, H.; Grubb, A.; Adolf, G.
#journal Eur. J. Haematol. (1989) 42:270-275
#title Isolation and characterization of a tumor necrosis factor binding protein from urine.
#accession A60594
##molecule_type protein
##residues 41-43,'X',45-53,'V',55-57,'XK',60 ##label OLS
##experimental_source renal failure patient urine

REFERENCE
#authors A35010
Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.
#journal JC2404
Engelmann, H.; Novick, D.; Wallach, D.
#title Biosci. Biotechnol. Biochem. (1994) 58:2266-2268
Two tumor necrosis factor-binding proteins purified from human urine. Evidence for immunological cross-reactivity with cell surface tumor necrosis factor receptors.
#accession JC2404
##molecule_type protein
##residues 41-53,'X',55-144,'X',146-150,'X',152-186,'X',188-201
#accession A35010
##molecule_type protein
##residues 41-45 ##label KAJ

REFERENCE
#authors A35010
Engelmann, H.; Novick, D.; Wallach, D.
#journal J. Biol. Chem. (1990) 265:1531-1536
#title Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified from human urine.
#accession JC2404
##molecule_type protein
##residues 41-45 ##label ENG
##experimental_source normal urine

COMMENT ##experimental_source urine
This protein is one of two known receptors for both TNF-alpha (cachectin) and TNF-beta (lymphotoxin).

GENETICS
#gene GDB:TNFR1
##cross-references GDB:125913; OMIM:191190
##map_position 12p13.2-12p13.2
#introns 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1

CLASSIFICATION #superfamily tumor necrosis factor receptor type 1; NGF receptor repeat homology duplication: glycoprotein; receptor; transmembrane protein

KEYWORDS alpha inhibitor; receptor; transmembrane protein
FEATURE
1-21 #domain signal sequence #status predicted #label SIG\
22-455 #product tumor necrosis factor receptor type 1 #status predicted #label MAT\
30-211 #domain extracellular #status predicted #label EXT\
41-201 #product TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status experimental #label TBP1\
44-82 #domain NGF receptor repeat homology #label NG1\
84-126 #domain NGF receptor repeat homology #label NG2\
127-167 #domain NGF receptor repeat homology #label NG3\
168-196 #domain NGF receptor repeat homology #label NG4\
212-234 #domain transmembrane #status predicted #label MEM\
235-455 #domain intracellular #status predicted #label INT\
54,145,151 #binding_site carbohydrate (Asn) (covalent) #status predicted

SUMMARY #length 455 #molecular-weight 50494 #checksum 153

Db 41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100

Query Match 52.0%; Score 1322; DB 1; Length 455;
Best Local Similarity 100.0%; Pred. No. 9.45e-253;
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   23  DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL   82
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  101  SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE  160

Qy   83  SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE  142
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  161  KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT          211

Qy  143  KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT          193
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RESULT   2

ENTRY 1EXTA #type complete
TITLE
PDB_TITLE tumor necrosis factor receptor extracellular domain, chain A
ORGANISM
 #note
 #formal_name Homo sapiens #common_name man
  expressed in Escherichia coli, the construct contains
  residues 12 to 172 of the mature sequence of the entire
  receptor. residue 11 is mutated to met as a result of the
  expression system

REFERENCE A65560
 #authors Naismith, J.H.; Sprang, S.R.
 #submission submitted to the Brookhaven Protein Data Bank, July 1996
 #cross-references PDB:1EXT

REFERENCE TN026248
 #authors Naismith, J.H.; Devine, T.Q.; Brandhuber, B.J.; Sprang, S.R.
 #journal J. Biol. Chem. (1995) 270:13303
 #title Crystallographic evidence for dimerization of unliganded
  tumor necrosis factor receptor.

REFERENCE TN026249
 #authors Rodseth, L.E.; Brandhuber, B.; Devine, T.Q.; Eck, M.J.; Hale,
  K.; Naismith, J.H.; Sprang, S.R.
 #journal J. Mol. Biol. (1994) 239:332
 #title Two crystal forms of the extracellular domain of type 1 tumor
  necrosis factor receptor.

REFERENCE A40737
 #authors Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
  H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
 #journal Cell (1993) 73:431-445
 #title Crystal structure of the soluble human 55 kd TNF
  receptor-human TNFbeta complex: Implications for TNF
  receptor activation.

COMMENT Resolution: 1.85 angstroms
COMMENT Determination: X-ray diffraction
COMMENT R-value: no refinement
KEYWORDS binding protein; cytokine; signalling protein
FEATURE
 66-68 #region helix (right hand 3-10)\
 151-154 #region helix (right hand 3-10)\
 7-9,17-19 #region helix (right hand alpha)\
 131-134,137-140 #region beta sheet\
 25-29,39-42 #region beta sheet\
 71-74,83-85 #region beta sheet\
 90-96,99-104 #region beta sheet\
 111-115,124-127 #region beta sheet\
 3-17 #region beta sheet\
 18-31 #region beta sheet\
 21-40 #region beta sheet\
 43-58 #region beta sheet\
 61-76 #region beta sheet\
 64-84 #region beta sheet\
 86-102 #region beta sheet\
 105-117 #region beta sheet\
 108-125 #region beta sheet\
 127-138 #region beta sheet\
 144-154 #region beta sheet\
 141-143 #disulfide_bonds\
 151-154 #disulfide_bonds\
  #disulfide_bonds\
  #disulfide_bonds\
SUMMARY #length 160 #molecular-weight 18065 #checksum 2297
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Query Match          49.5%;    Score 1257;   DB 5;   Length 160;
Best Local Similarity  100.0%;   Pred. No. 1.30e-238;
Matches  160;   Conservative  0;   Mismatches  0;   Indels  0;   Gaps  0;

Qy    1  SVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLS   60
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Db  121  SVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLS  60

Qy   24  SVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLS   83
         ...
Db   61  CSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLS 120

Qy   84  CSCKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEK 143
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   84  CSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLS 143

Db  144  QNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIEN          183
         ||||||||||||||||||||||||||||||||||||||||
Qy  121  QNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIEN          160
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RESULT   3

ENTRY 1EXTB #type complete
TITLE
PDB_TITLE tumor necrosis factor receptor extracellular domain, chain B
ORGANISM
 #note
 #formal_name Homo sapiens #common_name man
  expressed in Escherichia coli, the construct contains
  residues 12 to 172 of the mature sequence of the entire
  receptor. residue 11 is mutated to met as a result of the
  expression system

REFERENCE A65560
 #authors Naismith, J.H.; Sprang, S.R.
 #submission submitted to the Brookhaven Protein Data Bank, July 1996
 #cross-references PDB:1EXT

REFERENCE TN026251
 #authors Naismith, J.H.; Devine, T.Q.; Brandhuber, B.J.; Sprang, S.R.
 #journal J. Biol. Chem. (1995) 270:13303
 #title Crystallographic evidence for dimerization of unliganded
  tumor necrosis factor receptor.

REFERENCE TN026252
 #authors Rodseth, L.E.; Brandhuber, B.; Devine, T.Q.; Eck, M.J.; Hale,
  K.; Naismith, J.H.; Sprang, S.R.
 #journal J. Mol. Biol. (1994) 239:332
 #title Two crystal forms of the extracellular domain of type 1 tumor
  necrosis factor receptor.

REFERENCE A40737
 #authors Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
  H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
 #journal Cell (1993) 73:431-445
 #title Crystal structure of the soluble human 55 kd TNF
  receptor-human TNFbeta complex: Implications for TNF
  receptor activation.

COMMENT Resolution: 1.85 angstroms
COMMENT Determination: X-ray diffraction
COMMENT R-value: no refinement
KEYWORDS binding protein; cytokine; signalling protein
FEATURE
 68-70 #region helix (right hand 3-10)\
 143-145 #region helix (right hand 3-10)\
 9-11,19-21 #region helix (right hand 3-10)\
 133-136,139-142 #region beta sheet\
 27-31,41-44 #region beta sheet\
 73-76,85-87 #region beta sheet\
 92-98,101-106 #region beta sheet\
 113-117,126-129 #region beta sheet\
 5-19 #region beta sheet\
 20-33 #region beta sheet\
 23-42 #region beta sheet\
 45-60 #region beta sheet\
 63-78 #region beta sheet\
 66-86 #region beta sheet\
 88-104 #disulfide_bonds\
 107-119 #disulfide_bonds\
 110-127 #disulfide_bonds\
 129-140 #disulfide_bonds\
```

```
143-156         #disulfide_bonds\
146-152         #disulfide_bonds
SUMMARY      #length 158  #molecular-weight 17827  #checksum 5022

Query Match     48.7%;  Score 1238;  DB 5;  Length 158;
Best Local Similarity 100.0%;  Pred. No. 1.74e-234;
Matches  157;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 61
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 61

Qy    83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 121
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    62 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 82

Qy   143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLP 179
         |||||||||||||||||||||||||||||||||||
Db   122 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLP 158

RESULT
ENTRY       4         1NCFB          #type complete
TITLE       tumor necrosis factor receptor 55 kd extracellular domain
            contains residues 12 172 of the mature receptor sequence,
            chain B - hu
ALTERNATE_NAMES  stnfrl; type 1 receptor
ORGANISM    #formal_name Homo sapiens #common_name man
            expressed in Escherichia coli, residue 11 is mutated to met
            #note     as a result of the expression system
REFERENCE
            A66195
  *authors  Naismith, J.H.; Sprang, S.R.
  *submission  submitted to the Brookhaven Protein Data Bank, October 1994
  *cross-references PDB:1NCF
REFERENCE   TN029041
  *authors  Rodseth, L.E.; Brandhuber, B.; Devine, T.O.; Eck, M.J.; Hale,
            K.; Naismith, J.H.; Sprang, S.R.
  *journal  J. Mol. Biol. (1994) 239:332
  *title    Two crystal forms of the extracellular domain of type 1 tumor
            necrosis factor receptor.
REFERENCE   A40737
  *authors  Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
            H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
  *journal  Cell (1993) 73:431-445
  *title    Crystal structure of the soluble human 55 kd TNF
            receptor-human TNFbeta complex: implications for TNF
            receptor activation.
COMMENT     Resolution: 2.25 angstroms.
COMMENT     Determination: X-ray diffraction
COMMENT     R-value: no refinement
KEYWORDS    binding protein; cytokine; signalling protein
FEATURE
     2-16        #disulfide_bonds\
    17-30        #disulfide_bonds\
    20-39        #disulfide_bonds/
    42-57        #disulfide_bonds\
    60-75        #disulfide_bonds\
    63-83        #disulfide_bonds/
    85-101       #disulfide_bonds\
   104-116       #disulfide_bonds\
   107-124       #disulfide_bonds/
   126-137       #disulfide_bonds\
SUMMARY      #length 142  #molecular-weight 16046  #checksum 1225

Query Match     44.1%;  Score 1121;  DB 5;  Length 142;
Best Local Similarity 100.0%;  Pred. No. 4.07e-209;
Matches  142;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    25 VCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC 84
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 VCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC 60
```

```
Qy   145 NTVCTCHAGFFLRENECVSCSN 166
         |||||||||||||||||||||
Db   121 NTVCTCHAGFFLRENECVSCSN 142

Qy    85 SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQ 144
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQ 120

RESULT
ENTRY       5         1TNRR          #type complete
TITLE       tumor necrosis factor receptor type 1 (P55 extracellular
            receptor-human TNFbeta complex: implications for TNF
            receptor activation.
ORGANISM    #formal_name Homo sapiens #common_name man
            recombinant form expressed in Baculovirus SF9
REFERENCE   #note
            A52442
  *authors  Banner, D.W.
  *submission  submitted to the Brookhaven Protein Data Bank, May 1994
  *cross-references PDB:1TNR
REFERENCE   A40737
  *authors  Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
            H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
  *journal  Cell (1993) 73:431-445
  *title    Crystal structure of the soluble human 55 kd TNF
            receptor-human TNFbeta complex: implications for TNF
            receptor activation.
REFERENCE   TN034093
  *authors  D'Arcy, A.; Banner, D.W.; Janes, W.; Winkler, F.K.;
            Loetscher, H.; Schoenfeld, H.J.; Zulauf, M.; Gentz, R.;
            Lesslauer, W.
  *journal  J. Mol. Biol. (1993) 229:555
  *title    Crystallization and preliminary analysis of tnf-beta and a
            tnf-beta-55 kd tnf receptor complex.
COMMENT     Resolution: 2.85 angstroms
COMMENT     Determination: X-ray diffraction
KEYWORDS    Complex(lymphokineRECEPTOR)
FEATURE
     1-15        #disulfide_bonds\
    16-29        #disulfide_bonds\
    19-38        #disulfide_bonds/
    41-56        #disulfide_bonds\
    59-74        #disulfide_bonds\
    62-82        #disulfide_bonds/
    84-100       #disulfide_bonds\
   103-115       #disulfide_bonds\
   106-123       #disulfide_bonds/
   125-136       #disulfide_bonds\
SUMMARY      #length 139  #molecular-weight 15746  #checksum 5235

Query Match     43.5%;  Score 1105;  DB 5;  Length 139;
Best Local Similarity 100.0%;  Pred. No. 1.18e-205;
Matches  139;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    26 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCS 85
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCS 60

Qy    86 KCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQN 145
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 KCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQN 120

Qy   146 TVCTCHAGFFLRENECVSC 164
         |||||||||||||||||||
Db   121 TVCTCHAGFFLRENECVSC 139

RESULT
ENTRY       6         1NCFA          #type complete
TITLE       tumor necrosis factor receptor 55 kd extracellular domain
            contains residues 12 172 of the mature receptor sequence,
            chain A - hu
ALTERNATE_NAMES  stnfrl; type 1 receptor
```

ORGANISM   #formal_name Homo Homo sapiens #common_name man
#note   expressed in Escherichia coli, residue 11 is mutated to met
              as a result of the expression system
REFERENCE   A66195
#authors   Naismith, J.H.; Sprang, S.R.
#submission   submitted to the Brookhaven Protein Data Bank, October 1994
#cross-references PDB:1NCF
REFERENCE   TN029039
#authors   Rodseth, L.E.; Brandhuber, B.; Devine, T.Q.; Eck, M.J.; Hale,
              K.; Naismith, J.H.; Sprang, S.R.
#journal   J. Mol. Biol. (1994) 239:332
#title   Two crystal forms of the extracellular domain of type 1 tumor
              necrosis factor receptor.
REFERENCE   A40737
#authors   Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
              H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
#journal   Cell (1993) 73:431-445
#title   Crystal structure of the soluble human 55 kd TNF
              receptor-human TNFbeta complex: implications for TNF
              receptor activation.
COMMENT   Resolution: 2.25 angstroms
COMMENT   Determination: X-ray diffraction
COMMENT   R-value: no refinement
KEYWORDS   binding protein; cytokine; signalling protein
FEATURE
5-19   #disulfide_bonds\
20-33   #disulfide_bonds\
23-42   #disulfide_bonds\
45-60   #disulfide_bonds\
63-78   #disulfide_bonds\
66-86   #disulfide_bonds\
88-104   #disulfide_bonds\
107-119   #disulfide_bonds\
110-127   #disulfide_bonds\
129-140   #disulfide_bonds
SUMMARY   #length 140 #molecular-weight 15889 #checksum 6622

Query Match 43.2%; Score 1098; DB 5; Length 140;
Best Local Similarity 100.0%; Pred. No. 3.86e-204;
Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db   2 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 61
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db   62 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 121
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db 122 KQNTVCTCHAGFFLRENEC 140
         |||||||||||||||||||
Qy 143 KQNTVCTCHAGFFLRENEC 161

RESULT 7
ENTRY   I37412   #type fragment
TITLE   beta-gonadotropin - human (fragment)ORGANISM #formal_name Homo
DATE   21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change
            09-May-1997
ACCESSIONS I37231
REFERENCE   I37231
#authors   Talmadge, K.; Vamvakopoulos, N.C.; Fiddes, J.C.
#journal   Nature (1984) 307:37-40
#title   Evolution of the genes for the beta subunits of human
            chorionic gonadotropin and luteinizing hormone.
#cross-references MUID:84093590
#accession I37412
##status   preliminary; translated from GB/EMBL/DDBJ
##molecule_type DNA
##residues 1-145 ##label RES
##cross-references EMBL:X00265; NID:g31719
GENETICS

#introns
CLASSIFICATION 41/3
#superfamily pituitary glycoprotein hormone beta chain
SUMMARY   #length 145 #checksum 2358

Query Match 40.5%; Score 1030; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 1.88e-189;
Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db   7 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVCNYRDVRFES 66
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVCNYRDVRFES 257

Db   67 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPP 126
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPP 317

Db 127 SLPSPSRLPGPSDTPILPQ 145
         |||||||||||||||||||
Qy 318 SLPSPSRLPGPSDTPILPQ 336

RESULT 8
ENTRY   KTHUB   #type complete
TITLE   choriogonadotropin beta chain precursor - humanALTERNATE_NAMES chor
ORGANISM   #formal_name Homo sapiens #common_name man
DATE   20-Mar-1998
            23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change
ACCESSIONS A93230; I69972; I55224; I55250; I70007; I70008; A92303;
            A92181; A92142; PC1016; A61097; B56873; A01502
REFERENCE   A93230
#authors   Fiddes, J.C.; Goodman, H.M.
#journal   Nature (1980) 286:684-687
#title   The cDNA for the beta-subunit of human chorionic gonadotropin
            suggests evolution of a gene by readthrough into the
            3'-untranslated region.
#cross-references MUID:81012134
#accession A93230
##molecule_type mRNA
##residues 1-165 ##label FID
##cross-references GB:J00117; GB:M38559; GB:M54963; NID:g180436;

REFERENCE   I55224
#authors   Policastro, P.; Ovitt, C.E.; Hoshina, M.; Fukuoka, H.;
            Boothby, M.R.; Boime, I.
#journal   J. Biol. Chem. (1983) 258:11492-11499
#title   The beta subunit of human chorionic gonadotropin is encoded
            by multiple genes.
#cross-references MUID:84008141
#accession I69972
##status   translated from GB/EMBL/DDBJ
##molecule_type DNA
##residues 1-165 ##label POL
##cross-references GB:K03189; NID:g180450; PID:g180453
#accession I55224
##status   translated from GB/EMBL/DDBJ
##molecule_type DNA
##residues 1-23; /M, 25-136, /A, 138-165 ##label PO2
##cross-references GB:K03183; NID:g180442; PID:g180444
#note   clone CG-beta-e

REFERENCE   I55250
#authors   Policastro, P.F.; Daniels-McQueen, S.; Carle, G.; Boime, I.
#journal   J. Biol. Chem. (1986) 261:5907-5916
#title   A map of the hCG beta-LH beta gene cluster.
#cross-references MUID:86195987
#accession I55250
##status   preliminary; translated from GB/EMBL/DDBJ
##molecule_type DNA
##residues 1-5 ##label PO3
##cross-references GB:M13504; NID:g180419; PID:g463088
#note   CG-beta-3 gene
#accession I70007

```
##status          preliminary; translated from GB/EMBL/DDBJ
##molecule_type   DNA
##residues        1-5 ##label PO4
##cross-references GB:M13505; NID:g180429; PID:g463089
##note            CG-beta-6 gene
*accession        I70008
##status          preliminary; translated from GB/EMBL/DDBJ
##molecule_type   DNA
##residues        1-5 ##label RE5
##cross-references GB:M13503; NID:g180432; PID:g463090
##note            CG-beta-7 gene
REFERENCE         A92303
##authors         Birken, S.; Fetherston, J.; Canfield, R.; Boime, I.
#journal          J. Biol. Chem. (1981) 256:1816-1823
#title            The amino acid sequences of the prepeptides contained in the
                  alpha and beta subunits of human choriogonadotropin.
*accession        A92303
##molecule_type   protein
##residues        1-20 ##label BIR
##note            the identity of the residue at position 19 could not be
                  determined
REFERENCE         A92181
##authors         Morgan, F.J.; Birken, S.; Canfield, R.E.
#journal          J. Biol. Chem. (1975) 250:5247-5258
#title            The amino acid sequence of human chorionic gonadotropin. The
                  alpha subunit and beta subunit.
*accession        A92181
##molecule_type   protein
##residues        21-165 ##label MOR
REFERENCE         A92142
##authors         Carlsen, R.B.; Bahl, O.P.; Swaminathan, N.
#journal          J. Biol. Chem. (1973) 248:6810-6827
*accession        A92142
##molecule_type   protein
##residues        21-22,'Q',24-73,'ZL',76-140,142-157,'PB',160-165,'SLP'
                  ##label CAR
```

```
REFERENCE         PC1016
##authors         Shi, Z.P.; Du, G.G.; Li, W.X.; Liu, X.J.; Li, S.Z.; Xu, Y.S.;
                  Wang, Y.
#journal          Chinese Biochem. J. (1990) 6:558-562
#title            The immunological characteristics of the enzymatic fragments
                  of human chorionic gonadotropin beta-subunit.
*accession        PC1016
##molecule_type   protein
##residues        21-165 ##label SHI
##note            article in Chinese with English abstract
REFERENCE         A61097
##authors         Birken, S.; Armstrong, E.G.; Kolks, M.A.G.; Cole, L.A.;
                  Agosto, G.M.; Krichevsky, A.; Vaitukaitis, J.L.; Canfield,
                  R.E.
#journal          Endocrinology (1988) 123:572-583
#title            Structure of the human chorionic gonadotropin beta-subunit
                  fragment from pregnancy urine.
*accession        A61097
##molecule_type   protein
##residues        26-32,'X',34-49,'X',51-60,75-112 ##label BI2
##note            this material from pregnancy urine lacks sialic acid in
                  its carbohydrate and has been processed further from
                  the mature form into two chains linked by disulfide
                  bonds
*accession        A56873
##authors         Kardana, A.; Bagshawe, K.D.; Coles, B.; Read, D.; Taylor, M.
#journal          Br. J. Cancer (1993) 67:686-692
#title            Characterisation of UGP and its relationship with beta-core
                  fragment.
*accession        A56873
##molecule_type   protein
##residues        26-28,'X',30-32,'X',34-42,'X',44-45,'X',47-48;75-76,'X',
                  78-91,'G',93-102 ##label KAR
```

```
##note            experimental_source urine
                  sequence modified after extraction from NCBI backbone
                  this material was designated urinary gonadotrophin
                  peptide (peak 2)
REFERENCE         A44674
##authors         Lapthorn, A.J.; Harris, D.C.; Littlejohn, A.; Lustbader,
                  J.W.; Canfield, R.E.; Machin, K.J.; Morgan, F.J.; Isaacs,
                  N.W.
#title            Nature (1994) 369:455-461
#title            Crystal structure of human chorionic gonadotropin.
#contents         annotation; X-ray crystallography, 3.0 angstroms; correction
                  of disulfide bonds
GENETICS
##gene            GDB:CGB
##cross-references GDB:119055; OMIM:118860
##map_position    19q13.3-19q13.3
#introns          5/3; 61/3
#note             the choriogonadotropin beta chain locus contains six genes
                  (or pseudogenes)
CLASSIFICATION
KEYWORDS          #superfamily pituitary glycoprotein hormone beta chain
                  glycoprotein; hormone; pituitary
FEATURE
  1-20            #domain signal sequence #status experimental #label SIG\
  21-165          #product choriogonadotropin beta chain #status
                   experimental #label MAT\
  29-77,43-92,46-130,
  54-108,58-110,
  113-120         #disulfide_bonds #status experimental\
  33,50           #binding_site carbohydrate (Asn) (covalent) #status
                   experimental\
  138,150         #binding_site carbohydrate (Ser) (covalent) #status
                   predicted\
  141,147,152,158 #binding_site carbohydrate (Ser) (covalent) #status
                   experimental
SUMMARY           #length 165 #molecular-weight 17739 #checksum 6523
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Query Match           100.0%; Score 1030; DB 1; Length 165;
Best Local Similarity  40.5%;
Matches 139; Conservative 0; Pred. No. 1.88e-189; Mismatches 0; Indels 0; Gaps 0;

Db  27 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVCNYRDVRFES 86
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVCNYRDVRFES 257

Db  87 IRLPGCPRGVNPVVSYAVALSCQCCALCRRSTTDCGGPKDHPLTCDDPRRQDSSSSKAPP 146
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 258 IRLPGCPRGVNPVVSYAVALSCQCCALCRRSTTDCGGPKDHPLTCDDPRRQDSSSSKAPP 317

Db 147 SLPSPSRLPGPSDTPILPQ 165
        |||||||||||||||||||
Qy 318 SLPSPSRLPGPSDTPILPQ 336
```

```
RESULT 9

ENTRY         JC4302          #type complete
TITLE         tumor necrosis factor receptor p55 - pig
              ORGANISM                                     #formal_nam
DATE          29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change
              12-Dec-1997
ACCESSIONS    JC4302; PC4093
REFERENCE     JC4302
##authors     Suter, B.; Pauli, U.
#journal      Gene (1995) 163:263-266
#title        Cloning of the cDNA encoding the porcine p55 tumor necrosis
              factor receptor.
*accession    JC4302
##molecule_type mRNA
##residues    1-461 ##label SUT
##cross-references GB:U19994; NID:g1141752; PID:g1141753
*accession    PC4093
##molecule_type protein
##residues    1-7 ##label SU2
##experimental_source kidney cell line 15
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GENETICS
  #gene   tnfr
CLASSIFICATION
  #superfamily tumor necrosis factor receptor type 1; NGF
                receptor repeat homology
KEYWORDS   glycoprotein; kidney; receptor; transmembrane protein; tumor
FEATURE
  1-29   #domain signal sequence #status predicted #label SIG\
  30-461   #product tumor necrosis factor receptor p55 #status
                predicted #label MAT\
  44-194   #domain extracellular cysteine rich #status predicted
                #label EXT\
  44-82   #domain NGF receptor repeat homology #label NG1\
  211-231   #domain transmembrane #status predicted #label TMM\
  361-447   #domain signal transduction #status predicted #label
                SIT\
  54,145,151   #binding-site carbohydrate (Asn) (covalent) #status
                predicted
SUMMARY
  #length 461   #molecular-weight 50696 #checksum 8079

Query Match
Best Local Similarity   40.5%;   Score 1028; DB 2; Length 461;
Matches 125; Conservative 73.1%; Pred. 24; Mismatches 21; Indels 1; Gaps 1;

Db   41 ESLCPQGKYSHPQNRSICCTKCHKGTYLHNDCLGPGLDTDCRECDNGTFTASENHLTQCL 100
          :|::|:|| ||||:|||| |||||||:|| || |||||||| |||:|||::::|||:|| :|
Qy   23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db 101 SCSKCRSEMSQVEISPCTVRDTVCGCRKNQYRKYWSETLFQCLNCSLCPNGTVQLPCLE 160
          |:||:||:||::|:|||||||||||| |:|:|:|||||||||||||||:|:|:|:|:|:||
Qy   83 SCSKCRKEMGQVEISSCTVRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db 161 KQDTICNCHSGFFLRDKECVSCVNCKNA-DCKNLCPAISETRNDFQDTIGTT 210
          |:|:| ||||:|||:|:||::|::||| :||:||||||:||::|:||||:|||
Qy 143 KQNTVCTCHAGFFLRENECVSCGSNCKKSLECTKICLPQIENVKGTEDSGTT 193

RESULT 10
ENTRY   I37231   #type fragment
TITLE   beta-gonadotropin - human (fragment)
ORGANISM
  #formal_name Homo
DATE   21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change
        09-May-1997
ACCESSIONS   I37231
REFERENCE   I37231
  #authors   Talmadge, K.; Vamvakopoulos, N.C.; Fiddes, J.C.
  #journal   Nature (1984) 307:37-40
  #title   Evolution of the genes for the beta subunits of human
             chorionic gonadotropin and luteinizing hormone.
  #cross-references MUID:84093590
  #accession I37231
  ##status   preliminary; translated from GB/EMBL/DDBJ
  ##molecule_type DNA
  ##residues 1-145 ##label RES
  ##cross-references EMBL:X00266; NID:929907

GENETICS
  #introns   41/3
CLASSIFICATION
  #superfamily pituitary glycoprotein hormone beta chain
SUMMARY
  #length 145   #checksum 2349

Query Match
Best Local Similarity 40.3%;   Score 1024; DB 2; Length 145;
Matches 138; Conservative 99.3%; Pred. 0; Mismatches 1; Indels 0; Gaps 0;

Db   7 PRCRPINATLAVEKEGCPVCITVNTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 66
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 198 PRCRPINATLAVEKEGCPVCITVNTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Db   67 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQASSSSKAPP 126
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPP 317

Db 127 SLPSPSRLPGPSDTPILPQ 145
          |||||||||||||||||||
Qy 318 SLPSPSRLPGPSDTPILPQ 336

Qy 318 SLPSPSRLPGPSDTPILPQ 336

RESULT 11
ENTRY   GQMST1   #type complete
TITLE   tumor necrosis factor receptor type 1 precursor - mouse
ORGANISM
  #formal_name Mus musculus #common_name house mouse mouse
DATE   30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
        05-Sep-1997
ACCESSIONS   A38634; B40254; S16677; S19021; I54532
REFERENCE   A38634
  #authors   Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice,
             G.C.; Wong, G.H.W.; Chen, E.Y.; Goeddel, D.V.
  #journal   Proc. Natl. Acad. Sci. U.S.A. (1991) 88:2830-2834
  #title   Cloning and expression of cDNAs for two distinct murine tumor
             necrosis factor receptors demonstrate one receptor is
             species specific.
  #cross-references MUID:91187885
  #accession A38634
  ##molecule_type mRNA
  ##residues 1-454 ##label LEW
  ##cross-references GB:M60468; NID:g199825; PID:g199826
REFERENCE   A40254
  #authors   Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan,
             C.I.; Copeland, N.G.; Jenkins, N.A.; Smith, C.A.
  #journal   Mol. Cell. Biol. (1991) 11:3020-3026
  #title   Molecular cloning and expression of the type 1 and type 2
             murine receptors for tumor necrosis factor.
  #cross-references MUID:91246168
  #accession B40254
  ##molecule_type mRNA
  ##residues 1-454 ##label GO2
  #cross-references GB:M60468; NID:g199825; PID:g199826
REFERENCE   S16677
  #authors   Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissonerghis,
             A.M.; Gray, P.W.; Feldmann, M.; Foxwell, B.M.J.
  #journal   Eur. J. Immunol. (1991) 21:1649-1656
  #title   Cloning, expression and cross-linking analysis of the murine
             p55 tumor necrosis factor receptor.
  #cross-references MUID:91285014
  #accession S16677
  ##molecule_type mRNA
  ##residues 1-454 ##label BAR
  #cross-references EMBL:X59238; NID:g53578; PID:g53579
REFERENCE   S19021
  #authors   Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.
  #journal   Immunogenetics (1991) 34:338-340
  #title   Molecular cloning and expression of the mouse Tnf receptor
             type b.
  #cross-references MUID:92039815
  #accession S19021
  ##molecule_type mRNA
  ##residues 1-454 ##label ROT
  #cross-references EMBL:X57796; NID:g54848; PID:g54849
REFERENCE   I54532
  #authors   Bebo, B.F.
  #journal   Immunogenetics (1994) 39:450-451
  #title   Nucleotide sequence of the TNF type I receptor from a mouse
             endothelioma cell line.
  #cross-references MUID:94245292
  #accession I54532
  ##status   translated from GB/EMBL/DDBJ
  ##molecule_type mRNA
  ##residues 1-454 ##label RES
  ##cross-references GB:L26349; NID:g430732; PID:g430733
COMMENT This protein is one of two distantly related receptors for both
         TNF-alpha (cachectin) and TNF-beta (lymphotoxin).
CLASSIFICATION
  #superfamily tumor necrosis factor receptor type 1; NGF
               receptor repeat homology
KEYWORDS   duplication; glycoprotein; receptor; receptor; transmembrane protein
FEATURE
  1-29   #domain signal sequence #status predicted #label SIG\

SUMMARY
```
30-454    #product tumor necrosis factor receptor type 1 #status
          predicted #label MAT\
30-212    #domain extracellular #status predicted #label EXT\
44-82     #domain NGF receptor repeat homology #label NG1\
84-126    #domain NGF receptor repeat homology #label NG2\
127-167   #domain NGF receptor repeat homology #label NG3\
168-204   #domain NGF receptor repeat homology #label NG4\
213-235   #domain transmembrane #status predicted #label MEM\
236-454   #domain intracellular #status predicted #label INT\
54,151,202 #binding_site carbohydrate (Asn) (covalent) #status
          predicted
SUMMARY   #length 454 #molecular-weight 50129 #checksum 4839
```

```
Query Match          37.8%;  Score 960; DB 1; Length 454;
Best Local Similarity 68.6%; Pred. No. 2.26e-174;
Matches 118; Conservative 27; Mismatches 26; Indels 1; Gaps 1;

Db  41 DSLCPQGKYVHSKNNSICCTKCHKGTYLVSDCPSPGRDTVCRECEKGTFTASQNYLRQCL 100
        |:||||:|| |||||||||||||||||:|||||||||||:|:|| |:||||||||||||
Qy  23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db 101 SCKTCRKEMSQVEISPCQADKDTVCGCKENQFQRYLSETHFQCVDCSPCFNGTVTVIPCKE 160
        |||||||:|||||:||||:|:|||||||||||||||||:|||:|:|| :|||:||:||
Qy  83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db 161 TQNTVCNCHAGFFLRESECVPCSHCKKNEECMKLCLPPPLANVTNPQDSGTA 212
        |||| ||||||||||||| ||| |||||:||:||| ||| |:|||||||
Qy 143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQ-IENVKGTEDSGTT 193
```

RESULT   12

```
ENTRY      I57826           #type complete
TITLE      tumor necrosis factor receptor - mouseORGANISM
                            #formal_name Mus
DATE       02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
           23-May-1997
ACCESSIONS I57826
REFERENCE  I57826
           Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.;
 #authors  Steinmetz, M.
 #journal  Mol. Immunol. (1993) 30:165-176
 #title    Genomic organization and promoter function of the murine
           tumor necrosis factor receptor beta gene.
 #cross-references MUID:93156721
 #accession I57826
 #status   preliminary; translated from GB/EMBL/DDBJ
 #molecule_type DNA
 #residues 1-454  ##label RES
 #cross-references GB:M76656; NID:g202100; PID:g202102
```

```
Query Match          37.8%;  Score 960; DB 2; Length 454;
Best Local Similarity 68.6%; Pred. No. 2.26e-174;
Matches 118; Conservative 27; Mismatches 26; Indels 1; Gaps 1;

Db  41 DSLCPQGKYVHSKNNSICCTKCHKGTYLVSDCPSPGRDTVCRECEKGTFTASQNYLRQCL 100
        |:||||:|| |||||||||||||||||:|||||||||||:|:|| |:||||||||||||
Qy  23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db 101 SCKTCRKEMSQVEISPCQADKDTVCGCKENQFQRYLSETHFQCVDCSPCFNGTVTVIPCKE 160
        |||||||:|||||:||||:|:|||||||||||||||||:|||:|:|| :|||:||:||
Qy  83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db 161 TQNTVCNCHAGFFLRESECVPCSHCKKNEECMKLCLPPPLANVTNPQDSGTA 212
        |||| ||||||||||||| ||| |||||:||:||| ||| |:|||||||
Qy 143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQ-IENVKGTEDSGTT 193
```

GENETICS
```
 #gene     TNFR-2
 #introns  13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; 353/1
CLASSIFICATION #superfamily tumor necrosis factor receptor type 1; NGF
               receptor repeat homology
KEYWORDS   cytokine receptor
SUMMARY    #length 454 #molecular-weight 50030 #checksum 4267
```

RESULT   13

```
ENTRY      GQRTT1           #type complete
TITLE      tumor necrosis factor receptor type 1 precursor - ratCONTAINS
ORGANISM   #formal_name Rattus norvegicus #common_name Norway rat
DATE       30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change
           05-Sep-1997
ACCESSIONS B36555
           B36555
REFERENCE  A36555
 #authors  Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.;
           Pfizenmaier, K.; Lantz, M.; Olsson, I.; Hauptmann, R.;
           Stratowa, C.; Adolf, G.R.
 #journal  DNA Cell Biol. (1990) 9:705-715
 #title    Molecular cloning and expression of human and rat tumor
           necrosis factor receptor chain (p60) and its soluble
           derivative, tumor necrosis factor receptor-binding protein.
 #cross-references MUID:91090841
 #accession B36555
 #molecule_type mRNA
 #residues 1-461 ##label HIM
 #cross-references GB:M63122; NID:g207361; PID:g207362
COMMENT    This protein is one of two known receptors for both TNF-alpha
           (cachectin) and TNF-beta (lymphotoxin).
CLASSIFICATION #superfamily tumor necrosis factor receptor type 1; NGF
               receptor repeat homology
KEYWORDS   duplication; glycoprotein; receptor; transmembrane protein
FEATURE
1-29       #domain signal sequence #status predicted #label SIG\
30-461     #product tumor necrosis factor receptor type 1 #status
           predicted #label MAT\
30-201     #domain extracellular #status predicted #label EXT\
           #product tumor necrosis factor receptor binding protein #status
           predicted #label TBP\
44-82      #domain NGF receptor repeat homology #label NG1\
84-126     #domain NGF receptor repeat homology #label NG2\
127-167    #domain NGF receptor repeat homology #label NG3\
168-204    #domain NGF receptor repeat homology #label NG4\
212-234    #domain transmembrane #status predicted #label MEM\
235-461    #domain intracellular #status predicted #label INT\
54,151,201 #binding_site carbohydrate (Asn) (covalent) #status
           predicted
SUMMARY    #length 461 #molecular-weight 50969 #checksum 1617
```

```
Query Match          37.2%;  Score 944; DB 1; Length 461;
Best Local Similarity 67.3%; Pred. No. 6.21e-171;
Matches 115; Conservative 25; Mismatches 31; Indels 0; Gaps 0;

Db  41 DNLCPQGKYAHPKNNSICCTKCHKGTYLVSDCPSPGQETVCEVCDKGTFTASQNHVRQCL 100
        |::||||| | |:||||||||||||||||:||||||:|| || |:|||||||:||:||
Qy  23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db 101 SCKTCRKEMFQVEISPCKADMDTVCGCKKNQFQRYLSETHFQCVDCSPCFNGTVTVIPCKE 160
        |||||||| |||||:||:|||:|:|||||||||||:||||:|||:|:|| :|||:||:||
Qy  83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db 161 KQNTVCNCHAGFFLSGNECTPCSHCKKNQECMKLCLPPVANVTNPQDSGTA 211
        ||||||:||||||| :|||:||| ||||:||:||||| |||||||||||
Qy 143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 193
```

RESULT   14

```
ENTRY      KTBAB            #type complete
TITLE      choriogonadotropin beta chain precursor - olive baboonORGANISM
                            #common_name olive baboon
DATE       31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change
           03-May-1996
ACCESSIONS A25808
           A25808
REFERENCE  A25808
 #authors  Crawford, R.J.; Tregear, G.W.; Niall, H.D.
 #journal  Gene (1986) 46:161-169
 #title    The nucleotide sequences of baboon chorionic gonadotropin
```

```
            #cross-references genes MUID:87106851
            #accession A25808
            ##molecule_type mRNA
            ##residues 1-165 ##label CRA
COMMENT     There are at least five copies of CG-related genes and at least two
            of these are expressed in the baboon placenta.
CLASSIFICATION #superfamily pituitary glycoprotein hormone beta chain
KEYWORDS    glycoprotein; hormone; placenta; pregnancy maintenance
FEATURE
    1-165     #domain signal sequence #status predicted #label SIG\
   21-165     #product choriogonadotropin beta chain #status predicted
                #label CGB\
   29-77,43-92,46-130,
   54-108,58-110,
  113-120       #disulfide_bonds #status predicted\
   33,50         #binding_site carbohydrate (Asn) (covalent) #status
                  predicted\
  140,147,152    #binding_site carbohydrate (Ser) (covalent) #status
                  predicted
SUMMARY       #length 165 #molecular-weight 17592 #checksum 4960

Query Match          33.7%;  Score 857;  DB 1;  Length 165;
Best Local Similarity 81.3%;  Pred. No. 2.82e-152;
Matches 113; Conservative  14; Mismatches 12;  Indels  0;  Gaps  0;

Qy      27 PLCRPINATLAAEKEACPVCVTVNTTICAGYCPTMMRVLQAVLPPVPQVVCNYREVRFES  86
           | |||||||| ||||||||||||||||||||||||||||||||||:|||||||||||||||
Db     198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Qy      87 IRLPGCPPGVDPMVSVPVALSCRCALCRRSTSDCGGPKDHPLTCDDPNLQASSSKDPPP 146
           |:||||:|| :|:|| ||||||||||||||||||||||||||||||| |:|||||||||
Db     258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDRFQDSSSSKAPPP 317

Qy     147 SPPSPSRLLEPAGTPFLPQ 165
           | ||||| |:||||||||
Db     318 SLPSPSRLPGPSDTPILPQ 336
```

```
SUMMARY       #length 110 #molecular-weight 11906 #checksum 6414

Query Match          31.6%;  Score 803;  DB 5;  Length 110;
Best Local Similarity 100.0%;  Pred. No. 9.67e-141;
Matches 105; Conservative  0; Mismatches  0;  Indels  0;  Gaps  0;

Qy       6 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES  65
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Qy      66 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCD 110
           |||||||||||||||||||||||||||||||||||||||||||||
Db     258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCD 302

Search completed: Wed May  6 09:06:41 1998
Job time : 56 secs.
```

```
RESULT  15
ENTRY       1XULB          #type complete

TITLE       chorionic gonadotropin, chain B - humanPDB_TITLE         theoretical mod
            receptor complexed with human chorionic gonadotropin
ORGANISM    #formal_name Homo sapiens #common_name man
REFERENCE   A66957
    #authors   Jiang, X.; Dreano, M.; Buckler, D.R.; Cheng, S.; Ythler, A.;
               Wu, H.; Hendrickson, W.A.; El Tayar, N.
    #submission submitted to the Brookhaven Protein Data Bank, December 1996
    #cross-references PDB:1XUL
REFERENCE   TN032625
    #authors   Jiang, X.; Dreano, M.; Buckler, D.R.; Cheng, S.; Ythler, A.;
               Wu, H.; Hendrickson, W.A.; El Tayar, N.
    #journal   Structure (London) (1996) 3:1341
    #title     Structural predictions for the ligand-binding region of
               glycoprotein hormone receptors and the nature of
               hormone-receptor interactions structure.
REFERENCE   TN032626
    #authors   Wu, H.; Lustbader, J.W.; Liu, Y.; Canfield, R.E.;
               Hendrickson, W.A.
    #journal   Structure (London) (1994) 2:545
    #title     Structure of human chorionic gonadotropin at 2.6 a resolution
               from mad analysis of the selenomethionyl protein.
COMMENT     Resolution: not applicable
COMMENT     Determination: theoretical model
KEYWORDS    complex; glycoprotein hormone receptor glycoprotein; hormone;
            phosphorylation; receptor

FEATURE
   97-101,26-39,9-17    #region beta sheet\
   54-59,86-91          #region beta sheet\
   61-67,78-84          #region beta sheet\
    8-56                #disulfide_bonds\
   22-71                #disulfide_bonds\
```

```
beta-subunit genes have diverged from the human.

   25-109    #disulfide_bonds\
   33-87     #disulfide_bonds\
   37-89     #disulfide_bonds\
   92-99     #disulfide_bonds
```

```
 __  __ ____  ____  ____  ____ _   _
|  \/  |  _ \/ ___||  _ \ / ___| | | |
| |\/| | |_) \___ \| |_) | |   | |_| |
| |  | |  __/ ___) |  _ <| |___|  _  |  (TM)
|_|  |_|_|   |____/|_| \_\\____|_| |_|
```

```
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Distribution rights by Oxford Molecular Ltd
**************************************************************
```

MPsrch_pp   protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 6 09:03:29 1998;   MasPar time 9.80 Seconds
                859.610 Million cell updates/sec

Tabular output not generated.

Title:
Description: >US-08-804-166-8
Perfect Score: (1-336) from US00804166.pep
Sequence: 2541
                   1 SRTSLLLAFGLLCLPWLQEG.........PSLPSPSRLPGPSDTPILPQ 336

Scoring table: PAM 150
                   Gap 11

Searched: 69112 seqs, 25083644 residues

Post-processing: Minimum Match 0%
                   Listing first 45 summaries

Database: swiss-prot35
                   1:swiss1

Statistics: Mean 44.259; Variance 72.852; scale 0.608

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1322	52.0	455	1	TNR1_HUMAN	TUMOR NECROSIS FACTOR	6.45e-296
2	1030	40.5	165	1	CGHB_HUMAN	CHORIOGONADOTROPIN BET	1.12e-221
3	1028	40.5	461	1	TNR1_PIG	TUMOR NECROSIS FACTOR	3.59e-221
4	960	37.8	454	1	TNR1_MOUSE	TUMOR NECROSIS FACTOR	5.34e-204
5	944	37.2	461	1	TNR1_RAT	TUMOR NECROSIS FACTOR	5.76e-200
6	857	33.7	165	1	CGHB_PAPAN	CHORIOGONADOTROPIN BET	4.26e-178
7	740	29.1	141	1	LSHB_HUMAN	LUTROPIN BETA CHAIN PR	7.12e-149
8	709	27.9	164	1	CGHB_EQUAS	CHORIOGONADOTROPIN BET	3.56e-141
9	630	24.8	169	1	CGHB_CALJA	CHORIOGONADOTROPIN BET	1.18e-121
10	614	24.2	141	1	LSHB_BOVIN	LUTROPIN BETA CHAIN PR	1.01e-117
11	613	24.1	169	1	LSHB_HORSE	LUTROPIN/CHORIOGONADOT	1.77e-117
12	602	23.7	141	1	LSHB_SHEEP	LUTROPIN BETA CHAIN PR	8.87e-115
13	598	23.5	141	1	LSHB_PIG	LUTROPIN BETA CHAIN PR	8.48e-114
14	597	23.5	141	1	LSHB_RAT	LUTROPIN BETA CHAIN PR	1.49e-113
15	595	23.4	118	1	LSHB_BALAC	LUTROPIN BETA CHAIN (L	1.61e-113
16	587	23.1	138	1	LSHB_CANFA	LUTROPIN BETA CHAIN (L	4.19e-111
17	585	23.0	118	1	LSHB_PHYCA	LUTROPIN BETA CHAIN (L	1.29e-110
18	542	21.3	105	1	LSHB_MOUSE	LUTROPIN BETA CHAIN (L	4.00e-100
19	430	16.9	144	1	LSHB_CYPCA	LUTROPIN BETA CHAIN	3.62e-73
20	427	16.8	141	1	GTHB_HYPMO	GONADOTROPIN BETA CHAI	1.87e-72
21	426	16.8	146	1	GTHB_CTEID	GONADOTROPIN BETA CHAI	3.23e-72
22	416	16.4	142	1	GTH2_ONCKE	GONADOTROPIN BETA-II C	7.62e-70
23	411	16.2	138	1	GTHB_CLAGA	GONADOTROPIN BETA CHAI	1.16e-68
24	411	16.2	142	1	GTH2_ONCMA	GONADOTROPIN BETA-II C	1.16e-68
25	407	16.0	113	1	GTHB_MURCI	GONADOTROPIN BETA CHAI	1.03e-67
26	405	15.9	112	1	LSHB_RANCA	LUTROPIN BETA CHAIN (L	3.05e-67
27	403	15.9	140	1	GTH2_ANGAN	GONADOTROPIN BETA-II C	9.05e-67
28	398	15.7	142	1	GTHB_ONCTS	GONADOTROPIN BETA CHAI	1.37e-65
29	388	15.3	142	1	GTHB_CORAU	GONADOTROPIN BETA-II C	3.09e-63
30	371	14.6	166	1	LSHB_STRCA	LUTROPIN BETA CHAIN (L	2.98e-59
31	366	14.4	166	1	LSHB_COTJA	LUTROPIN BETA CHAIN PR	4.38e-58
32	355	14.0	115	1	GTH2_THOOB	GONADOTROPIN BETA-II C	1.59e-55
33	352	13.9	159	1	LSHB_MELGA	LUTROPIN BETA CHAIN PR	2.20e-55
34	319	12.6	136	1	GTHB_FUNHE	GONADOTROPIN BETA-II C	1.89e-47
35	320	12.6	138	1	TSHB_RAT	THYROTROPIN BETA CHAIN	3.63e-45
36	310	12.2	138	1	TSHB_PIG	THYROTROPIN BETA CHAIN	6.13e-45
37	309	12.2	138	1	TSHB_BOVIN	THYROTROPIN BETA CHAIN	6.13e-45
38	309	12.2	138	1	TSHB_SHEEP	THYROTROPIN BETA CHAIN	1.03e-44
39	308	12.1	130	1	TSHB_HUMAN	THYROTROPIN BETA CHAIN	4.98e-44
40	305	12.0	130	1	TSHB_MOUSE	THYROTROPIN BETA CHAIN	2.95e-44
41	306	12.0	138	1	TSHB_HORSE	THYROTROPIN BETA CHAIN	1.42e-43
42	303	11.9	130	1	TSHB_RAT	THYROTROPIN BETA CHAIN	2.07e-42
43	297	11.7	118	1	FSHB_RAT	FOLLITROPIN BETA CHAIN	3.24e-42
44	289	11.4	129	1	FSHB_HORSE	FOLLITROPIN BETA CHAIN	2.07e-40
45	281	11.1	129	1	FSHB_SHEEP	FOLLITROPIN BETA CHAIN	1.30e-38
					FSHB_HUMAN	FOLLITROPIN BETA CHAIN	

ALIGNMENTS

RESULT 1

```
ID   TNR1_HUMAN     STANDARD;      PRT;   455 AA.
AC   P19438;
DT   01-FEB-1991 (REL. 17, CREATED)
DT   01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (TUMOR NECROSIS FACTOR
DE   BINDING PROTEIN 1) (TBP1) (P60) (TNF-R1) (P55) (CD120A).
GN   TNFR1 OR TNFAR.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 90235284.
RA   LOETSCHER H., PAN Y.-C.E., LAHM H.-W., GENTZ R., BROCKHAUS M.,
RA   TABUCHI H., LESSLAUER W.;
RL   CELL 61:351-359(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 90235285.
RA   SCHALL T.J., LEWIS M., KOLLER K.J., LEE A., RICE G.C., WONG G.H.W.,
RA   GETANAGA T., GRANGER G.A., LENTZ R., RAAB H., KOHR W.J., GOEDDEL D.V.;
RL   CELL 61:361-370(1990).
RN   [3]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 41-53; 110-124 AND 199-201.
RX   MEDLINE; 91006021.
RA   NOPHAR Y., KEMPER O., BRAKEBUSCH C., ENGELMANN H., ZWANG R.,
RA   ADERKA D., HOLTMANN H., WALLACH D.;
RL   EMBO J. 9:3269-3278(1990).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91090841.
RA   HIMMLER A., MAURER-FOGY I., KRONKE M., SCHEURICH P., PFIZENMAIER K.,
RA   LANTZ M., OLSSON I., HAUPTMANN R., STRATOWA C., ADOLF G.R.;
RL   DNA CELL BIOL. 9:705-715(1990).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PLACENTA;
RX   MEDLINE; 91017509.
RA   GRAY P.W., BARRETT K., CHANTRY D., TURNER M., FELDMAN M.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 87:7380-7384(1990).
RN   [6]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 92250049.
RA   FUCHS P., STREHL S., DWORZAK M., HIMMLER A., AMBROS P.F.;
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RL   GENOMICS 13:219-224(1992).
RN   [7]
RP   SEQUENCE OF 41-45.
RX   MEDLINE; 90110215.
RA   ENGELMANN H., NOVICK D., WALLACH D.;
RL   J. BIOL. CHEM. 265:1531-1536(1990).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211.
RX   MEDLINE; 93258809.
RA   BANNER D.W., D'ARCY A., JANES W., GENTZ R., SCHOENFELD H.-J.,
RA   BROGER C., LOETSCHER H., LESSLAUER W.;
RL   CELL 73:431-445(1993).
RN   [9]
RP   X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.
RX   MEDLINE; 97094982.
RA   NAISMITH J.H., DEVINE T.Q., KOHNO H., SPRANG S.R.;
RL   STRUCTURE 4:1251-1262(1996).
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC   RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC   AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC   PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC   SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC   PROTEASES) MEDIATING APOPTOSIS.
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC   HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC   PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC   WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC   PROTEINS SUCH AS TRAF2, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC   TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC   ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC   NF-KAPPA B SIGNALING.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR   EMBL; X55313; G37224; -.
DR   EMBL; M33294; G339745; -.
DR   EMBL; M58286; G339754; -.
DR   EMBL; M63121; G339756; -.
DR   EMBL; M75866; G339750; -.
DR   EMBL; M75866; G339750; JOINED.
DR   EMBL; M75864; G339750; JOINED.
DR   EMBL; M75865; G339750; JOINED.
DR   EMBL; M60275; G339760; -.
DR   EMBL; A21522; G579600; -.
DR   PIR; A34899; GOHUT1.
DR   PIR; A35010; A35010.
DR   PIR; S12057; S12057.
DR   PIR; A38208; A38208.
DR   PDB; 1TNR; 31-JUL-94.
DR   PDB; 1EXT; 07-DEC-95.
DR   PDB; 1NCF; 11-JAN-97.
DR   MIM; 191190; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS;
KW   3D-STRUCTURE.
FT   SIGNAL   1   21
FT   CHAIN   22   455   TUMOR NECROSIS FACTOR RECEPTOR 1.
FT   CHAIN   41   291   TUMOR NECROSIS FACTOR BINDING PROTEIN 1.
FT   DOMAIN   22   211   EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   212   234   POTENTIAL.
FT   DOMAIN   235   455   CYTOPLASMIC (POTENTIAL).
FT   DOMAIN   43   196   4 X TNFR-CYS.
FT   REPEAT   43   82   TNFR-CYS 1.
FT   REPEAT   83   125   TNFR-CYS 2.
FT   REPEAT   126   166   TNFR-CYS 3.
FT   REPEAT   167   196   TNFR-CYS 4.
FT   DOMAIN   356   441   DEATH DOMAIN.
FT   DISULFID   44   58
FT   DISULFID   59   72
FT   DISULFID   62   81
FT   DISULFID   84   99
FT   DISULFID   102   117
FT   DISULFID   105   125

FT   DISULFID   127   143
FT   DISULFID   146   158
FT   DISULFID   149   166
FT   DISULFID   168   179
FT   DISULFID   182   191
FT   DISULFID   185   195
FT   CARBOHYD   54   54   POTENTIAL.
FT   CARBOHYD   145   145   POTENTIAL.
FT   CARBOHYD   151   151   POTENTIAL.
FT   CONFLICT   412   412   MISSING (IN REF. 4).
FT   CONFLICT   443   446   GPAA -> APP (IN REF. 4).
SQ   SEQUENCE   455 AA; 50494 MW; CE0EA06F CRC32;

Query Match   52.0%; Score 1322; DB 1; Length 455;
Best Local Similarity   100.0%;
Matches 171; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   23 DSVCPQGKYIHPQNNSICCTKCHKGTLYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   41 DSVCPQGKYIHPQNNSICCTKCHKGTLYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100

Qy   83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160

Qy   143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 193
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   161 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 211

RESULT 2
ID   CGHB_HUMAN   STANDARD;   PRT;   165 AA.
AC   P01233;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (CHORIONIC GONADOTROPIN BETA
DE   SUBUNIT).
GN   CGB.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 81012134.
RA   FIDDES J.C., GOODMAN H.M.;
RL   NATURE 286:684-687(1980).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 84093590.
RA   TALMADGE K., VAMVAKOPOULOS N.C., FIDDES J.C.;
RL   NATURE 307:37-40(1984).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 84008141.
RA   POLICASTRO P., OVITT C.E., HOSHINA M., FUKUOKA H., BOOTHBY M.R.,
RA   BOIME I.;
RL   J. BIOL. CHEM. 258:11492-11499(1983).
RN   [4]
RP   SEQUENCE OF 1-20.
RX   MEDLINE; 81117268.
RA   BIRKEN S., FETHERSTON J., CANFIELD R.E., BOIME I.;
RL   J. BIOL. CHEM. 256:1816-1823(1981).
RN   [5]
RP   SEQUENCE OF 21-165.
RX   MEDLINE; 75211304.
RA   MORGAN F.J., BIRKEN S., CANFIELD R.E.;
RL   J. BIOL. CHEM. 250:5247-5258(1975).
RN   [6]
RP   PRELIMINARY SEQUENCE OF 21-165.
RX   MEDLINE; 74011267.
RA   CARLSEN R.B., BAHL O.P., SWAMINATHAN N.;
RL   J. BIOL. CHEM. 248:6810-6827(1973).

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RN   [7]
RP   SEQUENCE OF 1-5 FROM N.A.
RX   MEDLINE; 8619987.
RA   POLICASTRO P.F., DANIELS-MCQUEEN S., CARLE G., BOIME I.;
RL   J. BIOL. CHEM. 261:5907-5916(1986).
RN   [8]
RP   PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.
RX   MEDLINE; 81215630.
RA   MISE T., BAHL O.P.;
RL   J. BIOL. CHEM. 256:6587-6592(1981).
RN   [9]
RP   DISULFIDE BONDS.
RX   MEDLINE; 90094415.
RA   SACCUZO BEEBE J., MOUNTJOY K., KRZESICKI R.F., PERINI F.,
RA   RUDDON R.W.;
RL   J. BIOL. CHEM. 265:312-317(1990).
RN   [10]
RP   STRUCTURE OF CARBOHYDRATES.
RX   MEDLINE; 93314469.
RA   WEISSHAAR G., HIYAMA J., RENWICK A.G.C.;
RL   GLYCOBIOLOGY 1:393-404(1991).
RN   [11]
RP   X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RX   MEDLINE; 94261179.
RA   LAPTHORN A.J., HARRIS D.C., LITTLEJOHN A., LUSTBADER J.W.,
RA   CANFIELD R.E., MACHIN K.J., MORGAN F.J., ISAACS N.W.;
RL   NATURE 369:455-461(1994).
CC   -!- FUNCTION: STIMULATES THE OVARIES TO SYNTHESIZE THE STEROIDS THAT
CC       ARE ESSENTIAL FOR THE MAINTENANCE OF PREGNANCY.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- TISSUE SPECIFICITY: PLACENTA.
CC   -!- DEVELOPMENTAL STAGE: MADE BY THE FIRST TRIMESTER PLACENTA.
DR   EMBL; J00117; G100437; -.
DR   EMBL; M13504; G463088; -.
DR   EMBL; M13505; G463089; -.
DR   EMBL; M13503; G463090; -.
DR   EMBL; K03189; G180453; -.
DR   EMBL; K03187; G180453; JOINED.
DR   EMBL; K03188; G180453; JOINED.
DR   PIR; A01502; KTHUB.
DR   PDB; 1HCN; 30-SEP-94.
DR   PDB; 1HRP; 01-NOV-94.
DR   MIM; 118860;
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL; 3D-STRUCTURE.
FT   SIGNAL        1     20
FT   CHAIN        21    165       CHORIOGONADOTROPIN BETA CHAIN.
FT   DISULFID     29     77
FT   DISULFID     43     92
FT   DISULFID     46    130
FT   DISULFID     54    108
FT   DISULFID     58    110
FT   DISULFID    113    120
FT   CARBOHYD     33
FT   CARBOHYD     50
FT   CARBOHYD    141    141
FT   CARBOHYD    147    147
FT   CARBOHYD    152    152
FT   CARBOHYD    158    158
FT   VARIANT     137    137       D -> A (IN GENE 6).
SQ   SEQUENCE    165 AA;  17739 MW;  FF1D4802 CRC32;

Query Match             40.5%;  Score 1030;  DB 1;  Length 165;
Best Local Similarity   100.0%;  Pred. No. 1.12e-221;
Matches  139;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Db         27 PRCRPINATLAVEKEGCPVCITVNNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 86
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy        198 PRCRPINATLAVEKEGCPVCITVNNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257
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Db         87 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPP 146
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy        258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSSKAPP 317

Db        147 SLPSPSRLPGPSDTPILPQ 165
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Qy        318 SLPSPSRLPGPSDTPILPQ 336
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RESULT   3
ID   TNR1_PIG      STANDARD;      PRT;    461 AA.
AC   P50555;
DT   01-OCT-1996 (REL. 34, CREATED)
DT   01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
GN   TNFR1.
OS   SUS SCROFA (PIG).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; ARTIODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=KIDNEY;
RX   MEDLINE; 96011645.
RA   SUER B., PAULI U.H.;
RL   GENE 163:263-266(1995).
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC       RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC       AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC       PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC       SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC       PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC       HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC       PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC       WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC       PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC       TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC       ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
EMBL; U19994; G1141753; -.
PROSITE; PS00652; TNFR_NGFR_1; 3.
PROSITE; PS50050; TNFR_NGFR_2; 2.
PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS.
FT   SIGNAL        1     21
FT   CHAIN        22    461       TUMOR NECROSIS FACTOR RECEPTOR 1.
FT   DOMAIN       22    210       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    211    233       POTENTIAL.
FT   DOMAIN      234    461       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       43    195       4 X TNFR-CYS.
FT   REPEAT       43     82       TNFR-CYS 1.
FT   REPEAT       83    125       TNFR-CYS 2.
FT   REPEAT      126    166       TNFR-CYS 3.
FT   REPEAT      167    195       TNFR-CYS 4.
FT   DOMAIN      362    447       DEATH DOMAIN.
FT   DISULFID     44     58       BY SIMILARITY.
FT   DISULFID     59     72       BY SIMILARITY.
FT   DISULFID     62     81       BY SIMILARITY.
FT   DISULFID     84     99       BY SIMILARITY.
FT   DISULFID    102    117       BY SIMILARITY.
FT   DISULFID    105    125       BY SIMILARITY.
FT   DISULFID    127    143       BY SIMILARITY.
FT   DISULFID    146    158       BY SIMILARITY.
FT   DISULFID    149    166       BY SIMILARITY.
FT   DISULFID    168    179       BY SIMILARITY.
FT   DISULFID    182    190       BY SIMILARITY.
FT   DISULFID    185    194       BY SIMILARITY.
FT   CARBOHYD     54     54       POTENTIAL.
FT   CARBOHYD     86     86       POTENTIAL.
FT   CARBOHYD    145    145       POTENTIAL.
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FT CARBOHYD 151 151 POTENTIAL.
SQ SEQUENCE 461 AA; 50696 MW; 8E2C350A CRC32;

Query Match 40.5%; Score 1028; DB 1; Length 461;
Best Local Similarity 73.1%; Pred. No. 3.59e-221;
Matches 125; Conservative 24; Mismatches 21; Indels 1; Gaps 1;

Db 41 ESLCPQGKYSHPQNRSICCTRCHKGTYLHNDCLGPGLDTDCRECDNGTFTASENHLTQCL 100
       ::!!||||||| ||||||| ||||||||||:|||||||||:|::||||||||||| :|| |
Qy 23 DSVCPQGKYIHPQNNSICCTRCHKGTVLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Db 101 SCSKCRKEMSQVEISPCTVRDTVCGCRKNQYRKTWSETLFQCLNCSLCPNGTVQLPCLE 160
        |||||||||||||:||||||:|||||||:||:||||| ||||:|||:|:||||:|||| |
Qy 83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db 161 KQDTICNCHSGFFLRDKECVSCVNCKNA-DCKNLCPAISETRNDFQDTGTT 210
        | |:||||||||||| |||||||||||| :|:|||||||| | :|:||||
Qy 143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGIEDSGTT 193

RESULT 4
ID TNR1_MOUSE STANDARD; PRT; 454 AA.
AC P25118;
DT 01-MAY-1992 (REL. 22, CREATED)
DT 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
GN TNFR1 OR TNFR-1.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91246168.
RA GOODWIN R.G., ANDERSON D., JERRY R., DAVIS T., BRANNAN C.I.,
RA COPELAND N.G., JENKINS N.A., SMITH C.A.;
RL MOL. CELL. BIOL. 11:3020-3026(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91187885.
RA LEWIS M., TARTAGLIA L.A., LEE A., BENNETT G.L., RICE G.C.,
RA WONG G.H., CHEN E.Y., GOEDDEL D.V.;
RL PROC. NATL. ACAD. SCI. U.S.A. 88:2830-2834(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91285014.
RA BARRETT K., TAYLOR-FISHWICK D.A., COPE A.P., KISSONERGHIS A.M.,
RA GRAY P.W., FELDMANN M., FOXWELL B.M.J.;
RL EUR. J. IMMUNOL. 21:1649-1656(1991).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93156721.
RA ROTHE J., BLUETHMANN H., GENTZ R., LESSLAUER W., STEINMETZ M.;
RL IMMUNOGENETICS 34:338-340(1991).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE; 9203981.
RA ROTHE J., GENTZ R., LESSLAUER W.;
RL IMMUNOGENETICS 34:338-340(1991).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94245292.
RA BEBO B.F., LINTHICUM D.S.;
RL IMMUNOGENETICS 39:450-451(1994).
CC -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC   RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC   AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC   PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC   SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC   PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC   HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS

CC   PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC   WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC   PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC   TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC   ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC   NF-KAPPA B SIGNALING (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL; M60468; G199826; -.
DR EMBL; M59377; G202097; -.
DR EMBL; X59238; G53579; -.
DR EMBL; X57796; G54849; -.
DR EMBL; L26349; G430733; -.
DR EMBL; M76656; G202102; -.
DR EMBL; M88067; G202102; -.
DR EMBL; M76655; G202102; JOINED.
DR PIR; A38634; GQMS T1.
DR PIR; S16677; S16677.
DR PIR; S19021; S19021.
DR HSSP; P19438; 1TNR.
DR MGD; MGI:98781; TNFR1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00050; TNFR_NGFR_2; 3.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 454 TUMOR NECROSIS FACTOR RECEPTOR 1.
FT DOMAIN 22 212 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 213 235 POTENTIAL.
FT DOMAIN 236 454 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 43 196 4 X TNFR-CYS.
FT DISULFID 44 58 BY SIMILARITY.
FT DISULFID 59 72 BY SIMILARITY.
FT REPEAT 43 82 TNFR-CYS 1.
FT REPEAT 83 125 TNFR-CYS 2.
FT REPEAT 126 166 TNFR-CYS 3.
FT REPEAT 167 196 TNFR-CYS 4.
FT DOMAIN 356 441 DEATH DOMAIN.
FT DISULFID 62 81 BY SIMILARITY.
FT DISULFID 84 99 BY SIMILARITY.
FT DISULFID 102 117 BY SIMILARITY.
FT DISULFID 105 125 BY SIMILARITY.
FT DISULFID 127 143 BY SIMILARITY.
FT DISULFID 146 158 BY SIMILARITY.
FT DISULFID 149 166 BY SIMILARITY.
FT DISULFID 168 179 BY SIMILARITY.
FT DISULFID 182 191 BY SIMILARITY.
FT DISULFID 185 195 BY SIMILARITY.
FT CARBOHYD 54 54 POTENTIAL.
FT CARBOHYD 151 151 POTENTIAL.
FT CARBOHYD 202 202 POTENTIAL.
FT CONFLICT 394 394 R -> G (IN REF. 6).
SQ SEQUENCE 454 AA; 50129 MW; 4B6EEC09 CRC32;

Query Match 37.8%; Score 960; DB 1; Length 454;
Best Local Similarity 68.8%; Pred. No. 5.34e-204;
Matches 118; Conservative 27; Mismatches 26; Indels 1; Gaps 1;

Db 41 SCKTCRKEMSQVEISPCCOADKDTVCGCKNENQFQRYLSETHFQCVDCSPCFNGTVTIPCKE 100
        |||||||||:|||:||| | ||||:|||:||:||||| : |||||| :||:|:|| |||||
Qy 23 DSVCPQGKYIHPQNNSICCTRCHKGTVLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100

Db 101 SCKTCRKEMSQVEISPCCOADKDTVCGCKNENQFQRYLSETHFQCVDCSPCFNGTVTIPCKE 160
        |||||||||||:|||| ||||||||:|||||:||:||||:|||:|||:|:|||||:||:||
Qy 83 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Db 161 TQNTVCNCHAGFFLRSECVCGHSHCRKNEEECMKLCLPPPLANVTNPQDSGTA 212
        |||||||:||||||| ||||:|||| ||:||:|:||||| :|||| |||:||
Qy 143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQ-IENVKGIEDSGTT 193

RESULT 5
ID TNR1_RAT STANDARD; PRT; 461 AA.

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AC   P22934;
DT   01-AUG-1991 (REL. 19, CREATED)
DT   01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
GN   TNFR1 OR TNFR-1.
OS   RATTUS NORVEGICUS (RAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91090841.
RA   HIMMLER A., MAURER-FOGY I., KRONKE M., SCHEURICH P., PFIZENMAIER K.,
RA   LANTZ M., OLSSON I., HAUPTMANN R., STRATOWA C., ADOLF G.R.;
RL   DNA CELL BIOL. 9:705-715(1990).
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC       RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC       AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC       PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC       SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC       PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC       HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS SPECIFICALLY
CC       PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC       WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC       PROTEINS SUCH AS TRAF2, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC       TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC       ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
PIR; B36555; B36555.
HSSP; P19438; 1TNR.
PROSITE; PS00652; TNFR_NGFR_1; 3.
PROSITE; PS00050; TNFR_NGFR_2; 3.
PROSITE; PS00017; DEATH_DOMAIN; 1.
KW   RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS.
FT   SIGNAL          1     21       POTENTIAL.
FT   CHAIN          22    455       TUMOR NECROSIS FACTOR RECEPTOR 1.
FT   DOMAIN         22    211       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM      212    234       POTENTIAL.
FT   DOMAIN        235    461       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN         43    196       4 X TNFR-CYS.
FT   REPEAT         43     82       TNFR-CYS 1.
FT   REPEAT         83    125       TNFR-CYS 2.
FT   REPEAT        126    166       TNFR-CYS 3.
FT   REPEAT        167    196       TNFR-CYS 4.
FT   DOMAIN        363    448       DEATH DOMAIN.
FT   DISULFID       44     58       BY SIMILARITY.
FT   DISULFID       59     72       BY SIMILARITY.
FT   DISULFID       62     81       BY SIMILARITY.
FT   DISULFID       84     99       BY SIMILARITY.
FT   DISULFID      102    117       BY SIMILARITY.
FT   DISULFID      105    125       BY SIMILARITY.
FT   DISULFID      127    143       BY SIMILARITY.
FT   DISULFID      146    158       BY SIMILARITY.
FT   DISULFID      149    166       BY SIMILARITY.
FT   DISULFID      168    179       BY SIMILARITY.
FT   DISULFID      182    191       BY SIMILARITY.
FT   DISULFID      185    195       BY SIMILARITY.
FT   CARBOHYD       54     54       POTENTIAL.
FT   CARBOHYD      151    151       POTENTIAL.
FT   CARBOHYD      201    201       POTENTIAL.
SQ   SEQUENCE    461 AA;  50969 MW;  82F68B08 CRC32;

Query Match             37.2%;  Score 944;  DB 1;  Length 461;
Best Local Similarity   67.3%;  Pred. No. 5.76e-200;
Matches  115;  Conservative  25;  Mismatches 31;  Indels  0;  Gaps  0;

Db         41 DNLCPQGKYAHPKNNSICCTKCHKGTYLVSDCPSPGQETVCEVCDKGTFTASQNHVRQCL 100
              :|::|||||| || ||:|||||||||||||||||| |::||| |||||||| ::|:|||
Qy         23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82
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RESULT  6
ID   CGHB_PAPAN     STANDARD;       PRT;    165 AA.
AC   P07434;
DT   01-APR-1988 (REL. 07, CREATED)
DT   01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (CHORIONIC GONADOTROPHIN BETA
DE   SUBUNIT).
GN   CGB.
OS   PAPIO ANUBIS (OLIVE BABOON).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 87106851.
RA   CRAWFORD R.J., TREGEAR G.W., NIALL H.D.;
RL   GENE 46:161-169(1986).
CC   -!- FUNCTION: STIMULATES THE OVARIES TO SYNTHESIZE THE STEROIDS THAT
CC       ARE ESSENTIAL FOR THE MAINTENANCE OF PREGNANCY.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- TISSUE SPECIFICITY: PLACENTA.
CC   -!- THERE ARE AT LEAST FIVE COPIES OF CG-RELATED GENES AND AT LEAST
CC       TWO OF THESE ARE EXPRESSED IN THE BABOON PLACENTA.
EMBL; M14966; G176573; -.
PIR; A25808; KTBAB.
HSSP; P01233; 1HCN.
PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL          1     20       BY SIMILARITY.
FT   CHAIN          21    165       CHORIOGONADOTROPIN BETA CHAIN.
FT   DISULFID       29     77       BY SIMILARITY.
FT   DISULFID       43     92       BY SIMILARITY.
FT   DISULFID       46    130       BY SIMILARITY.
FT   DISULFID       54    108       BY SIMILARITY.
FT   DISULFID       58    110       BY SIMILARITY.
FT   DISULFID      113    120       BY SIMILARITY.
FT   CARBOHYD       33     33       BY SIMILARITY.
FT   CARBOHYD       50     50       BY SIMILARITY.
FT   CARBOHYD      141    141       BY SIMILARITY.
FT   CARBOHYD      147    147       BY SIMILARITY.
FT   CARBOHYD      152    152       BY SIMILARITY.
SQ   SEQUENCE    165 AA;  17592 MW;  78987D30 CRC32;

Query Match             33.7%;  Score 857;  DB 1;  Length 165;
Best Local Similarity   81.3%;  Pred. No. 4.26e-178;
Matches  113;  Conservative  14;  Mismatches 12;  Indels  0;  Gaps  0;

Db        101 SCKTCRKEMFQVEISPCKADMDTVCCGEKKNQFQRYLSETHFQCVDCSPCFNGTVTIPCKE 160
              || ||||||||||||||||||:|||||:||||||||||::|| ||| | ||||| ::|| |
Qy         83 SCSKCRKEMGQVEISSCTVDRDTVCGGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCCE 142

Db        161 KQNTVCNCHAGFFLSGNECTPCSHCKKNQECMKLCLPVANVTNPQDSGTA 211
              ||||||| |||||||||:|:|||||||| ||:||||:|||||| |||| |:
Qy        143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIENVKGTEDSGTT 193
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Query Match             81.3%;  Score 857;  DB 1;  Length 165;
Best Local Similarity  113;  Conservative 14;  Mismatches 12;  Indels  0;  Gaps  0;

Db         27 PLCRPINATLAAEKEACPVCTVNTTICAGYCPTMMRVLQAVLPPVPQVVCNYREVRFES 86
              | |||||||||||:|||||||||||||:|||||||||||||||||||:||||||||||||
Qy         198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMRVLQGVLPALPQVVCNYRDVRFES 257

Db          87 IRLPGCPPGVDPMVSVPVALSCRCALCRRSTSDCGGPKDHPLTCDDPNLQASSSSSKDPP 146
              |||||||||| |||||| |||||||:|:|||||||||||||||||||||||| |||| ||
Qy         258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPP 317

Db         147 SPPSPSRLLEPAGTPFLPQ 165
              | |||||| | :||:||||
Qy         318 SLPSPSRLPGSDTPILPQ 336
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RESULT 7

ID   LSHB_HUMAN     STANDARD;      PRT;   141 AA.
AC   P01229;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT   01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE   LUTROPIN BETA CHAIN PRECURSOR (LUTEINIZING HORMONE) (LSH-B) (LH-B).
GN   LHB.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 84093590.
RA   TALMADGE K., VAMVAKOPOULOS N.C., FIDDES J.C.;
RL   NATURE 307:37-40(1984).
RN   [2]
RP   SEQUENCE OF 21-141.
RX   MEDLINE; 76025547.
RA   SAIRAM M.R., LI C.H.;
RL   BIOCHIM. BIOPHYS. ACTA 412:70-81(1975).
RN   [3]
RP   PRELIMINARY SEQUENCE OF 21-141.
RX   MEDLINE; 73090987.
RA   SHOME B., PARLOW A.F.;
RL   J. CLIN. ENDOCRINOL. METAB. 36:618-621(1973).
RN   [4]
RP   PRELIMINARY PARTIAL SEQUENCE.
RX   MEDLINE; 73221227.
RA   KEUTMANN H.T., HUA Q.-X., WEISS M.A.;
RL   MOL. ENDOCRINOL. 6:904-913(1992).
RN   [5]
RP   STRUCTURE OF CARBOHYDRATE.
RX   MEDLINE; 91122088.
RA   WEISSHAAR G., HIYAMA J., RENNICK A.G.C., NIMTZ M.;
RL   EUR. J. BIOCHEM. 195:257-268(1991).
RN   [6]
RP   STRUCTURE BY NMR OF 58-77.
RX   MEDLINE; 92357029.
RA   KEUTMANN H.T., HUA Q.-X., WEISS M.A.;
RL   MOL. ENDOCRINOL. 6:904-913(1992).
RN   [7]
RP   VARIANT ARG-74.
RX   MEDLINE; 92085985.
RA   WEISS J., AXELROD L., WHITCOMB R.W., HARRIS P.E., CROWLEY W.F.,
RA   JAMESON J.L.;
RL   NEW ENGL. J. MED. 326:179-183(1992).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- TISSUE SPECIFICITY: PITUITARY.
CC   -!- DISEASE: DEFECTS IN LHB ARE A CAUSE OF HYPOGONADISM WHICH IS
CC       CHARACTERIZED BY INFERTILITY AND PSEUDOHERMAPHRODITISM.
DR   EMBL; X00264; E28368; -.
DR   EMBL; S71273; E91454; -.
DR   PIR; A01497; UTHUB.
DR   HSSP; P01233; 1HCN.
DR   MIM; 152780;
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL; PSEUDOHERMAPHRODITISM;
KW   DISEASE MUTATION.
FT   SIGNAL        1     20
FT   CHAIN        21    141       LUTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   CARBOHYD     50     50       BY SIMILARITY.
FT   VARIANT      74     74       O -> R (IN HYPOGONADISM; LACK OF
FT                                RECEPTOR-BINDING).
FT   CONFLICT     39     39       E -> Q (IN REF. 2).
FT   CONFLICT     76     76       MISSING (IN REF. 2).
FT   CONFLICT    132    135       HPQL -> PQH (IN REF. 2).
SQ   SEQUENCE   141 AA;  15345 MW;  A257F6F CRC32;

Query Match             29.1%;  Score 740;  DB 1;  Length 141;
Best Local Similarity   84.4%;  Pred. No. 7.12e-149;
  Matches   92;  Conservative   12;  Mismatches    5;  Indels    0;  Gaps    0;

Db         27 PWCHPINAILAVEKEGCPVCITVNTTICAGYCPTMMRVLQAVLPPLPQVVCTYRDVRFES 86
              : :|:|||:| |||||||||||||||||||||||| |||||:|||:||||||| ||||||||
Qy        198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMRVLQGVLPALPQVVCNYRDVRFES 257

Db         87 IRLPGCPRGVDPVVSFPVALSCRCGPCRRSTSDCGGPKDHPLTCDHPQL 135
              |||||||||||:|||:|:|||||:||:|||||:||||||||||||| ::
Qy        258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRF 306

RESULT 8

ID   CGHB_CALJA     STANDARD;      PRT;   164 AA.
AC   P51500;
DT   01-OCT-1996 (REL. 34, CREATED)
DT   01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (CHORIONIC GONADOTROPHIN BETA
DE   SUBUNIT).
GN   CGB.
OS   CALLITHRIX JACCHUS (COMMON MARMOSET).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PLACENTA;
RX   MEDLINE; 96115012.
RA   SIMULA A.P., AMATO F., FAAST R., LOPATA A., BERKA J., NORMAN R.J.;
RL   BIOL. REPROD. 53:380-389(1995).
CC   -!- FUNCTION: STIMULATES THE OVARIES TO SYNTHESIZE THE STEROIDS THAT
CC       ARE ESSENTIAL FOR THE MAINTENANCE OF PREGNANCY.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- TISSUE SPECIFICITY: PLACENTA.
DR   EMBL; U04447; G606607; -.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL        1     20       BY SIMILARITY.
FT   CHAIN        21    164       CHORIOGONADOTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   CARBOHYD     50     50       BY SIMILARITY.
FT   CARBOHYD    146    146       BY SIMILARITY.
FT   CARBOHYD    151    151       BY SIMILARITY.
SQ   SEQUENCE   164 AA;  17712 MW;  E364DB3 CRC32;

Query Match             27.9%;  Score 709;  DB 1;  Length 164;
Best Local Similarity   64.7%;  Pred. No. 3.56e-141;
  Matches   90;  Conservative   25;  Mismatches   23;  Indels    1;  Gaps    1;

Db         27 PLCRPVNAILAAEKEGCPVCVAFNTTICAGYCSSMVRVLQTILPPLPQSVCNYHELRFTS 86
              | |:|:|| || ||||||||| | |||||||| ::||||| ::|||||:||:|::|||:|
Qy        198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMRVLQGVLPALPQVVCNYRDVRFES 257

Db         87 VRLPGCPRGVDPVVSMPVALSCRCGLCRRSYSDCGSLRNEPLGCDYSTFQDSSS-KDPPR 145
              :|||||||||:|||| |||||| || |||| ::|||      :||:|:::|||| |:.|||
Qy        258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSSKRAPPP 317
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Db    146 NLTSPSQLLEPADPPLVPQ 164
          :|||:||  |:|| |:::||
Qy    318 SLPSPSRLPGPSDTPILPQ 336

RESULT   9
ID   LSHB_EQUAS              STANDARD;     PRT;   169 AA.
AC   P19794;
DT   01-FEB-1991 (REL. 17, CREATED)
DT   01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   LUTROPIN/CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (LSH-B/CG-B).
GN   LHB.
OS   EQUUS ASINUS (DONKEY).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PERISSODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   CHOPINEAU M., COMBARNOUS Y., ALLEN W.R., STEWART F.;
RL   SUBMITTED (JUL-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN   [2]
RP   PRELIMINARY SEQUENCE OF 105-169 FROM N.A.
RX   MEDLINE; 90262634.
RA   LEIGH S.E.A., STEWART F.;
RL   J. MOL. ENDOCRINOL. 4:143-150(1990).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   EMBL; X80116; G510971; -.
DR   EMBL; X53669; E27544; ALT_SEQ.
DR   PIR; S15676; S15676.
DR   HSSP; P01233; 1HCN.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL        1     20       BY SIMILARITY.
FT   CHAIN        21    169       LUTROPIN/CHORIOGONADOTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   CARBOHYD     33     33       PROBABLE.
SQ   SEQUENCE   169 AA;  17943 MW;  9D4B5421 CRC32;

Query Match             24.8%;  Score 630;  DB 1;  Length 169;
Best Local Similarity   63.4%;
Matches   85;  Conservative  21;  Mismatches  23;  Indels   5;  Gaps   4;

Db    27 PLCRPINATLAAEKEACPICITFTTSICAGYCRSMVRVNMPAALPPIPQPVCTYRELRFGS 86
          ||||||||  ||| | || |||:|||:||  :|:|| :| |||||||||  |  |||
Qy   198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Db    87 IRLPGCPPGVDPMVSFPVALSCHCGPCRLKTTDCGGPRDHPLACA-P--QTSSSCKDPPS 143
          :|||||||||||||||:||||||||||||| || ::|||| | |  |::||| |
Qy   258 IRLPGCPRGVNPVVSYAVALSCQCALCRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPS 317

Db   144 QPLTSTSTPTPGAS 157
          :| | | |:|
Qy   318 SLPSPS-RLPGPS 329

RESULT  10
ID   LSHB_BOVIN              STANDARD;     PRT;   141 AA.
AC   P04651;
DT   13-AUG-1987 (REL. 05, CREATED)
DT   01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   LUTROPIN BETA CHAIN PRECURSOR (LUTEINIZING HORMONE) (LSH-B) (LH-B).
GN   LHB.
OS   BOS TAURUS (BOVINE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; ARTIODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 85207729.
RA   VIRGIN J.B., SILVER B.J., THOMASON A.R., NILSON J.H.;
RL   J. BIOL. CHEM. 260:7072-7077(1985).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 85182575.
RA   MAURER R.A.;
RL   J. BIOL. CHEM. 260:4684-4687(1985).
RN   [3]
RP   SEQUENCE OF 21-139.
RX   MEDLINE; 74075724.
RA   MAGHUIN-ROGISTER G., HENNEN G.;
RL   EUR. J. BIOCHEM. 39:235-253(1973).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   EMBL; M10077; G163301; -.
DR   EMBL; M11506; G163299; -.
DR   PIR; A01499; UTBOB.
DR   HSSP; P01233; 1HCN.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   HORMONE; SIGNAL; GLYCOPROTEIN.
FT   SIGNAL        1     20
FT   CHAIN        21    141       LUTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   CARBOHYD     33     33
FT   CONFLICT      1      2       MISSING (IN REF. 2).
FT   CONFLICT     74     74       Q -> E (IN REF. 3).
FT   CONFLICT    112    112       P -> S (IN REF. 2).
FT   CONFLICT    122    123       GP -> PG (IN REF. 3).
FT   CONFLICT    126    126       Q -> E (IN REF. 3).
SQ   SEQUENCE   141 AA;  15202 MW;  82879D1F CRC32;

Query Match             24.2%;  Score 614;  DB 1;  Length 141;
Best Local Similarity   64.9%;
Matches   72;  Conservative  22;  Mismatches  17;  Indels   0;  Gaps   0;

Db    27 PLCQPINATLAAEKEACPVCITFTTSICAGYCPSMKRVLPVILPPMPQRVCTYHELRFAS 86
          | ::|||||| |||:|| | ||||||||||  |||:||||| || |  |:||:|||||| |
Qy   198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Db    87 VRLPGCPPGVDPMVSFPVALSCHCGPCRLSSTDCGGPRTQPLACDHPPLPD 137
          :|||||||||||||||:||||||||| |||| || :||| | |
Qy   258 IRLPGCPRGVNPVVSYAVALSCQCALCRSTTDCGGPKDHPLTCDDPRFQD 308

RESULT  11
ID   LSHB_HORSE              STANDARD;     PRT;   169 AA.
AC   P08751; P01234;
DT   01-AUG-1988 (REL. 08, CREATED)
DT   01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   LUTROPIN/CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (LSH-B/CG-B).
GN   LHB.
OS   EQUUS CABALLUS (HORSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PERISSODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
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RX   MEDLINE; 92357035.
RA   SHERMAN G.B., WOLFE M.W., FARMERIE T.A., CLAY C.M.,
RA   THREADGILL D.S., SHARP D.C., NILSON J.H.;
RL   MOL. ENDOCRINOL. 6:951-959(1992).
RN   [2]
RP   SEQUENCE OF 21-169.
RX   MEDLINE; 87250476.
RA   BOUSFIELD G.R., LIU W.-K., SUGINO H., WARD D.N.;
RL   J. BIOL. CHEM. 262:8610-8620(1987).
RN   [3]
RP   SEQUENCE OF 21-169.
RX   MEDLINE; 87250475.
RA   SUGINO H., BOUSFIELD G.R., MOORE W.T. JR., WARD D.N.;
RL   J. BIOL. CHEM. 262:8603-8609(1987).
RN   [4]
RP   CHORIOGONADOTROPIN, PARTIAL SEQUENCE.
RA   WARD D.N., MOORE W.T. JR., BURLEIGH B.D.;
RL   J. PROTEIN CHEM. 1:263-280(1982).
RN   [5]
RP   STRUCTURE OF CARBOHYDRATES.
RX   MEDLINE; 90235854.
RA   DAMM J.B.L., HARD K., KAMERLING J.P., VAN DEDEM G.W.K.,
RA   VLIEGENTHART J.F.G.;
RL   EUR. J. BIOCHEM. 189:175-183(1990).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- PTM: AT LEAST FOUR O-GLYCOSYLATION SITES ARE PRESENT.
DR   EMBL; S41704; G252741; -.
DR   PIR; A01503; KTHOB.
DR   PIR; A29304; A29304.
DR   PIR; A29305; A29305.
DR   PIR; A41917; A41917.
DR   HSSP; P01233; 1HCN.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
HORMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL        1     20
FT   CHAIN        21    169       LUTROPIN/CHORIOGONADOTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   CARBOHYD     33     33       GLYCAN SHOWING A REMARKABLY STRUCTURAL
FT                                HETEROGENEITY.
SQ   SEQUENCE    169 AA;  17865 MW;  9AB1CAA3 CRC32;
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Query Match   24.1%;   Score 613;   DB 1; Length 169;
Best Local Similarity   62.7%;   Pred. No. 1.77e-117;
Matches   84; Conservative   22; Mismatches   23; Indels   5; Gaps   4;

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Qy   318 -SLPSPS-RLPGPS 329
         :| |:| |:|
Db   144 QPLTSTSTPPGAS 157

Qy   258 IRLPGCPRGVNPVVSVAVALSCCQCALCRRSTTDCCGPKDHPLTCDDPRFQDSSSSSKRAPP 317
         |::||||:|:|| ||:|:|:|||  ||||||||:||| |||::  |||| || |:||
Db    87 IRLPGCPPGVDPMVSFPVALSCHCGPCQIKTTDCGVFRDQPLACA-P--QASSSSKDPPS 143

Qy   198 PRCRPINATLAVEKEGCPVCITVNTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257
         |:|||||||| :||||| ||| ||||||||:|||||||||||||:||||||||||
Db    27 PLCRPINATLAAEKEACPICTTFTTSICAGYCPSMVRVMPAALPALPQPVCTYRELRFAS 86
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RESULT 12
ID   LSHB_SHEEP   STANDARD;   PRT;   141 AA.
AC   P01231;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   LUTROPIN BETA CHAIN PRECURSOR (LUTEINIZING HORMONE) (LSH-B) (LH-B).
GN   LHB.
OS   OVIS ARIES (SHEEP).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; ARTIODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PITUITARY;
RX   MEDLINE; 93351742.
RA   BROWN P., MCNEILLY J.R., WALLACE R.M., MCNEILLY A.S., CLARK A.J.;
RL   MOL. CELL. ENDOCRINOL. 93:157-165(1993).
RN   [2]
RP   SEQUENCE OF 21-139.
RX   MEDLINE; 90245669.
RA   D'ANGELO-BERNARD G., MOUMNI M., JUTISZ M., COUNIS R.;
RL   NUCLEIC ACIDS RES. 18:2175-2175(1990).
RN   [3]
RP   SEQUENCE OF 21-139.
RX   MEDLINE; 72211145.
RA   LIU W.-K., NAHM H.S., SWEENEY C.M., HOLCOMB G.N., WARD D.N.;
RL   J. BIOL. CHEM. 247:4365-4381(1972).
RN   [4]
RP   SEQUENCE OF 21-139.
RX   MEDLINE; 7319035.
RA   SAIRAM M.R., SAMY T.S.A., PAPKOFF H., LI C.H.;
RL   ARCH. BIOCHEM. BIOPHYS. 153:572-586(1972).
RN   [5]
RP   STRUCTURE OF CARBOHYDRATE.
RX   MEDLINE; 91006170.
RA   WEISSHAAR G., HIYAMA J., RENWICK A.G.C.;
RL   EUR. J. BIOCHEM. 192:741-751(1990).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   EMBL; X52488; G1320; -.
DR   EMBL; S64695; G408241; -.
DR   PIR; A01500; UTSHB.
DR   HSSP; P01233; 1HCN.
DR   PIR; S09232; S09232.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   HORMONE; SIGNAL; GLYCOPROTEIN.
FT   SIGNAL        1     20
FT   CHAIN        21    141       LUTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   CARBOHYD     33     33       BY SIMILARITY.
FT   MOD_RES      21     21       BLOCKED.
FT   VARIANT     138    141       MISSING (IN SOME MOLECULES).
FT   CONFLICT     30     30       Q -> E (IN REF. 4).
FT   CONFLICT     59     59       L -> V (IN REF. 1).
FT   CONFLICT     63     63       R -> Q (IN REF. 2).
FT   CONFLICT     71     72       PM -> PPM (IN REF. 4).
FT   CONFLICT     81     81       E -> Q (IN REF. 4).
FT   CONFLICT    122    122       GP -> PG (IN REF. 3 AND 4).
FT   CONFLICT    123    123       Q -> E (IN REF. 3 AND 4).
SQ   SEQUENCE    141 AA;  15184 MW;  BA2C0204 CRC32;
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Query Match   23.7%;   Score 602;   DB 1; Length 141;
Best Local Similarity   54.0%;   Pred. No. 8.87e-115;
Matches   71; Conservative   22; Mismatches   18; Indels   0; Gaps   0;

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Qy   198 PRCRPINATLAVEKEGCPVCITVNTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257
         |:|||||||| :||||| |||| ||||||| :|:||| |:| || || |::| |||||
Db    27 PLCQPINATLAAEKEACPVCITFTTSICAGYCLSMRRVLPVILPPMPQRVCTYHELRFAS 86
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Db   87  VRLPGCPPGVDPMVSFPVALSCHGCPRLSSSTDCGGPRTOPLACDHPPLPD  137
         :|||||| |||| |:| ||||||||||||||||  |||||  ||| :  | |
Qy  258  IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQD  308

RESULT  13
ID   LSHB_PIG          STANDARD;      PRT;    141 AA.
AC   P01232;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   LUTROPIN BETA CHAIN PRECURSOR (LUTEINIZING HORMONE) (LSH-B) (LH-B).
GN   LHB.
OS   SUS SCROFA (PIG).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; ARTIODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91063934.
RA   EZASHI T., HIRAI T., KATO T., WAKABAYASHI K., KATO Y.;
RL   J. MOL. ENDOCRINOL. 5:137-146(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 89306142.
RA   KATO Y., HIRAI T.;
RL   MOL. CELL. ENDOCRINOL. 62:47-53(1989).
RN   [3]
RP   SEQUENCE OF 21-139.
RX   MEDLINE; 74075724.
RA   MAGHUIN-ROGISTER G., HENNEN G.;
RL   EUR. J. BIOCHEM. 39:235-253(1973).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   EMBL; D00579; G217694; -.
DR   PIR; A30322; UTPGB.
DR   PIR; A48170; A48170.
DR   HSSP; P01233; 1HCN.
DR   PROSITE; PS002261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   HORMONE; SIGNAL; GLYCOPROTEIN.
FT   SIGNAL        1     20
FT   CHAIN        21    141       LUTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   CARBOHYD     33     33       BY SIMILARITY.
FT   MOD_RES      21     21       BLOCKED.
FT   VARIANT      30     30       R -> Z.
FT   CONFLICT     40     40       N -> D (IN REF. 3).
FT   CONFLICT     62     62       V -> R (IN REF. 3).
FT   CONFLICT     83     83       S -> I (IN REF. 3).
FT   CONFLICT     87     87       I -> S (IN REF. 3).
FT   CONFLICT    122    123       GP -> PG (IN REF. 3).
SQ   SEQUENCE   141 AA;  14889 MW;  DA2EF539 CRC32;

Query Match    23.5%;        Score 598;  DB 1;  Length 141;
Best Local Similarity   66.4%;  Pred. No. 8.48e-114;
Matches    71;  Conservative   19;  Mismatches   17;  Indels   0;  Gaps   0;

Qy   27  PLCRPINATLAAENEACPVCIFFTSICAGYCPSMVRVLPAALPPVPQPVCTYRELSFAS   86
         | ||||||| |  ::||||:|:||||||||||||||||:||| ||| || ||  ||| |
Db  198  PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMRVLQGVLPALPQVVCNYRDVRFES  257

Db   87  IRLPGCPPGVDPTVSFPVALSCHGCPRLSSSDCGGPRAQPLACDRP  133
         || ||||  ||| |:| |||||||||||||||| |  ||| |||
Qy  258  IRLPGCPRGVNPVVSYAVALSCQCALCRSTTDCGGPKDHPLTCDDP  304
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Db   87  VRLPGCPPGVDPMVSFPVALSCHGCPRLSSSTDCGGPRTOPLACDHPPLPD  137
         :|||||| |||| |:| ||||||||||||||||  |||||  ||| :  | |
Qy  258  IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQD  308

RESULT  14
ID   LSHB_RAT          STANDARD;      PRT;    141 AA.
AC   P01230;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   LUTROPIN BETA CHAIN PRECURSOR (LUTEINIZING HORMONE) (LSH-B) (LH-B).
GN   LHB.
OS   RATTUS NORVEGICUS (RAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 85080043.
RA   JAMESON L., CHIN W.W., HOLLENBERG A.N., CHANG A.S., HABENER J.F.;
RL   J. BIOL. CHEM. 259:15474-15480(1984).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 83273673.
RA   CHIN W.W., GODINE J.E., KLEIN D.R., CHANG A.S., TAN L.K.,
RA   HABENER J.F.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 80:4649-4653(1983).
RN   [3]
RP   SEQUENCE OF 4-141 FROM N.A.
RC   STRAIN=WISTAR-IMAMICHI; TISSUE=ANTERIOR PITUITARY;
RA   KATO Y., EZASHI T., HIRAI T., KATO T.;
RL   ZOOL. SCI. 7:877-885(1990).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   EMBL; V01542; G758262; -.
DR   EMBL; J00749; G205176; -.
DR   EMBL; D00576; G220808; -.
DR   PIR; A01498; UTRTB.
DR   PIR; S42527; S42527.
DR   HSSP; P01233; 1HCN.
DR   PROSITE; PS002261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   HORMONE; SIGNAL; GLYCOPROTEIN.
FT   SIGNAL        1     20
FT   CHAIN        21    141       LUTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   CARBOHYD     33     33       PROBABLE.
SQ   SEQUENCE   141 AA;  15177 MW;  6EOC19BA CRC32;

Query Match    23.5%;        Score 597;  DB 1;  Length 141;
Best Local Similarity   64.2%;  Pred. No. 1.49e-113;
Matches    70;  Conservative   23;  Mismatches   16;  Indels   0;  Gaps   0;

Qy   27  PLCRPVNATLAAENEFCPVCITFTTSICAGYCPSMVRVLPAALPPVPQPVCTYRELRFAS   86
         | |||:|||| |  :||||| |:||||||||||||||||||||||||:||| |  || |
Db  198  PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMRVLQGVLPALPQVVCNYRDVRFES  257

Db   87  VRLPGCPPGVDPIVSFPVALSCRGCPCRLSSSDCGGPRAQPLACDRP  135
         :||||||:|:||||||||||||||:||| | ||| || |  || |:
Qy  258  IRLPGCPRGVNPVVSYAVALSCQCALCRSTTDCGGPKDHPLTCDDPRF  306

RESULT  15
ID   LSHB_BALAC        STANDARD;      PRT;    118 AA.
AC   P33088;
DT   01-OCT-1993 (REL. 27, CREATED)
DT   01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
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DE   LUTROPIN BETA CHAIN (LUTEINIZING HORMONE) (LSH-B) (LH-B).
GN   LHB.
OS   BALAENOPTERA ACUTOROSTRATA (MINKE WHALE) (LESSER RORQUAL).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; CETACEA.
RN   [1]
RP   SEQUENCE.
RA   KARASEV V.S., PANKOV Y.A.;
RL   BIOKHIMIIA 50:1972-1986(1985).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR   PIR; PN0139; PN0139.
DR   HSSP; P01233; 1HCN.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; FALSE_NEG.
KW   HORMONE; GLYCOPROTEIN.
FT   DISULFID      9     57       BY SIMILARITY.
FT   DISULFID     23     72       BY SIMILARITY.
FT   DISULFID     26    110       BY SIMILARITY.
FT   DISULFID     34     88       BY SIMILARITY.
FT   DISULFID     38     90       BY SIMILARITY.
FT   DISULFID     93    100       BY SIMILARITY.
FT   CARBOHYD     13              BY SIMILARITY.
FT   CARBOHYD     13
SQ   SEQUENCE   118 AA;  12414 MW;  DE251ECF CRC32;

Query Match             23.4%;  Score 595;  DB 1;  Length 118;
Best Local Similarity   60.6%;  Pred. No. 4.61e-113;
Matches     66;  Conservative  25;  Mismatches 17;  Indels  1;  Gaps  1;

Db         7 PLCRPINATLAAAZBZACPVCITFTTSICAGYCPSMVRVLPAALPPVPZPVCTYRZLRFAS 66
             |||||||| | ||||| |       ::::||||||| | ||:|||||:||:||:||||||||
Qy       198 PRCRPINATLAVEKEGCPVCITVNTIICAGICPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Db        67 IRLPGCPPGVBPMVSFPVALSCHCGPCRLSSSBCGPGRAZPLACBRSPR 115
             |||||||  |:||:||:||::|||||:|| | |:::|| : ||:||: ||
Qy       258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCD-DPR 305
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| |\/| || |_) |\___ \| |_) | |   | |_| |
| |  | ||  __/  ___) |  _ <| |___|  _  |   (TM)
|_|  |_||_|    |____/|_| \_\\____|_| |_|
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MPsrch_pp   protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 6 09:04:08 1998;   MasPar time 17.16 Seconds
                                  824.654 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-8
Description: (1-336) from US08804166.pep
Perfect Score: 2541
Sequence: 1 SRTSLLAFGLLCLPWLQEG..........PSLPSPSRLPGPSDTPILPQ 336

Scoring table: PAM 150
                  Gap 11

Searched: 140555 seqs, 42109429 residues

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database: sptremb15
        1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
        5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
        9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
        13:sp_unclassified

Statistics: Mean 43.140; Variance 76.550;   scale 0.564

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1024	40.3	145	2	Q13991	BETA-GONADOTROPIN.	1.18e-204
2	1024	40.3	165	2	Q14000	CHORIONIC GONADOTROPIN.	1.18e-204
3	975	38.4	471	4	Q19131	TUMOR NECROSIS FACTOR-	3.72e-193
4	945	37.2	180	4	Q95185	TUMOR NECROSIS FACTOR	3.95e-186
5	596	23.5	135	4	Q19102	LUTEINIZING HORMONE BE	2.28e-105
6	595	23.4	139	10	Q62778	TESTICULAR LUTEINIZING	2.86e-105
7	582	22.9	141	10	Q60844	LUTEINIZING HORMONE BE	3.51e-102
8	430	16.9	140	12	Q60849	LUTEINIZING HORMONE BE	4.94e-68
9	391	15.4	80	10	Q63013	TESTICULAR LUTEINIZING	1.91e-59
10	361	14.2	147	12	Q91121	GONADOTROPIN II BETA S	6.60e-53
11	353	13.9	137	12	Q90225	GONADOTROPIN BETA-SUBU	3.56e-51
12	321	12.6	130	12	Q13050	GONADOTROPIN I BETA SU	2.68e-44
13	312	12.3	130	12	Q98848	GONADOTROPIN I BETA SU	2.21e-42
14	306	12.0	138	4	P79357	GONADOTROPIN BETA CHAIN	1.14e-41
15	304	12.0	138	4	Q28376	GONADOTROPIN BETA CHAIN	1.10e-40
16	303	11.9	138	2	Q16163	THYROID-STIMULATING HO	1.79e-40
17	301	11.8	150	12	Q13051	THYROTROPIN BETA SUBUN	4.73e-40
18	294	11.6	147	12	Q13052	THYROTROPIN BETA SUBUN	1.42e-38
19	289	11.4	150	12	Q13049	THYROTROPIN BETA SUBUN	1.60e-37
20	271	10.7	101	10	Q62590	BETA-THYROTROPIN (FRAG	9.17e-34
21	250	9.8	253	2	O00276	LYMPHOCYTE ASSOCIATED	1.96e-29
22	249	9.8	277	2	O14866	SOLUBLE DEATH RECEPTOR	3.14e-29
23	250	9.8	380	2	O00280	LYMPHOCYTE ASSOCIATED	1.96e-29
24	250	9.8	418	2	O00275	LYMPHOCYTE ASSOCIATED	1.96e-29
25	249	9.8	426	2	O14865	DEATH RECEPTOR 3 BETA.	3.14e-29
26	214	8.4	348	11	Q85407	HOMOLOG OF VACCINIA VI	3.49e-22
27	214	8.4	349	11	Q99098	GARCIA-1966 RIGHT NEAR	3.49e-22
28	214	8.4	349	11	Q89118	SOMALIA-1977 RIGHT NEA	3.49e-22
29	210	8.3	87	2	Q15962	THYROTROPIN BETA SUBUN	2.15e-21
30	210	8.3	355	11	Q55308	SECRETED RECEPTOR BIND	2.15e-21
31	205	8.1	61	10	Q53012	TESTICULAR LUTEINIZING	2.07e-20
32	206	8.1	459	10	Q62327	TUMOR NECROSIS FACTOR	1.32e-20
33	187	7.4	267	4	O22764	OX40 PRECURSOR (FRAGME	6.32e-17
34	182	7.2	259	2	O14755	TRAIL RECEPTOR 3.	5.67e-16
35	180	7.1	283	2	Q92956	HERPESVIRUS ENTRY MEDI	1.36e-15
36	180	7.1	299	2	O08727	CYTOTOXIC TRAIL RECEPT	1.36e-15
37	180	7.1	401	10	O63199	CYTOTOXIC TRAIL RECEPT	1.36e-15
38	179	7.0	324	10	O00300	FAS ANTIGEN PRECURSOR.	3.24e-15
39	179	7.0	401	2	O00300	OSTEOPROTEGERIN.	2.10e-15
40	179	7.0	401	2	O15517	OSTEOPROTEGERIN.	2.10e-15
41	178	7.0	411	2	O15508	P53-REGULATED DNA DAMA	3.24e-15
42	178	7.0	411	2	O14720	DEATH RECEPTOR 5.	3.24e-15
43	179	7.0	425	2	Q16042	TUMOR NECROSIS FACTOR	2.10e-15
44	178	7.0	440	2	O14763	APOPTOSIS INDUCING REC	3.24e-15
45	178	7.0	440	2	O15531	APOPTOSIS INDUCING PRO	3.24e-15

ALIGNMENTS

RESULT 1

ID	Q13991 PRELIMINARY; PRT; 145 AA.
AC	Q13991;
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT	01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE	BETA-GONADOTROPIN.
OS	HOMO SAPIENS (HUMAN).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC	EUTHERIA; PRIMATES.
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE; 84093590.
RA	TALMADGE K., VAMVAKOPOULOS N.C., FIDDES J.C.;
RL	NATURE 307:37-40(1984).
DR	EMBL; X00266; E27486; -.
KW	SIGNAL.
SQ	SEQUENCE 145 AA; 15488 MW; AC321C60 CRC32;

Query Match   40.3%;   Score 1024;   DB 2;   Length 145;
Best Local Similarity   99.3%; Pred. No. 1.18e-204;
Matches   138;   Conservative   0;   Mismatches   1;   Indels   0;   Gaps   0;

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Db   7 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVCNYRDVRFES  66
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVCNYRDVRFES 257

Db  67 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQASSSSKAPP 126
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPP 317

Db 127 SLPSPSRLPGPSDTPILPQ 145
         |||||||||||||||||||
Qy 318 SLPSPSRLPGPSDTPILPQ 336
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RESULT 2

ID	Q14000 PRELIMINARY; PRT; 165 AA.
AC	Q14000;
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
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DE   CHORIONIC GONADOTROPIN BETA SUBUNIT.
GN   CGB.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 84008141.
RA   POLICASTRO P., OVITT C.E., HOSHINA M., FUKUOKA H., BOOTHBY M.R.,
RA   BOIME I.;
RL   J. BIOL. CHEM. 258:11492-11499(1983).
DR   EMBL; K03183; G1804444; -.
DR   EMBL; K00092; G1804444; JOINED.
DR   EMBL; K03182; G1804444; JOINED.
SQ   SEQUENCE   165 AA; MW; B1CAA0B1 CRC32;

Query Match   40.3%; Score 1024; DB 2; Length 165;
Best Local Similarity   99.3%;   Pred. No. 1.18e-204;
Matches 138; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Qy   27 PRCRPINATLAVEKEGCPVCITVNTIICAGYCPTMRVLQGVLPALPQVVCNYRDVRFES 86
         ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db 198 PRCRPINATLAVEKEGCPVCITVNTIICAGYCPTMRVLQGVLPALPQVVCNYRDVRFES 257

Qy   87 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQASSSSKAPP 146
         ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db 258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPP 317

Qy 147 SLPSPSRLPGPSDTPILPQ 165
         |||||||||||||||||||
Db 318 SLPSPSRLPGPSDTPILPQ 336

RESULT 3
ID   O19131   PRELIMINARY;   PRT;   471 AA.
AC   O19131;
DT   01-JAN-1998 (TREMBLREL. 05, CREATED)
DT   01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   TUMOUR NECROSIS FACTOR-RECEPTOR I.
GN   TNF-RI.
OS   BOS TAURUS (BOVINE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; ARTIODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=AORTA;
RA   LEE E.-K., TALYOR M.J., KEHRLI M.E.;
RL   SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U90937; G2290398; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
SQ   SEQUENCE   471 AA; 51368 MW; 1D60FF4A CRC32;

Query Match   38.4%; Score 975; DB 4; Length 471;
Best Local Similarity   67.8%;   Pred. No. 3.72e-193;
Matches 116; Conservative   27; Mismatches   27; Indels   1; Gaps   1;

Qy   41 ESPCPQGKYNHPQNSTICCTKCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCL 100
         : ||||||| ||| |||||||||||||||||||||||||| : :||||:||:||||||:||
Db   23 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 82

Qy 101 SCSRCRDEMFQVEISPCVVDRDTVCCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQE 160
         |||:||::|||||||:|:||||||| |||||||||:|||:|:|||||||||||:||:||||
Db   83 SCSKCRREMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 142

Qy 161 RQDTICHCHMGFFLKGAKCISCHDCKNK-ECERLCPTRPSTGKDSQDPGTT 210
         : ||:| |||||||::|:||:||::::|:|:|| ||| :||:|||||||||
Db 143 KONTVCTCHAGFFLRENECVSGSNCKKSLECTKLCLPQIENVKGTEDSGTT 193

RESULT 4
ID   Q95185   PRELIMINARY;   PRT;   180 AA.

AC   Q95185;
DT   01-FEB-1997 (TREMBLREL. 02, CREATED)
DT   01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   TUMOR NECROSIS FACTOR RECEPTOR P60 (FRAGMENT).
GN   TNFR-1.
OS   FELIS SILVESTRIS CATUS (CAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; CARNIVORA.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   DUTHIE S., NASIR L., ECKERSALL P.D.;
RL   SUBMITTED (OCT-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U72344; G1613880; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
FT   NON_TER   1   1
FT   NON_TER   180   180
SQ   SEQUENCE   180 AA; 20399 MW; 5452A6B2 CRC32;

Query Match   37.2%; Score 945; DB 4; Length 180;
Best Local Similarity   86.0%;   Pred. No. 3.95e-186;
Matches 117; Conservative   9; Mismatches   10; Indels   0; Gaps   0;

Qy   45 CPQGKYIHPQDNSICCTKCHKGTYLYNDCAGPGLDTDCRECENGTFFTASENHLRQCLSCS 104
         |||||||||| |||||||||||||||||||.||| |||||||||.:|.||||||||:||||||
Db   26 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCS 85

Qy 105 KCRKEMTQVEISPCTVYRDTVCGCCRKNQYRYWSETHFQCLNCSLCLNGTVQISCKETQN 164
         |||||| ||||| |||.|||||||.|||||||.||| .||:|||||||||||.:||:|.||
Db   86 KCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKON 145

Db 165 TVCTCHAGFFLRGNEC 180
         ||||||||||| |||
Qy 146 TVCTCHAGFFLRENEC 161

RESULT 5
ID   O19102   PRELIMINARY;   PRT;   135 AA.
AC   O19102;
DT   01-JAN-1998 (TREMBLREL. 05, CREATED)
DT   01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT   01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE   LUTEINIZING HORMONE BETA SUBUNIT (FRAGMENT).
OS   CERATOTHERIUM SIMUM (WHITE RHINOCEROS) (SQUARE-LIPPED RHINOCEROS).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PERISSODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PITUITARY GLAND;
RX   MEDLINE; 97449288.
RA   SHERMAN G.B., LUND L.A., BUNICK D., WINN R.J.;
RL   GENE 195:131-139(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PITUITARY GLAND;
RA   SHERMAN G.B., LUND L.A.;
RL   SUBMITTED (SEP-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U72659; G2462779; -.
FT   NON_TER   1   1
SQ   SEQUENCE   135 AA; 14212 MW; F4F196D2 CRC32;

Query Match   23.5%; Score 596; DB 4; Length 135;
Best Local Similarity   66.4%;   Pred. No. 2.28e-105;
Matches   71; Conservative   20; Mismatches   16; Indels   0; Gaps   0;

Db   21 PLCRPINATLAAENEACPVCIFTTTSICAGYCPSMRVLPAALPPPAQPVCTVHELRFAS 80
         |.||||||||| ::. ||||| .||.||||||||:||||..:||| .|||| :::||:||
Qy 198 PRCRPINATLAVEKEGCPVCITVNTICAGYCPTMRVLQGVLPALPQVVCNYRDVRFES 257

Db   81 IRLPGCPPGVDPMVSFPVALSCRCGPCRLSSSDCGGPRAQPLACCDRP 127
         |||||||.||:| ||.|||:||:|| || ||:|||||||: || ||:

Qy 258 IRLPGCPRGVNPVVSYAVALSCCQCALCRSTTDCGGPRKDHPLTCDDP 304

RESULT 6
ID 062778   PRELIMINARY;   PRT;   139 AA.
AC 062778;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE TESTICULAR LUTEINIZING HORMONE BETA-SUBUNIT.
GN TLHB1.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE DAWLEY;
RX MEDLINE; 95283549.
RA ZHANG F.P., RANNIKKO A., HUHTANIEMI I.;
RL BIOCHEM. BIOPHYS. RES. COMMUN. 210:858-865(1995).
DR EMBL; U25653; G915217; -.
SQ SEQUENCE 139 AA; 14880 MW; 5B2E7DBF CRC32;

Query Match   23.4%; Score 595; DB 10; Length 139;
Best Local Similarity 63.3%; Pred. No. 3.86e-105;
Matches   69; Conservative   24; Mismatches 16; Indels   0; Gaps   0;

Qy 198 PRCRPINATLAVEKEGCGPCVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNRDVRFES 257
       |:|:|||:||||| ||:|:|||:|| ||||||||||| || |:||||||||||||::|||||
Db 25 PLCRPVNATLAAENEFCPVCITFTTSICAGYCPSMVRILPAALPPVPQPVCTYRELRFAS 84

Db 85 VRLPGCPPGVDPIVSFPVALSCRCGPCRLSSSSDCGGPRTQPMACDLPHL 133
       :||||||||||||:|:|||||||:||||| |:||||| :|||| ::||||
Qy 258 IRLPGCPRGVNPVVSYAVALSCCQCALCRSTTDCGGPRKDHPLTCDDPRF 306

RESULT 7
ID 060844   PRELIMINARY;   PRT;   141 AA.
AC 060844;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE LUTEINIZING HORMONE BETA (LUTENIZING HORMONE BETA-SUBUNIT).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129 SVEV;
RA KAPUR V., MATZUK M.M.;
RL SUBMITTED (AUG-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR EMBL; U25145; G930345; -.
DR MGD; MGI:96782; LHB.
SQ SEQUENCE 141 AA; 15028 MW; BE50AB2B CRC32;

Query Match   22.9%; Score 582; DB 10; Length 141;
Best Local Similarity 62.4%; Pred. No. 3.51e-102;
Matches   68; Conservative   24; Mismatches 17; Indels   0; Gaps   0;

Qy 198 PRCRPINATLAVEKEGCGPCVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNRDVRFES 257
       |:|:|||:||||| ||:|:|||:|| ||||||||||| || |:||||||||||||::|| |
Db 27 PLCRPVNATLAAENEFCPVCITFTTSICAGYCPSMVRVLPAALPPVPQPVCTYRELAFAS 86

Db 87 VRLPGCPPGVDPIVSFPVALSCRCGPCRLSSSSDCGGPRTQPMACDLPHL 135
       :||||||||||||:|:|||||||:||||| |:||||| :|||| ::||||
Qy 258 IRLPGCPRGVNPVVSYAVALSCCQCALCRSTTDCGGPRKDHPLTCDDPRF 306

RESULT 8
ID Q98849   PRELIMINARY;   PRT;   140 AA.
AC Q98849;
DT 01-FEB-1997 (TREMBLREL. 02, CREATED)
DT 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
DT 01-FEB-1997 (TREMBLREL. 02, LAST ANNOTATION UPDATE)
DE GONADOTROPIN II BETA SUBUNIT PRECURSOR.
OS CARASSIUS AURATUS (GOLDFISH).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OC OSTEICHTHYES; ACTINOPTERYGII; CYPRINIFORMES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PITUITARY GLAND;
RA YOSHIURA Y., KOBAYASHI M., KATO Y., AIDA K.;
RL SUBMITTED (OCT-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR EMBL; D88024; G1644243; -.
KW SIGNAL.
FT SIGNAL   1   23   POTENTIAL.
FT CHAIN   24   140   GONADOTROPIN II BETA SUBUNIT.
SQ SEQUENCE 140 AA; 15533 MW; 7205FD03 CRC32;

Query Match   16.9%; Score 430; DB 12; Length 140;
Best Local Similarity 50.0%; Pred. No. 4.94e-68;
Matches   54; Conservative   22; Mismatches 32; Indels   0; Gaps   0;

Qy 198 PRCRPINATLAVEKEGCGPCVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNRDVRFES 257
       | | :|| |||||||| |:| | |||| | | | || :|| || | | | | |
Db 27 PPCEPVNETVAVEKEGCPKCLIVLQTTICSGHCLIKEPVYKSPFSTVYQHVCTYRDVRYET 86

Db 87 VRLPDCPPGVDPHITYPVALSCDCSLCTMDTSDCTIESLQPDFCMSQR 134
       :|||:||||||| |: |||||| | | | |::||:||| :| | ||
Qy 258 IRLPGCPRGVNPVVSYAVALSCCQCALCRSTTDCGGPRKDHPLTCDDPR 305

RESULT 9
ID 063013   PRELIMINARY;   PRT;   80 AA.
AC 063013;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE TESTICULAR LUTEINIZING HORMONE BETA SUBUNIT.
GN TLHB3.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE DAWLEY;
RX MEDLINE; 95283549.
RA ZHANG F.P., RANNIKKO A., HUHTANIEMI I.;
RL BIOCHEM. BIOPHYS. RES. COMMUN. 210:858-865(1995).
DR EMBL; U25803; G904026; -.
SQ SEQUENCE 80 AA; 8515 MW; 74FA772D CRC32;

Query Match   15.4%; Score 391; DB 10; Length 80;
Best Local Similarity 60.0%; Pred. No. 1.91e-59;
Matches   45; Conservative   18; Mismatches 11; Indels   1; Gaps   1;

Qy   1 MVRVLPAALPPVPQPVCTYRE-RFASVRLPGCPPGVDPIVSFPVALSCRCGPCRLSSSSDC 59
       | ||| :||| || || | | | |:||||||||:||||||||||:|| ||||||||:||
Db 232 MTRVLQGVLPALPQVVCNRDVRFESIRLPGCPRGVNPVVSYAVALSCCQCALCRSTTDC 291

Db 60 GGPRTQPMTCDLPHL 74
       ||||::| |:|| |:
Qy 292 GGPRKDHPLTCDDPRF 306

RESULT 10
ID Q91121   PRELIMINARY;   PRT;   147 AA.
AC Q91121;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)

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DT   01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE   GONADOTROPIN II BETA SUBUNIT PRECURSOR.
OS   MORONE SAXATILIS (STRIPED BASS).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OC   OSTEICHTHYES; ACTINOPTERYGII; PERCIFORMES;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PITUITARY GLAND;
RX   MEDLINE; 96020549.
RA   HASSIN S., ELIZUR A., ZOHAR Y.;
RL   J. MOL. ENDOCRINOL. 15:23-35(1995).
DR   EMBL; L35096; G598255; -.
KW   SIGNAL.
FT   SIGNAL        1     32
FT   CHAIN        33    147
SQ   SEQUENCE    147 AA;   16398 MW;   292F2F62 CRC32;

POTENTIAL.
GONADOTROPIN II BETA SUBUNIT.

Db            14.2%;    DB 12;          Length 147;
Qy   198 PRCRPINATLAVEKEGCPVCITIVNTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Db    36 PPCQLINQTVSLEKEGCPKCHPVETTICSGHCITKDPVIKIPFSNYQHVCTYRDLHYKT 95
         ||||||:|:::||||||||:|::||||||||  ::|  ||||  |||||||||
Qy   198 PRCRPINATLAVEKEGCPVCITIVNTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Query Match    14.4%;
Best Local Similarity   44.5%;   Pred. No. 6.60e-53;
Matches         49;   Conservative    24;   Mismatches  36;   Indels   1;   Gaps   1;
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RESULT  11
ID   Q90225                       PRELIMINARY;   PRT;   137 AA.
AC   Q90225;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE   GONADOTROPIN BETA-SUBUNIT.
OS   ACANTHOPAGRUS LATUS.
OC   EUKARYOTA; ANIMALIA; METAZOA; CHORDATA; VERTEBRATA; OSTEICHTHYES;
OC   ACTINOPTERYGII; PERCIFORMES; PERCOIDEI; SPARIDAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   TSAI H.J., YANG L.T.;
RL   SUBMITTED (JAN-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; L11722; G437308; -.
SQ   SEQUENCE    137 AA;   15330 MW;   F8757785 CRC32;

         ||||||||||||||:|:||||||||||||||| |:|:  |:| |:|||  |||:|:||:||:
Qy    96 FELPDCPPGVDPTVTFPVAQSCHCGRCAMDTSDCTFESLQPNFCMNDIPF 145

Db    28 PPCQLINQTVSLEKEGCPKCHPVETTICSGHCITKDPVMKTRY-VTQHV-CTYRDLHYKT 85
         || |:|:|:||||||||| |:||:|| ||| |||  |:| |||: ::| ||||||||||
Qy   198 PRCRPINATLAVEKEGCPVCITIVNTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Db    86 FELPDCPLGVDPTVTFPVAVSCNCGLCAMDTSDCTFESLQPNFCMNDIPF 135
         ||||||||||||||:|:||||||||:||||||||||||||||||||||||
Qy   258 IRLPGCPRGVNPVVSVAVALSCQCALCRRSTTDCGGPKDHPLTC-DDPRF 306

Query Match    13.9%;
Best Local Similarity   44.5%;   Pred. No. 3.56e-51;
Matches         49;   Conservative    22;   Mismatches  36;   Indels   3;   Gaps   3;
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RESULT  12
ID   O13050                       PRELIMINARY;   PRT;   130 AA.
AC   O13050;
DT   01-JUL-1997 (TREMBLREL. 04, CREATED)
DT   01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT   01-JUL-1997 (TREMBLREL. 04, LAST ANNOTATION UPDATE)
DE   GONADOTROPIN I BETA SUBUNIT PRECURSOR.
OS   CYPRINUS CARPIO (COMMON CARP).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OC   OSTEICHTHYES; ACTINOPTERYGII; CYPRINIFORMES.
RN   [1]
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RP   SEQUENCE FROM N.A.
RA   KOBAYASHI M., IWASAKI M., RONDO H., YOSHIURA Y., WATABE S.;
RL   SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; AB003583; D1020895; -.
KW   SIGNAL.
FT   SIGNAL        1     18
FT   CHAIN        19    130
SQ   SEQUENCE    130 AA;   14393 MW;   3D37E6B1 CRC32;

POTENTIAL.
GONADOTROPIN I BETA SUBUNIT.

Db    26 CRLTNISITVESEBCGSCITIDDTTACAGLCKTQESVTRSPL-MLSYQNTCNFREWTYETY 84
         || |  :|||||||| |:||| |:|| |||:|||  |::| :|||::||:| |:|
Qy   200 CRPINATLAVEKEGCPVCITIVNTICAGYCPTMTRVLQGVLPALP-QVVCNYRDVRFESI 258

Db    85 EFKGCPARADSVFTIPVALSCECSKCNSDITDCGALSQQTLSCN 128
         ||:|||  |  ::| |||:|:| |:| : : ||| ::||:|:
Qy   259 RLPGCPRGVNPVVSVAVALSCQCALCRRSTTDCGGPKDHPLTCD 302

Query Match    12.6%;
Best Local Similarity   41.3%;   Pred. No. 2.60e-44;
Matches         43;   Conservative    24;   Mismatches  35;   Indels   2;   Gaps   2;
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RESULT  13
ID   Q98848                       PRELIMINARY;   PRT;   130 AA.
AC   Q98848;
DT   01-FEB-1997 (TREMBLREL. 02, CREATED)
DT   01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
DT   01-FEB-1997 (TREMBLREL. 02, LAST ANNOTATION UPDATE)
DE   GONADOTROPIN I BETA SUBUNIT PRECURSOR.
OS   CARASSIUS AURATUS (GOLDFISH).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OC   OSTEICHTHYES; ACTINOPTERYGII; CYPRINIFORMES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PITUITARY GLAND;
RA   YOSHIURA Y., KOBAYASHI M., KATO Y., AIDA K.;
RL   SUBMITTED (OCT-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; D88023; G1644241; -.
KW   SIGNAL.
FT   SIGNAL        1     18
FT   CHAIN        19    130
SQ   SEQUENCE    130 AA;   14422 MW;   3C2222BFD CRC32;

POTENTIAL.
GONADOTROPIN I BETA SUBUNIT.

Db    26 CRLTNISITVESEBCGSCITIDDTTACAGLCKTQESVTRSPL-MLSYQNTCNFREWTYETY 84
         || |  :|||||||| |:||| |:||||||:|||  |::| :|||::||:| |:|
Qy   259 RLPGCPRGVNPVVSVAVALSCQCALCRRSTTDCGGPKDHPLTCD 302

Db    85 EFKGCPARADSIFTIPVALSCECSKCNSDITDCGVLSQQTLGCN 128
         ||:|||  |  ::| ||:|:| |:| : : ||:  ::||:|:
Qy   259 RLPGCPRGVNPVVSVAVALSCQCALCRRSTTDCGGPKDHPLTCD 302

Query Match    12.3%;
Best Local Similarity   40.4%;   Pred. No. 2.1e-42;
Matches         42;   Conservative    23;   Mismatches  37;   Indels   2;   Gaps   2;
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RESULT  14
ID   P79357                       PRELIMINARY;   PRT;   138 AA.
AC   P79357;
DT   01-MAY-1997 (TREMBLREL. 03, CREATED)
DT   01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT   01-MAY-1997 (TREMBLREL. 03, LAST ANNOTATION UPDATE)
DE   THYROTROPIN BETA CHAIN.
OS   LAMA GLAMA (LLAMA).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; ARTIODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PITUITARY;
RA   KANIA S.A., FRANK L.A., ODOM T.F.;
RL   SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
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DR    EMBL; U89294; G1872550; -.
SQ    SEQUENCE   138 AA;  15571 MW;  332E4E82 CRC32;

Query Match            12.0%;   Score 305;  DB 4;  Length 138;
Best Local Similarity  47.9%;   Pred. No. 4.14e-41;
Matches   46;  Conservative  18;  Mismatches  26;  Indels  6;  Gaps  4;

Db    22  CIPTEYMMHVERKECAYCLTINTTICAGYC--MTRDFNGKLFLPKFALSQDVCTYRDFMY  79
          | | :  |:  |:  :|:|:||||||||||    ||| :| | || |||| :
Qy   200  CRPINATLAVEKEGCPVCITVNTTICAGYCPPIMTRVLQG-V-LP--ALPQVVCNYRDVRF 255

Db    80  KTVEIPGGPHHVTPYFSYPVAVSCKCGKCDTDYSDC 115
          ::|||:  |  |  ||||:|| |:|  |:|
Qy   256  ESIRLPGCPRGVNPVSYAVALSCQCALCRRSTTDC 291


RESULT   15
ID    Q28376                  PRELIMINARY;     PRT;   138 AA.
AC    Q28376;
DT    01-NOV-1996 (TREMBLREL.  01, CREATED)
DT    01-NOV-1996 (TREMBLREL.  01, LAST SEQUENCE UPDATE)
DT    01-NOV-1996 (TREMBLREL.  01, LAST ANNOTATION UPDATE)
DE    THYROTROPIN BETA CHAIN.
GN    TSH-BETA.
OS    EQUUS CABALLUS (HORSE).
OC    EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC    EUTHERIA; PERISSODACTYLA.
RN    [1]
RP    SEQUENCE FROM N.A.
RC    TISSUE=PITUITARY;
RA    KANIA S.A., OLCHOWY T.W., FRANK L.A.;
RL    SUBMITTED (MAR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR    EMBL; U51789; G1262916; -.
SQ    SEQUENCE   138 AA;  15663 MW;  2DA6B024 CRC32;

Query Match            12.0%;   Score 304;  DB 4;  Length 138;
Best Local Similarity  47.9%;   Pred. No. 1.10e-40;
Matches   46;  Conservative  17;  Mismatches  27;  Indels  6;  Gaps  4;

Db    22  CIPTEYMMHVERKECAYCLTINTTICAGYC--MTRDINGKLFLPKYALSQDVCTYRDFMY  79
          | | :  |:  |:  :|:|:||||||||||    ||| : |  ||:| ||| ||| :
Qy   200  CRPINATLAVEKEGCPVCITVNTTICAGYCPPIMTRVLQG-V-LP--ALPQVVCNYRDVRF 255

Db    80  KTVEIPGCPDHVTPYFSYPVAVSCKCGKCNTDYSDC 115
          ::|||   |  | ||||:|| |:|:|  :||
Qy   256  ESIRLPGCPRGVNPVSYAVALSCQCALCRRSTTDC 291


Search completed: Wed May  6 09:05:27 1998
Job time : 79 secs.
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